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AUTHORS Hoon, M.A., Adler, E., Lindemeier, J., Battey, J.F., Ryba, N.J. and Zuker, C.S.

TITLE Putative mammalian taste receptors: a class of taste-specific GPCRs with distinct topographic selectivity

JOURNAL Cell 96 (4), 541-551 (1999)

MEDLINE 99159821

REFERENCE 2 (bases 1 to 2520)

AUTHORS Hoon, M.A., Adler, E., Lindemeier, J., Battey, J.F., Ryba, N.J.P. and Zuker, C.S.

TITLE Direct Submission

JOURNAL Submitted (10-FEB-1999) Taste and Smell Unit, NIDCR, 10 Center Drive MSC 1188, Bethesda, MD 20892-1188, USA

FEATURES Location/Qualifiers

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CDS 1..2520

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/product="putative taste receptor TR1"

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BASE COUNT 479 a 749 c 676 g 616 t

ORIGIN

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 Best Local Similarity 79.9%; Pred. No. 0;
 Matches 1866; Conservative 0; Mismatches 464; Indels 4; Gaps 2;

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 ORGANISM Homo sapiens
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 Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
 Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 270)
 MURRAY, V., SHEFFIELD, V., WEBER, J. L., DUYK, G. and BUELOW, K. H.
 TITLE Cooperative Human Linkage Center
 JOURNAL Unpublished (1995)

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REFERENCE   1 (bases 1 to 5275)  
AUTHORS    Brown,E.M., Fuller,F.H., Hebert,S.C. and Garrett,J.E. Jr.  
TITLE       Calcium receptor-active molecules  
JOURNAL     Patent: US 5688938-A 1 18-NOV-1997;  
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ACCESSION	175053
VERSION	175053.1 GI:301194
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REFERENCE	Unclassified.
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TITLE	Brown,E.M., Fuller,F.H., Hebert,S.C. and Garrett,J.E. Jr.
JOURNAL	Calcium receptor-active molecules
FEATURES	Patent: US 5688938-A 3 18-NOV-1997;
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QY	2130	gccttcttcaacagcgcagcgtcgtctagcagcgaatgtacctgtcgtgcgcgaacaatgtg	2189
Db	2830	TCCCTTATTCAGGCTTATGTCACAGACTTATGGCAGATTTGTCTGTCCGTAGAGGTATT	2889
QY	2190	gctgt	2249
Db	2890	GCATCTCTGACACGACGCTTGTGCTGTGCGGTGATCTTCTTCACAAAGTCTACATC	2949
QY	2250	atctctgtgcgcgcgaagactcctaacagcaagaaggaacttgc	2289
Db	2950	ATTCTCTTCAAGCCATCCGCAACACCATTCAGAGAGGTGC	2989

RESULT 12				
HSPCARI				
LOCUS	HSPCARI	3234 bp	DNA	PRI
DEFINITION	H. sapiens PCAR1 gene.			
ACCESSION	X81086			
VERSION	X81086.1	GI:599819		


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source
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  /db_xref="taxon:9606"
  /chromosome="3"
  /dev_stage="adult"
  /map="21.25"
1. .3234
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1. .>3234
CDS
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Best Local Similarity	47.0%;	Pred. No. 1.7e-20;		
Matches 498;	Conservative 0;	Mismatches 556;	Indels 6;	Gaps 2;

Db	1681	TGCGCTTTAGAGTGTGGAGTCTCTCTGATGGGAGATATAGATGACACATGCCAGT	1745
Qy	1410	agatgccagccctgtgtgaaagaagaggtgtcccaactgagaggaagccagacctgtctccg	1458
Db	1741	GCCGTACAAAGTGCCAGATGACTCTTGTGTCMAAGCAACCAACCTCTGCATTGCC	1800
Qy	1470	cgacatgtgttcttttggatcttggtagaacaacctctgtgtgtctgtgcagctaac	1528
Db	1801	AAGGAGATGAGATTTCTGTGCTGAGACGGAGCCCTTTGGATGCACTACCTCTTTGCC	1866
Qy	1530	acgtgtctgtctgtctgtctgtctgtggaatctgtgaccttctgtccctggacatacac	1588
Db	1861	GTGTGGGCAATTTTCTGAGACAGCCTTTGTGCTGGGTGCTTTATCAAGTTCGGCAACA	1922
Qy	1590	ctctgtgtgaggtcaagcaagggtgcgcgcctgttcttctatgtctgtgtccctgtcaaga	1648
Db	1921	CCCATTTGTCAAGGCCACCAACCGAGAGCTCTCTACTCTCTTCTTCCCTGCTGTGC	1988
Qy	1650	ggtatgtgagagcctctatgtgtctcttggtagaaccaagaagcccggtgtctgtatgc	1709
Db	1981	TGCTTCTCCAGCTCCCTGTTCTTCACTGGGAGACCCCAAGACTGACAGCTGCGCTGTGC	2040
Qy	1710	caagccctcttctgtccctgtgtttacaacatctctctgtccctgtcaagttgcacattc	1769
Db	2041	CAGCGGGCCTTTGGATCTAGACTCTGTGCTCTGATCTCATGATCTTGTAANAACAC	2100
Qy	1770	caactaatcatcatcttcaagttttccacaagaagtcatatcttacaagccttggct	1828
Db	2101	CGTGTCTCTCTGGTGTTTTGAGG---CCAAGATGCCACACAGCTTCCACGGCAAGGTGG	2157
Qy	1830	caaaacacaggtgtctgtgctgttgtgtgaagtacagctcaaggtgccagctgtattctgt	1888
Db	2158	GGGCTCAACCTGAGTTCCTCGTGGTTTCCTGTGACTTTCATGCAATTTGTCACTGT	2217
Qy	1890	ctaacctgt	1944
Db	2218	GTGATCTGCTCTACACACGCGGCCCTCTAAGCTACCGAACAGAGAGCTGGAGATGAG	2277
Qy	1950	ctgtgtatgtctgt	2009
Db	2278	ATCATCTTCAACGATGACGACGAGGAGCTCCCTCATGTGGCCCTGGGCTCTGATGGGCTAC	2337
Qy	2010	aatgtgtctctctccatcaagtgtaccttgtctgtcaagtactgtgtgtgtgtgtgtgtgt	2068
Db	2238	ACCTGCTGCTGGCTGCCATCTGCTCTTCTTGTGCTTCACTCCGGAAGCTGCCGAG	2397
Qy	2070	aactacaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	2129
Db	2398	AACCTCAATTAAGCCAAAGTTCACTACCTTTCACATGCTCATTTTTCATCTCTGGATC	2457
Qy	2130	gacctcttccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	2189
Db	2458	TCCATCTTCCACGCTATGACAGACACTTGTGGCAGTTGTGTCTGCGGTGAGAGTGATT	2517
Qy	2190	gtctgt	2249
Db	2518	GCCATCTGGCAACCAAGCTTTGGCTTGTGCTGTGATCTTCTTCAACAAAGTCTATCATC	2577
Qy	2250	atctctgtgcgcgcagacctcaacagcacaagcagcagcagcagcagcagcagcagcagcagc	2289
Db	2578	ATTCTCTTCAAGCCATCCGCAACACCACTCGAGAGGTGC	2617
RESULT 13			
HUMCASR			
LOCUS	HUMCASR	3361 bp	mRNA
DEFINITION	Human mRNA for Ca-sensing receptor, complete cds.		
ACCESSION	D50855		
VERSION	D50855.1	GI:904209	
KEYWORDS	Ca-sensing receptor.		
SOURCE	Homo sapiens kidney cDNA to mRNA.		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2000, 10:28:19 ; Search time 2238.04 seconds
(without alignments)
3935.865 Million cell updates/sec

Title: US-09-361-652-6
Perfect score: 2333
Sequence: 1 aggtctgtgacttcaatga.....ggcgcgcgcgcctccaccctga 2333

Scoring table: IDENTITY_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:*

Word size : 0

Number of hits that pass the threshold : 9077268

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- 2: em_est2:*
- 3: em_est3:*
- 4: em_est4:*
- 5: em_est5:*
- 6: em_est6:*
- 7: em_est7:*
- 8: em_est8:*
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- 10: em_est10:*
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- 13: em_est13:*
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- 100: gb_est11:*
- 101: em_est12:*
- 102: gb_est12:*
- 103: gb_est13:*
- 104: gb_est14:*
- 105: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	380	16.3	562	51	AI742401	AI742401 wg40e02.x
c 2	279	12.0	496	39	AA853967	AA853967 a15le10.s
c 3	210.4	9.0	525	45	AI390993	AI390993 mb98d01.y
c 4	196.8	8.4	421	46	AI415100	AI415100 mb98d01.x
c 5	178.2	7.6	298	48	AI562167	AI562167 vw73d10.x
c 6	131.6	5.6	247	26	W18663	W18663 mb98d01.r1
c 7	108	4.6	514	105	AO615201	AO615201 HS_5138_B

C	8	85	3.6	464	60	AA937218	AA937218	OK13f08.x
C	9	85	3.6	498	64	AM051287	AM051287	wY83g12.x
C	10	68.6	2.9	732	64	AL040113	AL040113	DKFEP343C
C	11	61	2.6	497	70	AM157397	AM157397	au95a09.x
C	12	61	2.6	498	70	AM157806	AM157806	au80f01.x
C	13	60.4	2.6	476	42	AI090099	AI090099	qb28a01.x
C	14	60.4	2.6	438	43	AI200353	AI200353	qf98a02.x
C	15	60.4	2.6	488	44	AI283030	AI283030	gm56b04.x
C	16	60.4	2.6	474	47	AI475867	AI475867	tc95b01.x
C	17	60.4	2.6	483	47	AI499186	AI499186	lc08c01.x
C	18	60.4	2.6	479	49	AI625563	AI625563	tw57e12.x
C	19	60.4	2.6	485	50	AI680129	AI680129	ty65b07.x
C	20	60.4	2.6	453	51	AI735731	AI735731	at20g01.x
C	21	60.4	2.6	468	62	AI928061	AI928061	w066f07.x
C	22	60.4	2.6	465	64	AM083236	AM083236	xc01d01.x
C	23	60.4	2.6	495	70	AM156922	AM156922	au89f04.x
C	24	60.4	2.6	510	70	AM157053	AM157053	au91c10.x
C	25	60.4	2.6	418	72	AM161036	AM161036	au78a10.y
C	26	60.4	2.6	445	72	AM161303	AM161303	au80f01.y
C	27	60.4	2.6	466	72	AM162175	AM162175	au89f04.y
C	28	60.4	2.6	502	72	AM162417	AM162417	au74d11.x
C	29	60.4	2.6	488	72	AM162603	AM162603	au78a10.x
C	30	60.4	2.6	497	72	AM162988	AM162988	au96h03.x
C	31	60.4	2.6	437	72	AM163020	AM163020	au91c10.y
C	32	60.4	2.6	428	72	AM163458	AM163458	au95a09.y
C	33	60.4	2.6	436	72	AM163636	AM163636	au96h03.y
C	34	58.8	2.5	464	62	AI913962	AI913962	wd04f06.x
C	35	58.6	2.5	440	47	AI523924	AI523924	tg98b08.x
C	36	57.8	2.5	386	50	F24619	HSPD11067	H
C	37	57.4	2.5	474	41	AI183682	AI183682	UI-M-AP0-
C	38	57	2.4	444	42	AI165888	qG78f04.x	
C	39	56.4	2.4	440	51	A1718867	at15b07.x	
C	40	56	2.4	379	45	A1365577	ao95e03.x	
C	41	56	2.4	477	62	AA984440	wm05d12.x	
C	42	55.6	2.4	448	40	AA945538	ESF201037	
C	43	55	2.4	573	49	A1657897	fc14h06.y	
C	44	55	2.4	699	64	AL118996	DKFEP761I	
C	45	54.8	2.3	458	64	AM021371	d12e12.y	

ALIGNMENTS

Query Match	Best Local Similarity	Matches	Conservative	Score	DB %	Length	Indels	Gaps
1993	gtgatgcttgatgtgcacagaaacccaacccctctggcttcataactgagccttccttaacat	16.3%	99.7%	380	51	562	1	0
552	gtgatgcttgatgtgcacagaaacccaacccctctggcttcataactgagccttccttaacat	0	0	1	0	503	0	0
2013	ggccctccctccatcaatgctgctcttggccgcgcgcacccctgggtaagagacttgcacaagaaac	16.3%	99.7%	380	51	562	1	0
502	ggccctccctccatcaatgctgctcttggccgcgcgcacccctgggtaagagacttgcacaagaaac	0	0	1	0	443	0	0
2073	tacaacagagccaatgctgtacacttcaagcctgctcttcaacttcgtgtcctgtagtcgc	16.3%	99.7%	380	51	562	1	0
442	tacaacagagccaatgctgtacacttcaagcctgctcttcaacttcgtgtcctgtagtcgc	0	0	1	0	383	0	0

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RESULT      1
LOCUS       AT1742401/c
DEFINITION  wq40e02.x1 Soares_NSF_F8_WU_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:2367578 3' similar to TR:093557 093557 PUTATIVE ODORANT
RECEPTOR ;, mRNA sequence.
ACCESSION   AT1742401
VERSION     AT1742401.1  GI:5110689
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE   1 (bases 1 to 562)
NCI-CCAP    http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     On Dec 20, 1995 this sequence version replaced gi:1130951.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LIND ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq Primer: -40UP from Gldco
High quality sequence stop: 468.
location/Qualifiers
    1..562
/organism="Homo sapiens"
/db_xref="taxon:9606"

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Db	3422	ggcgctgagcaaacctcgagagacgagctcggtggtgattcttcgcctaaagtgcgtatc	263
OY	2253	ctctgcgcgcacagacctcaacagacagagaccttcagagctccattccagactacag	2312
Db	2652	ctctgcgcgcacacagacctcaacagacagagaccttcagagctccattccagactacag	203
QY	2313	aggcgctgagcgctcctcacctga	2333
Db	202	aggcgctgagcgctcctcacctga	182
RESULT	2		
LOCUS	AA853967/c		
DEFINITION	AA853967	496 bp	mRNA
	aj51e0.0.s1 Soares_testes_NHT Homo sapiens cDNA clone IMAGE:1393866		EST
	3. similar to SW:GASR_RAT P46442 EXTRACELLULAR CALCIUM-SENSING RECEPTOR PROTEIN; mRNA sequence.		
ACCESSION	AA853967		
VERSION	AA853967.1	GI:2941505	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
	Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 496)		
	NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap .		
TITLE	National Cancer Institute, Human Genome Anatomy Project (CGAP),		
	Tumor Gene Index		

QY	1901	ggtgtgtgagcccccaactgctctgtagggatataccagcgcttcccccatctgtgatgtct	1960
Db	249	-----	249
QY	1961	tgaatgcacagaaagaccacactccctctgggcttcatactgctctctctcaaatgycctct	2020
Db	249	-----	261
QY	2021	ctccatcaatgycctcttgccttcgcagctactcctgggtaaagacttgcagagaactacaaga	2080
Db	262	cttcacatagagcacccttcttctgcagactaacctgaggaagaaacgcggaaactatmaaga	321
QY	2081	ggccaaatgtgtcaacctcaagccctgcctctcaactcgtctgtccctgatgcctcttcaac	2140
Db	322	agccaaatggtctacacctcttgcagcctctgcctctccactctgtaattcctggatgcctt	381
QY	2141	caacggcagcgtctctacgaacggcgaagtacactgccttcgcgcgaacatgatgtgctggctag	2200
Db	382	catgtccagacatttaccagaagggcagcttaccacccggggcattatgctgctggcagggcgtgc	441
QY	2201	caagccttgaacagcggctcgtgtgtgtatttcttgcttaagtgtactatgatactcttcgcg	2260
Db	442	cacactctagtgccggccttgcagcggcctattttcccttaattgctacgtgatcttctgccg	501
QY	2261	cccaagacctcaacagcacagagaaga	2284
Db	502	ttccagaactcacacacacagaaca	525

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RESULT 4
LOCUS A1415100/c
DEFINITION mb98d01.x1 Soares et al. 1998. Mus musculus cDNA clone IMAGE:337441.3 similar to SW:045814.1 (P48442) EXTRACTED FROM CALCULUM-SENSING RECEPTOR PRECURSOR ; mRNA sequence.
ACCESSION A1415100
VERSION 1
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 421)
AUTHORS Merritt, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritten, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
COMMENT The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
TITLE On Apr 21, 1998 this sequence version replaced gi:3073000.
CONTACT: Marra W/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
FEATURES
SOURCE 1..421
LOCATION/Qualifiers

```

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGGCGCCGCGCATTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldi. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

	Query Match	Similarity	8.4%	Score 196.8	DB 46	Length 421
	Best Local	Similarity	84.1%	Pred. No. 4e-18		
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					Gaps	0
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Db	421	AACCTTAAACGAAGGCCAAATGTGTCACTTCAAGCCCTGCCTCTCCACTTGTTATCCGGGATC	362			
QY	2130	gcctcttcacacagcgcagcgtctctacagcagcaatgatactgcctgcgcgcgaacatgata	2189			
Db	361	GCTTCTTCAACCATTTCCAGCATTTACCAAGGCAAGCTACCTACACCGGGTCAATGTGCTG	302			
QY	2190	gctggccttgagcagcctctgaacagcgcgcttggtggtatcttctgcctaaagtgtcaagt	2249			
Db	301	GCAGGGCGTGGCCACTCTATGATGGCGGCTTACGCGGCATTTTCTCTCCATAATGTCTACTGTG	242			
QY	2250	atccctctgcgcgccacagaccttaacacagacagagacacactccagcgcctccatccagactac	2309			
Db	241	ATTCTCTCCGCTCCAGAACTCAACACACAGAACACTTTCAGGCGCTCATCAGAGACTTAC	182			
QY	2310	acgagagcgctggcggtctccaactgta	2333			
Db	181	ACGAGGCGCTGGGCGACTTACCTGA	158			

RESULT	5
A1562167/c	
LOCUS	
DEFINITION	AI562167.1 298 bp mRNA EST 25-MAR-1999 WVJ3d0LxI Strataegene mouse heart (#937316) Nus musculus cDNA clone IMAGE:1260595 3 similar to SW:CASR_HUMAN P41180 EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR ; , mRNA sequence.
ACCESSION	AI562167
VERSION	EST. A1562167.1 GI:4513512
KEYWORDS	
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Scuriongnathi; Muridae; Murinae; Mus. 1 (bases 1 to 298)
AUTHORS	Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T., Ponderwood,K., Steptoe,M., Thelsting,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurr,R., Ritter,E., Korn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterson,R. and Wilson.R
TITLE	The WashU-NCI Mouse EST Project 1999
JOURNAL	Unpublished (1999)
COMMENT	On Mar 10, 1998 this sequence version replaced gi:2948814. Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel.: 314 286 1800 Fax: 314 286 1810

```

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:337441"
/clone_lib="Soares mouse p31MP19.5"
/dev_stage="19.5 dpc total fetus"
/lab_name="DH10B (ampicillin resistant)"
/notes="Vector: pT73D (Pharmacia) with a modified

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QY	2043	agctaccggggaagagactgctgcagagaaactacaacgaagcgcaaatgtgtcaaccttcagc	2102
Db	496	GCCTTCAAGACTCGCAAGAGCGCCCAAAACTTCAACGAGGCCAAGTTCATTGCGCTTACAC	555
QY	2103	ctgtctcttcaactcgtgtctgtgatctgcctctcttcacacgagcgcaagcgtctacgaagc	2162
Db	556	ATGTACACACCATCGATCATCTGTGGTGGCATCTTCGCCATCTTGTATGTACACTTCAGT	615
QY	2163	aagtaacctgcctgcgagcaacatgtg	2189
Db	616	GACTACCGGTACAGACCAACACATG	642
RESULT	11		
LOCUS	AM157397/c		
DEFINITION	AM157397 497 bp mRNA EST 04-NOV-1999		
	au55a09.x1 schneider fetal brain 00004 Homo sapiens CDNA clone		
	IMAGE:27831992.3 similar to gb:J02984.40S RIBOSOMAL PROTEIN S15		
	(HUMAN); mRNA sequence.		
ACCESSION	AM157397		
VERSION	AM157397.1 GI:6228798		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
	Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 497)		
	Hallier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,		
	Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Matra, M.,		
	Martin, J., Moore, B., Schellenberg, K., Stepien, M., Tan, F.,		
	Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.		
	WashU-NCI human EST Project		
	Unpublished (1997)		
TITLE	On Dec 20, 1995 this sequence version replaced gi:1135775.		
JOURNAL	Washington University School of Medicine		
COMMENT	4444 Forest Park Parkway, Box 850L, St. Louis, MO 63108		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: est@watson.wustl.edu		
	This clone is available royalty-free through LNL; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
	Seq primer: -400p from Glbo		
	High quality sequence stop: 467.		
FEATURES	Location/Qualifiers		
source	1..497		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:27831992"		
	/clone_lib="Schneider fetal brain 00004"		
	/sex="male"		
	/tissue.type="frontal lobe"		
	/dev.stage="5 months post-conception"		
	/lab_host="DH10B"		
	/note="Organ: brain; Vector: pBluescript SK (Stratagene);		
	Site_1: SctI; Site_2: XhoI; Double-stranded cDNA was		
	prepared from human fetal brain tissue. 5' and 3'		
	adaptors were used in cloning as follows: 5' adaptor		
	sequence:		
	5'-GAGAGAGAGAGAGCTCAGAGTCTTAAATTAATATATCCCCCCCCCCC-3'		
	and 3' adaptor sequence:		
	5'-GAGAGAGAGAGCTCGAGTTTGTGTGTGTGTGT-3'. The library was		
	size-selected for >0.5 kb inserts and has an average		
	insert size estimated at 1.2 kb. This library was		
	constructed using the CAP-trapper method for full-length		
	enrichment and has not undergone amplification. Library		
	was constructed by Dr. Claudio Schneider (LMCIB-Area		
	Science Park, Trieste, Italy). "		
BASE COUNT	74 a 151 c 150 g 121 t		1 others
ORIGIN			

Query Match	2.6% ; Score 61 ; DB 70 ; Length 497 ;
Best Local Similarity	47.4% ; Pred. No. 9,5e-05 ;
Matches 181 ; Conservative 0 ; Mismatches 201 ; Indels 0 ; Gaps 0 ;	
OY	366 ggcacacccatcccaatgacaagtaaccaggtgagagacaatggtgtctgtctgcagaaatt 425
Db	450 GCGGCGACTTCGGCAAGTGTACCTACCTACCGCGCGGTGAGACTCGACACGAGCTGGACATGTC 391
OY	426 cgggtggaccctggatctctctgtgttgtagagagatgagacatattggcagctcaaggtgtgca 485
Db	390 CTACGACGAGNTGATGACGCTGTACAGTGGCGGCACGCGCGGCGCTGAACCGGGGCGCT 331
OY	486 ggcactgtgagagaccaaagcgcctgtgcaaggggtgagctctgtctttcaagagatcatatgcc 545
Db	330 GCGGCGGGAAGCAGCAGCACTCCCTGCTGAAAGCGCCTCGCAGAGCCCAAGAAAGAGGGCGCCGC 271
OY	546 ctctctctgcccaaggttggcgcgtgagagatgcaatgtgcctcatctgcgcacactgtgcagagc 605
Db	270 CATGAGAAAGCCCGGAAGTGTGTAAGACGACACTCGGGGACATGATCATCTACCCGAGAT 211
OY	606 cggggccaccgttgtgtgtgttttttccagccgcgcagtttggccaaggtgtgttttcagatc 665
Db	210 GGTGGCGAGCATGGTGGGCGCTCTCAAAAGGCAACACTTCAACAGGAGGAGATCAACCC 151
OY	666 cgtgtgtgtgaccaaaccctgactggcaaggtgtgtgtgcctccagaagccctgcgcctctc 725
Db	150 CGAGATGATTCGGCCACTCTCTGGCGGAGTCTTCATCATCACTACAAAGCCCTGTAAGCATAG 91
OY	726 caggacatcatcttgggtgtgcgc 747
Db	90 CCGGCCCGCATCGGGGCCACC 69
RESULT 12	
AM157806/c	
LOCUS	
DEFINITION	AM157806 498 bp mRNA EST 04-NOV-1999
	au0f01.x1 schneider fetal brain 00004 Homo sapiens CDNA clone
	IMAGE:2782585.3, similar to gb:02984.405 RIBOSOMAL PROTEIN S15
	(HUMAN), mRNA sequence.
ACCESSION	AM157806
VERSION	AM157806.1 GI:6229207
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS	Eutheria; Primates; Catarrhini; Homidae; Homo.
	1 (bases 1 to 498)
	Hillier,L., Allen,M., Bowles,L., Dubugue,T., Gelsel,G., Jost,S.,
	Kitzman,D., Kucaba,T., Lacey,M., Le,N., Lennon,G., Marra,M.,
	Mattlin,J., Moore,B., Scheinberg,K., Steptoe,M., Tan,F.,
	Thelings,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.
	WashU-NCI human EST Project
	Unpublished (1997)
TITLE	On May 18, 1998 this sequence version replaced gi:3136531.
JOURNAL	Other ESTs: au0f01.y1
COMMENT	Contact: Wilson RK
	Washington University School of Medicine
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
	Tel: 314 286 1800
	Fax: 314 286 1810
	Email: est@wustl.edu
	This clone is available royalty-free through LNL ; contact the
	IMAGE Consortium (info@image.llnl.gov) for further information.
	Seq primer: -40UP from GIDCO
	High quality sequence stop: 343.
FEATURES	Location/Qualifiers
SOURCE	1..498
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="IMAGE:2782585"
	/clone_id="Schneider fetal brain 00004"
	/sex="male"
	/tissue_type="frontal lobe"

Oy 726 caggcaccatcactgggtgcc 747
| | | | | | | | | |
Db 96 cggcccgccgcatcgccgccacc 75

Search completed: March 18, 2000, 10:28:32
Job time: 2317 sec



GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2000, 09:49:55 : Search time 2238.04 seconds
(without alignments)
4674.789 Million cell updates/sec

Title: US-09-361-652-4

Perfect score: 2771

Sequence: 1 attcacatcagagctgtgct.....aaaaaaaaaaaaaaaaaaaaa 2771

Scoring table: IDENTITY_NUC

Searched: 4538634 seqs, 1887831982 residues

Database: EST:*

Word size: 0

Number of hits that pass the threshold: 9077268

1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
31: gb_est12:*
32: gb_est13:*
33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
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45: gb_est26:*
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48: gb_est29:*
49: gb_est30:*

50: gb_est31:*
51: gb_est32:*
52: em_est20:*
53: em_est21:*
54: em_est22:*
55: em_est23:*
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61: gb_est35:*
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65: em_est27:*
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69: gb_est39:*
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73: gb_est43:*
74: gb_est44:*
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76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_gss1:*
80: gb_gss2:*
81: gb_gss3:*
82: gb_gss4:*
83: em_gss1:*
84: em_gss2:*
85: em_gss3:*
86: em_gss4:*
87: gb_gss5:*
88: gb_gss6:*
89: gb_gss7:*
90: gb_gss8:*
91: gb_gss9:*
92: em_gss5:*
93: em_gss6:*
94: em_gss7:*
95: em_gss8:*
96: em_gss9:*
97: em_gss10:*
98: em_gss11:*
99: gb_gss10:*
100: gb_gss11:*
101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	333.6	12.0	421	46	A1415100	A1415100 mb98d01.x
C 2	301.4	10.9	525	45	A1390993	A1390993 mb98d01.y
C 3	294.8	10.6	562	51	A1742401	A1742401 wg40e02.x
C 4	229.2	8.3	298	48	A1562167	A1562167 vw73d10.x
C 5	212.8	7.7	496	39	AA853967	AA853967 aj51e10.s
6	175.6	6.3	247	26	W18663	W18663 mb98d01.r1
7	140.6	5.1	260	71	AV278654	AV278654 AV278654

SOURCE	house mouse
ORGANISM	Mus musculus
REFERENCE	Eukariyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 525)
AUTHORS	Marrin,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theisinger,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk, Walter,E., Korn,S., Shih,T., Jackson,Y., Cardenas,M., McCann, Mattern,R. and Wilson,R. The Mashu-NCI Mouse EST Project 1999 Unpublished (1999) On Jan 17, 1998 this sequence version replaced gi:2044280.
TITLE	
JOURNAL	
COMMENT	

Email: mousestew@watson.wustl.edu
This clone is available royalty-free through LNCI; contact the IMAG Consortium (infoimage.jhmi.gov) for further information.
This read is a RESOURCE of a previously sequenced mouse clone.
This read has been verified (found to hit its original self in the correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 481.

FEATURES
source

Location/Qualifiers
1. .525

```

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:337441"
/clone_lib="Soares mouse p3NM19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/notes="Vector: pT73b (pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGGAGCGCGCATTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fátima Bonaldo. RNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."
```

Query Match	10.98;	Score 301.4;	DB 45;	Length 525;
Best Local Similarity	75.58;	Pred. No. 2e-61;		
Matches 443;	Conservative 0;	Mismatches 31;	Indels 113;	Gaps 1

QY	1944	tgatgtgtgtgaagcccccttctctctcgggtttgacatcttctctccgcctatga	2003
Db	52	ttctctgtgggtcagcccccttctctctcgggtttgacatcttctctccgcctatga	111
QY	2004	atccgcctctctccaactggtatcattcattcttaagtcttctcacaagggtgcacattcac	2063
Db	112	atccgcctctctccaactggtatcattcattcttaagtcttctcacaagggtgcacattcac	171
QY	2064	cgtaacctcggggcccaaaacacatggttcaggtctcttcgtatgtcagctcccaaggtccat	2122
Db	172	cacacgtttgggcccacaaacacatggttcaggtctcttcgtatgtcagctcccaaggtccat	231
QY	2124	ttggtatcctcgtctccatcattgcttgaatgtagtaccaccacagaccacacaggaataaccag	2183
Db	232	ttggtatcctcgtctccatcattgcttgaatgtagtaccaccacagaccacacaggaataaccag	248
QY	2184	cgctctcccccattcgtgattcttcgcagtgtagcagaggtacaactcgttagcttctctgtg	2243
Db	248	cgctctcccccattcgtgattcttcgcagtgtagcagaggtacaactcgttagcttctctgtg	248

Accession	Sequence	Position
Oy	gcttcaaccccaaacatctccctccctccatcaagtaacttgcctcagatgaactgggttag	2303
Oy	2244	
Db	-----CACAAATCCCTCCTCTCCATCAGACACTTTGTGTGAGCTACTGGGTAAAG	298
Db	248	
Oy	gaactgcacagaagaactaataagaagcaaaagtacccctcagactggtcccaattc	2353
Oy	2304	
Db	GAATGGCGGAGAACTTAACGAAGCAATAGTGTACCTTCAGGCTGTGCTCCATTC	358
Db	299	
Oy	gtaccctggatgcctcttccaccatcagcagcatttaccagggaagctactcgtgcg	2423
Oy	2364	
Db	GTATCTCGATGGTTTCTTCCACCATGTCACGATTTACCAAGGACGCTACTACCCCG	418
Db	359	
Oy	gtcaatgtctggcaagctcctccacacacacacagcggcggtcctcagcgtatctctccc	2483
Oy	2424	
Db	GTCATATGCTGGGAGGCGTGGCCACTGTGAAGGGCGGCTTCAGGGGCTATTTCTCCT	478
Db	419	
Oy	aagcgcatatgatctctctcgcgtccagaactcaaaaataacagaca	2530
Oy	2484	
Db	AAATGCTTAAGGATCTCTCTCCGTCGAGAACTTAATAACAGCAACA	525
Db	479	

RESULT	3	562 bp	EST	21-JUN-1999
LOCUS	A1742401/c			
DEFINITION		mRNA		
	A1742401			
	W9406002.x1 Soaree.NF.F8.9M.OT.PA.P.S1 Homo sapiens cDNA clone			
	IMAGE:267578.3	similar to TR:093557	093557	PUTATIVE ODORANT RECEPTOR ;, mRNA sequence.

ACCESSION	AI742401
VERSION	AI742401.1
KEYWORDS	GI:5110689
SOURCE	EST.
ORGANISM	human. Homo sapiens

REFERENCE
1 (bases 1 to 562)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 562)

JOURNAL
COMMENT
On Dec 20, 1995 this sequence version replaced gi:1130951.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the IMAG Consortium (info@lmage.llnl.gov) for further information.
Seq primer: -400P from G1bco
High quality sequence stop: 468

FEATURES
source

Location/Qualifiers
1. .562

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1="IMAGE:2367578"
/clone_1_id="Soares_NSF"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneids: Soares NBHSF pool 1:
1409384-310919, 333208-325895 Soares NB2HP pool 1:
1405032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152337 Soares NB2HR8-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-322823, 326280-325663 Soares NBHOT
pool 1: 723720-726407, 735080-740999 Subtraction: by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT
116 a 161 c 167 g 117 t 1 others
ORIGIN

```


Query Match 10.6%; Score 294.8; DB 51; Length 562;
 Best Local Similarity 72.4%; Pred. No. 7.8e-60;
 Matches 409; Conservative 0; Mismatches 153; Indels 3; Gaps 2;

QY 2199 gtgattcctcaggtgacagaggaactcgttaagctcctgtgtgtgttccaccacaac 2258
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 562 GTGATGCTTGAAGTGCACGAGACCAACTCCNTGGCTTCATACAGGCTTCCTACAAAT 503
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 2259 attccctccatcaggaactctgtcgcagcctcctggttaaggaactccagagaac 2318
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 502 GGCTCCCTCCATCAGGCTTGGCTTGGCTGACGCTACCTGGGTAAGGAGCTTGCCAGAGAAC 443
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 2319 tataatgaagcacaatgtgtacacttcagcctcctcctcaactcgtatcctggtatcgc 2378
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 442 TACAACGAGGCCAATGTCACCTTCAGCTGCTCTTCAACTGCTGCTCTGATGCC 383
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 2379 ttcttccatcagcgaacttaccaggggaagcactcctcctggtcaatgtgtgtgca 2438
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 382 TTCTTCAACAGGCGCAGCTTACGAGCGCAAGTACCTGCTGGGCGCAACATGATGGCT 323
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 2439 gggctgacacacactgagcgggagcttcagcgttactctccccaagtctgtatgatt 2498
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 322 GGGCTGAGCAGCCCTGACAGCGGCTTGGTGGTATTCTGCTAAGTCTACGTGATC 263
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 2499 cctgtccgtccagaactcaacatacagaacacttccagcctccatccagagactaacg 2558
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 262 CTGCGCGCCGACACCTCAACAGCAGACGACTTCACGCGCTCCATTCAGGACTACAGC 203
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 2559 agggcgctggcgactactatccactcgtgaaggtgacagcgggaaggaagcctctctc 2618
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 202 AGGCGCTGGCGCTTCACCTTACACAGTGGTGCACAG--GCACGCGTGGCGCTTCTGTC 145
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 2619 ttgtgtcgaaggtggtggtcaggtggtggtggtggtggtggtggtggtggtggtg 2678
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 144 CCTGAGAGGTGGAAGTGCAGAGCGCGGGGTGTCCGGAGGCTCTTGGG-CATGCCG 86
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 2679 ggcacgttcctgattgtataagcagcgggaagaaactcagtgcaataagaacgggaagtg 2738
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 85 TCTGGGGTGTGGAGGTGTAAGCGCTGGGAGAGCTTACAGAGCTCCGGGCTGCCAATA 26
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 2739 aaaaaaaaaaaaaaaaaaaaaa 2763
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 25 AAGAAAAAATCGTAAAAAAA 1
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
 A1562167 298 bp mRNA EST 25-MAR-1999
 LOCUS vw73d10.x1 Stratagene mouse heart (#937316) Mus musculus cDNA clone
 DEFINITION IMAGE:1260595 3' similar to SW:CA5R_HUMAN P41180 EXTRACELLULAR
 CALCIUM-SENSING RECEPTOR PRECURSOR ; mRNA sequence.
 A1562167
 ACCESSION A1562167.1 GI:4513512
 VERSION A1562167
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 298)
 Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
 Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R.,
 Ritter, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R.,
 Waterston, R. and Wilson, R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 On Mar 10, 1998 this sequence version replaced gi:2948814.
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@wustl.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:663147
 This clone was previously sequenced on the 5' end only, this new
 data is from the 3' end
 Possible reversed clone: similarity on wrong strand
 Possible reversed clone: polyA not found
 High quality sequence stop: 286.
 Location/Qualifiers
 1..298
 /organism="Mus musculus"
 /strain="NIH/Swiss"
 /db_xref="taxon:10090"
 /clone="IMAGE:1260595"
 /clone_id="Stratagene mouse heart (#937316)"
 /sex="pooled"
 /tissue_type="heart"
 /dev_stage="13 day embryos"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: heart; Vector: pBluescript SK-; Site 1:
 EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts.
 Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
 adaptor sequence: 5' GAATTCGGCAGCAG 3'-3' adaptor
 sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'."

BASE COUNT 59 a 101 c 87 g 51 t
 ORIGIN

Query Match 8.3%; Score 229.2; DB 48; Length 298;
 Best Local Similarity 85.6%; Pred. No. 2.3e-44;
 Matches 255; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 546 cccctgtacagctatgagcgaagcagcgtgtactacagtcgcaagcgaagtcctccctc 605
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 298 CCACAGGTACAGCTATGAGGAGCAGCAGCGTGTCTCTAGTGGGAAGCCCAAGTTCCTGTC 239
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 606 ttccctgtacgctcccaagtgacagcagcagcagcagcagcagcagcagcagcagcagc 665
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 238 TTCTTGGCAGCAGCTCCACAGGATMACTACAGTGTGAGTGTGCTGCTGCTGAG 179
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 666 agtttggt 725
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 178 AGCTTGGGCTGGT 119
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 726 gtgcagcgcgtgtgagagagcgtgcgcgtgtgcgcgcgcgcgcgcgcgcgcgcgcgc 785
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 118 GTACAGGCGGTGAGAGAGTGTGCGCACGCGGAGCATGTGCTTCGCTTCAAGAGCGTG 59
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 786 gtgccttctcctgc 843
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 58 GTGCTCTCTCCGCCAGGCGGCGGTGACCCAGAGATCAGAGCATGTGCTGCTGCG 1

RESULT 5
 AA853967 496 bp mRNA EST 31-DEC-1998
 LOCUS a51e10.s1 Soares testis_NBT Homo sapiens cDNA clone IMAGE:1393866
 DEFINITION 3 similar to SW:CA5R_RAT P48442 EXTRACELLULAR CALCIUM-SENSING
 RECEPTOR PRECURSOR ; mRNA sequence.
 AA853967
 ACCESSION AA853967.1 GI:2941505
 VERSION AA853967
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 496)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

On Jan 14, 1998 this sequence version replaced g1:1797381.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.lnl.gov/bdrip/image/image.html

FEATURES

Location/Qualifiers
 1. 496
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:1393866"
 /sex="male"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from Clontech
 Laboratories, Inc., and primed with a Not I - oligo(dT)
 primer [5'
 TGTACCAATCTGAAGTGGAGCGGCCCAATTTTTTTTTTTT 3']
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization to Cot5, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 102 a 145 c 148 g 100 t 1 others
 ORIGIN

Query Match

Best Local Similarity 7.7%; Score 212.8; DB 39; Length 496;
 Matches 331; Conservative 0; Mismatches 123; Indels 5; Gaps 4;

2262 ctctctccatcagtaacctgctgctgagctgagctgtaagaaactgcagaaactat 2321
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 493 CTCCTTCCATCAGTGCCTTCCCTGCAGTACCTGGTAGACTTGCAGAACTAC 434
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2322 aatgaagcacaatgtgtaacctgaacctgctcctcaacttgatctgagtccttc 2381
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 433 AACGAGCCCAATGTGTACCTTCAGCCTGCTTCAAAATCGTCTGGATCGCCTTC 374
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2382 ttaacatgacagcagatcttccagagcagcagcagcagcagcagcagcagcagc 2441
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 373 TTCAACAGGCGCAGGTCTTACGAGGCAAGTA-ANCCITGGGCCCAACATGATGTC- 316
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2442 ctgaccacactgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2501
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 315 CTGAGCAGCCTGAGCAGCGGCTTGGTGGATTTTCTGCTAAGTGTCTACGTATCTTC 256
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2502 tggcgtccagaactcaacaaacacacttcaagcagcagcagcagcagcagcagcagc 2561
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 255 TGGCGCCCAACCTCAACAGCAGACACACTTCCAGGCTTCATTCAGACTACAGAGG 196
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2562 cgcgcggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2621
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 195 GCGTGGCGCTCCACTCAGTGGTGCAGAGGCAAC--GCTGGCAGCCTTCTCTGCC 138
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2622 tgcgtgaagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2681
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 137 TGAAGGTGGAAGTGCAGAGCGCGGGGGGTGTCCGGGAGAGTCTTTGGG-CATCCGGGTCT 79
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2682 cagctacgataagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2720
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 78 GGGGTGGAGCTGTAGCCCTGGAGAGCCTAGACCA 40

RESULT 6

LOCUS W18663 247 bp mRNA EST 10-SEP-1996
 DEFINITION MB98401.r1 Soares mouse p3NMF19.5 Mus musculus CDNA clone
 IMAGE:337441 5', mRNA sequence.
 W18663
 ACCESSION W18663.1 GI:1294371
 VERSION EST.
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 247)
 Maira,N., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Scheilenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

THE WASHU-HMT MOUSE EST PROJECT
 Unpublished (1996)
 On May 9, 1995 this sequence version replaced g1:802427.
 CONTACT: Maira M/Mouse EST Project
 WASHU-HMT Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@wustl.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:218841
 Seq primer: mob.REGA+ET
 High quality sequence stop: 225.

FEATURES

source

Location/Qualifiers
 1. 247
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone_lib="IMAGE:337441"
 /clone_lib="Soares mouse p3NMF19.5"
 /dev_host="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Vector: pT73D (Pharmacia) with a modified
 polylinker; Site_1: Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGGAGCGGCCCAATTTTTTTTTTTT 3']
 Double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M. Fatima Bonaldo. RNA was kindly provided by
 Dr. Minoru Ko (Wayne State University)."

BASE COUNT

44 a 89 c 42 g 72 t

Query Match

Best Local Similarity 6.3%; Score 175.6; DB 26; Length 247;
 Matches 184; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

1944 tgccttgctgctcagccctctctctctggttgcacatctctctctgcccagaa 2003
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 46 TTCTTGTGGTGCAGCGCCCTTTTCTCTGCGGTTTGGCCATTTCTCTCTCTGACA 105
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2004 atcgcgcctctcaacatgcgcacatcttcaagttctcaccaagtgccacacattac 2063
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 106 ATCCGCTCTTCCACTGCTGATCATCTTCAAGTTTCTTACCAAGGTACCCACATTTTAC 155
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2064 cgtacctggcccaaaacatggtgagctctatctgcatctgagctcacaagctcat 2123
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

DB	166	CACACTTGGGCCCCAAACCATGTGGCCGGAATTTGTCATTGTGACGCCACGCTCAT	225
OY	2124	ttgtcatctgtctcaca	2141
Db	226	TTGTTCTCTGTCTCACA	243
RESULT	7		
AV278654			
LOCUS			
DEFINITION	AV278654	260 bp mRNA	EST 05-NOV-1999
ACCESSION	AV278654	RIKEN full-length enriched, adult male testis (DH10B) mus-	
VERSION	AV278654	musculus cDNA clone 4933403B08.3, mRNA sequence.	
KEYWORDS	AV278654.1	GI:6266691	
SOURCE		EST.	
ORGANISM		house mouse.	
		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
AUTHORS		Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
		1 (bases 1 to 260)	
		Konno,H., Alzawa,K., Akahire,S., Akiyama,J., Carninci,P., Endo,T.,	
		Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.	
		Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I.,	
		Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,	
		Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,	
		Owa,C., Ozawa,T., Saito,H., Sano,M., Sato,K., Shibata,K.,	
		Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y.,	
		Suzuki,H., Suzuki,H., Takahashi,F., Tateo,M., Tomihata,N.,	
		Tanoda,Y., Watabiki,A., Watanabe,S., Yamamura,T., Yasunishi,A.,	
		Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.	
TITLE		RIKEN Mouse ESTs (Konno,H., et al.)	
COMMENT		Unpublished (1999)	
		On Mar 10, 1998 this sequence version replaced gi:2948605.	

```

FEATURES
SOURCE

location/Qualifiers
1..260

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4933403B08"
/clone_lib="RIKEN full-length enriched, adult male testis
(DH10B)"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: Sali; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken

```

Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCGTCCTTTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGAGATCTCGAGTTAATTAATGATCCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pluescript KS(+) after bulk excision from Lambda
FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

	Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
	5.1%;	Score 140.6;	DB 71;	Length 260;			
	74.5%;	Pred. 2.6-23;					
			0;	59;	7;	1;	
QY	2475	ttccctcccgaagtgctatgtaattctctgcgcgtccagaactccaacatacagaacacttt	2534				
Db	5	ttcttttccatattccatagtgatttaaaccttctctgattttttatcatattacagttt	64				
QY	2535	cagccctccatccagagactacacagagcgctgcgcgcactacactatccatcgaaagtg	2594				
Db	65	cagcgttccattccagagattacacagggccgacatgacattacttatccgcctggggctatt	124				
QY	2595	cagacggsaaggaagcctctcttcttctgtcgaagtggtgcggtccagtggtgcccagag	2654				
Db	125	gagatgggcgaagc-----agatgggcgtgaagtgctgcggcgatctggggcgggaag	177				
QY	2655	cttaagtggtctgggaagcctccgcgcacaggttaacatgtaaaagcacgcggaagatcc	2714				
Db	178	cttgagcgtgcttgggagagatcacccacacggcttgcgatgcttaagcacacgaaggaatcc	237				
QY	2715	agtcacataaagacgggaa	2733				
Db	238	agtcgaataaagacctgaa	256				

LOCUS AA937218 464 bp MWNA EST 09-JUN-1998
DEFINITION ok13f08.91 Soares NSF.F8.9G PA.P.S1 Homo sapiens cDNA clone
IMAGE:15072719.3 similar to SW:CCSR.HUMAN P41180 EXTRACELLULAR
CALCIUM-SENSING RECEPTOR PRECURSOR ;, mRNA sequence.
ACCESSION AA937218
VERSION AA937218.1 GI:3095329
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 464)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jan 19, 1998 this sequence version replaced gi:2150441.
CONTACT: Robert Strausberg, Ph.D.
TEL: (301) 496-1550
EMAIL: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 1252 Std Error: 0.00
Seq Primer: -40ml3 fwd. ER from AmerSham
High quality sequence stop: 398.
location/Qualifiers
1..464
/organism="Homo sapiens"
/db_xref="taxon:9606"


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/clone="IMAGE:1507719"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P1"
/lab_host="DH10B"
/notes="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site.1: Not I; Site.2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneids: Soares NBHSP pool 1:
309384-310919, 323208-325895, Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151175-152327 Soares NB2H8-9W pool 1:
758280-760583, 772104-774407 Soares NBHBP pool 1:
304775-306511, 320136-322823, 326280-32653 Soares NBHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Ronaldo."

```

```

FEATURES
    source

High quality sequence stp: 440.
    Location/Qualifiers
        ..498
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="IMAGE:2555206"
        /clone_id="Soares_NSF_F8_9W_OT_PA_P_S1"
        /lab_host="DH10B"
        /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
        a modified polylinker; Site_1: Not I; Site_2: Eco R1;
        Equal amounts of plasmid DNA from five normalized
        libraries were mixed, and ss circles were made in vitro.
        Following HAP purification, this DNA was used as tracer in
        a subtractive hybridization reaction. The driver was
        PCR amplified cDNAs from pools of 5,000 clones made from
        the same 5 libraries. The pools consisted of the following
        libraries and cloneIDs: Soares NBHSF pool 1:
        309584-310919, 333208-325895 Soares NB2HP pool 1:
        145032-147335, 147720-148103, 148872-149255, 15002 -
        15007, 151176-152327 Soares NB2HH8-9W pool 1:
        758880-760583, 772104-774407 Soares NB4PA pool 1:
        304776-306331, 320136-322823, 32680-326653 Soares NB2OR
        pool 1: 723720-726407, 739080-740999 Subtraction by Bento
        Soares and M. Fatima Donaldo."
122 a 119 c 135 g 121 t 1 others
BASE COUNT
ORIGIN

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RESULT	9				
AM051287/c					
LOCUS	AM051287	498 bp	mRNA	EST	20-SEP-1999
DEFINITION	W539g12.1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone				
IMAGE	2:551206 3' similar to SW:CA8_HUMAN P41180 EXTRACELLULAR				
ACCESSION	CALCIUM-SENSING RECEPTOR PRECURSOR ; mRNA sequence.				
VERSION	AM051287				
KEYWORDS	AM051287.1	GI:5813557			
SOURCE	EST.				
ORGANISM	human.				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
	Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
REFERENCE	1 (bases 1 to 498)				
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP)				
	Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	On Dec 20, 1995 this sequence version replaced gi:1134450.				
	Contact: Robert Strausberg, Ph.D.				
	Tel: (301) 496-1550				
	Email: Robert.Strausberg@nih.gov				
	This clone is available royalty-free through LNL ; contact the				
	IMAGE Consortium (Info@image.llnl.gov) for further information.				
	Seq primer: -40UP from Gibco				

Qy	755	gcgtgccttcaaggacatcgt	787
Db	41	GCATTCGACTTCAGTCGAACTCAT	20
RESULT	10		
LOCUS	A0615201/c		
DEFINITION	A0615201	514 bp	DNA
ACCESSION	HS_5158_B2.C04_Sp6E PRC1-11		GSS
VERSION	A0615201		15-JUN-1999
KEYWORDS	A0615201.1	GI:5076477	Human Male BAC Library Homo sapiens genomic clone Plate=714 Col=8 Row=F, genomic survey sequence.
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Mammalia; Eutheria; Primates: Catarrhini; Hominoidea; Homo.		
AUTHORS	1 (bases 1 to 514) Meharitas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.		
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome		
JOURNAL	Proc. Natl. Acad. Sci. U. S. A.	96 (17)	9739-9744 (1999)
MEDLINE	99380589		

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 442)
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT Unpublished (1997)
On May 18, 1998 this sequence version replaced gi:3138688.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Oligo-dt track not found. Not 1 site shown in beginning of sequence is likely internal to the message. CDNA library preparation: M.B. Soares lab clone distribution: NCI-CGAP clone distribution
Information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.llni.gov/dbfp/image/image.html
Seq primer: M13 forward
POLYA=No.

FEATURES

source

1..442 Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2710331"
/clone_lib="NCI-CGAP_Sub1"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-pac (Pharmacia) with a modified polylinker. Site_1: Not 1; Site_2: Eco RI; The NCI-CGAP_Sub1 library is a subtracted library derived from B1. B1 constitutes a mixture of 21 normalized or subtracted NCI-CGAP libraries: NCI-CGAP_C04, NCI-CGAP_P22, NCI-CGAP_P28, NCI-CGAP_C01, NCI-CGAP_C016, NCI-CGAP_Kid5, NCI-CGAP_C012, NCI-CGAP_Kid3, NCI-CGAP_Kid11, NCI-CGAP_LYn2, NCI-CGAP_Br2, NCI-CGAP_C08, NCI-CGAP_C1L1, NCI-CGAP_Le12, NCI-CGAP_Brn23, NCI-CGAP_Lu5, NCI-CGAP_Lu24, NCI-CGAP_Lu19, NCI-CGAP_GC4, NCI-CGAP_G6, NCI-CGAP_Brn25.
These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below: NCI-CGAP_Kid3 pool 1 L1AM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clonesids 132376-132391, 1456008-145675, 15028855)
NCI-CGAP_Kid5 pool 1 L1AM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonesids 1323912-132531, 1471368-1472903, 1492104-1493255)
NCI-CGAP_Lu5 pool 1 L1AM 3575-3582, 3581-3854 (IMAGE Clonesids 1414920-1417991, 1520904-1522439)
NCI-CGAP_GC4 pool 1 L1AM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonesids 1257096-1258631, 1459064-1470983, 1475592-1476743)
NCI-CGAP_P22 pool 1 L1AM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonesids 985608-986759, 1101192-1101959, 1217928-1220515)
NCI-CGAP_C010 pool 1 L1AM 2644-2653, 2871-2872 (IMAGE Clonesids 1057416-1051255, 1144584-1145351)
The resulting subtracted library contained 530,000 recombinants.
Subtraction was performed as previously described [Bonaldi, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.
TAG_LIB="NCI-CGAP_Le12"
TAG_TISSUE="leiomyosarcoma"
TAG_SEQ="AATCG"

BASE COUNT

118 a 97 c 127 g 100 t

Query Match 2.1%; Score 58.6; DB 63; Length 442;
Best Local Similarity 47.0%; Pred. No. 0.001;

Matches 181; Conservative 0; Mismatches 204; Indels 0; Gaps 0;

534 ccttcctgtagccctgctgagcgtatgagcagcgctggtactcagtgccaagcgc 593

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 11 CTTTCAACATACCTCAGATTGCTTACTCAGCAACCATCATGATCTGATGACACACT 70
Qy 594 aagtcctccgtcttcctctgctacccgtcccaagtgaccgagccagcggtgaggtatggtg 653
Db 71 CTGTTCAAAATATTTCAAGAGGTTTGCTTCAGATGCTCAGCAGGAGAGGTCATGTG 130
Qy 654 cagctgctgcagagatttgggtggtggtatcctgcctatctggcactacgtggtatc 713
Db 131 GACATAGTGAAGAGGTCAACTGACCTATGATACCCGTACACAGAGCAACTAT 190
Qy 714 gggcagctgggtgtgcagcgctggaagagctgcccgtgcccgaggacatcgtcgc 773
Db 191 GGACAAAGTGGATGAGGAGGCTTCAAGATATGTCAGCGAAGAGGATTTGCATGCC 250
Qy 774 ttcaagacatcggtccttctcgtcccggtgtgtatcccgagatgcagagcatatg 833
Db 251 CACTCTTCAAAATCTACACTAAATGCGAGGAGAGGAGCTTTGATAGCTGCTGAAGAG 310
Qy 834 cagcatctgctcagcgacagccacccgtgtgtgtgctctcctaacgagccactgct 893
Db 311 CTCACAGTCACTTGTCCCAAGGCCCGGCTGTGCTTCTTCTGTGAGGCAATGACGCTG 370
Qy 894 agagtgcttcaggtcgtgtgtgc 918
Db 371 AGAGTCTGCTGATGCCCATGAGGC 395

RESULT 13

Al657897

LOCUS

Al657897

DEFINITION

fc14h06.y1 zebrafish Washu MPING EST Danio rerio cDNA 5' similar to

Ca²⁺/CaSR, RAT P48442 EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR

; mRNA sequence.

ACCESSION

Al657897

VERSION

Al657897.1 GI:4755565

KEYWORDS

EST.

SOURCE

zebrafish.

ORGANISM

Danio rerio

REFERENCE

1 (bases 1 to 573)

AUTHORS

Clark, S., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Bddy, S., Hillier, L., Kueba, T., Martin, J., Beck, C., Wyllie, T.,

TITLE

underwood, K., Steptoe, M., Treising, B., Allen, M., Bowers, Y.,

JOURNAL

Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R.,

COMMENT

Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

OTHER

Waterson, R. and Wilson, R.

WASHTU

Washu zebrafish EST Project 1998

UNPUBLISHED

On Jun 5, 1998 this sequence version replaced gi:3189643.

OTHER

ESTs: fc14h06.x1

CONTACT

Other: Stephen L. Johnson

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4444

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314 286 1800

FAX

314 286 1810

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zdr@fish.wustl.edu

CDNA

Library Preparation: Matthew Clark. CDNA library Arrayed by:

MATTHEW

Clark. DNA Sequencing by: Washington University Genome

SEQUENCING

Center Clone distribution: Genome Systems, St. Louis,

MISSOURI

(web address: www.genomesystems.com) (email contact:

INFOGENOMESYSTEMS

.com) and Research Genetics, Huntsville, Alabama

WEB

addresses: www.resgen.com (email contact: info@resgen.com) and

RESSOURCECENTRUM

PrimateRatBank, Berlin, Germany (web address:

WWW

.resgen.de)

SEQ

primer: T3 RT from Amersham

HIGH

quality sequence stop: 460.

LOCATION

Qualifiers

1..573

/organism

"Danio rerio"

/db_xref

"taxon:7955"

/clone_lib

"zebrafish Washu MPING EST"


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/sex="mixed"
/tissue.type="26 somite embryos, adult livers, shield
stage embryos"
/lab_host="XLI-blue MRF"
/node="vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st
strand cDNA was primed with a Not I - oligo(dT)15 primer
[5'gacacagatcctcagatccgcagccgcgcctttttttttttt3'];
double-stranded cDNA was ligated to Sal I adaptors (BRL)
digested with Not I and cloned into the Not I and Sal I
sites of the pSPORT1 vector (BRL). Library was constructed
by Matthew Clark (Lehrnach Lab, ICRF, London and Max Planck
Institut fuer Molekulare Genetik, Berlin). cDNAs for EST
hybridization fingerprinting of arrayed clones from
zebrafish late somitogenesis (26 ss), adult liver or
embryonic shield stage (5-6 h) libraries. Fingerprint
data were used to computationally cluster cDNAs, and a
single cDNA from each cluster was chosen for sequencing.
In some cases multiple members of the same cluster were
sequenced to assess clustering parameters or single clones
were sequenced additional times to assess quality
control."

```

	Query Match	2.0%	Score 55.2%	DB 49	Length 573
	Best Local Similarity	53.2%	Pred. No. 0.0075		
	Matches	117	Conservative	0	Mismatches 103
					Indels 0
					Gaps 0
QY	496	acacgacacacagcgtctcactaccgctgcctcgtcgttgccttcctatgagccctgaca	555		
DB	225	ACTCGAGCTATCCATCCGCTATCGGCAAGCTCCTACGCTTCATCCGTCCTCAGGCA	284		
QY	556	gctatgagcgcaagcagcagcgtggtacacagtcagtcacgaagcgcaagctccgttcctcgtta	615		
DB	285	GCAGCTCCTCCTCTTCTCCGGTTCGTGAGTGATGAACCTGGCGCTACCCGTCCTCATAGCGTG	344		
QY	616	ccgtccccaagtcacccgcaaccagctgtgagatcatgtgtgcagctgtcgaagatttgggt	675		
DB	345	TGATCCCAAGTATGTGTACCGAGCTCAGGCGCCTGGTCAAGCTCATGTCTATTTCTCCT	404		
QY	676	gggtgtgagctcgcgtcaatgagcagctaaagtgatataagg	715		
DB	405	GGAACTGGGTGGTGTCTGTATACGGAGATGATGATCATATGG	444		

RESULT	14
LOCUS	FR0044372
DEFINITION	Fr0044372 615 bp DNA GSS 22-OCT-1999 Fugu rubripes GSS sequence, clone 184F17A8, genomic survey sequence.
ACCESSION	ALJ31864
VERSION	ALJ31864.1 GI:6113810
KEYWORDS	GSS; genome survey sequence.
SOURCE	Fugu rubripes.
ORGANISM	Fugu rubripes. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
REFERENCE	1 (bases 1 to 615) Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K., Umanita,Y., Williams,G. and Brenner,S.
AUTHORS	Direct Submission
TITLE	Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB. UK Email:
COMMENT	biohelp@hmp.mrc.ac.uk vector: plusescript II KS V type: phagemid PRIMER: KS DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.

[illegible]

RESULT	15
LOCUS	FR0013504
DEFINITION	FR0013504 285 bp DNA GSS 18-SEP-1997
ACCESSION	F.rubripes GSS sequence, clone 124A16a11, genomic survey sequence.
VERSION	AL0004753
KEYWORDS	AL0004753.1 GI:2450323
SOURCE	GSS: genome survey sequence.
ORGANISM	Fugu rubripes.
	Fugu rubripes
	Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;
	Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
	Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
REFERENCE	1 (bases 1 to 285)
AUTHORS	Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umranta,Y., Williams,G. and Brenner,S.
TITLE	Direct Submission
JOURNAL	Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource
COMMENT	Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@mp.mrc.ac.uk
	V_type: phagemid
	PRIMER: KS
	DESCR:
	One pass dye-terminator sequencing of cosmid cloned genomic
	sequence.

FEATURES		Location/Qualifiers
source	1..285	/organism="Fugu rubripes" /db_xref="taxon:31033" /clone_11p="cosmid:124A16" /clone_124A16a11"
BASE COUNT	82 a 70 c 53 g 71 t	9 others
ORIGIN		
Query Match	1.9%	Score 53; DB 79; Length 285;
Best Local Similarity	50.7%	Pred. No. 0.018;
Matches 116; Conservative	0; Mismatches 113; Indels	0; Gaps 0;
OY	2305	aactgcagagaactataatgaagccaatgtygtacccttaagcgtgctctcaactcg 2364
Db	21	AAATGCCAGACNACCTCAACGAGNCACACAAATCNCCTTAGCATATTTNTGTG 80
OY	2365	tatcctgatgcgtctcttcgaccagcgcaagcattaccagcgagcgtacctgctgcg 2424
Db	81	CAGTGTGGGTGCCCTTTCTCCAGCTTTATATACGCTCTCCACGGAAATACCTCCACGCTCA 140

Oy	2425	tcaatgctgcgcgacagagcttaccacaacactgagcgcgcgcttcaagcggttaacttccccc	2484
Db	141	CGGAATCTTTGCCACTCTAGACCTCCAGTACCGATGCTGGGCTGTGCATATGACCCA	200
Oy	2485	agctctctgcatctctctgcgcgcgcgaactctcaacatctagaacactt	2533
Db	201	AGTCTATATATTTCTATGATANTCTGAAAGACCAAGGAAACACTT	249

Search completed: March 18, 2000, 10:28:08
Job time: 2293 sec

WISKEY (TM)

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MSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Mar 17 13:05:22 2000; Maspar time 113.50 Seconds
Tabular output not generated. 513.137 Million cell updates/sec

Title: >US-09-361-652-1
Description: (1-840) from US09361652.pep
Perfect Score: 6338
Sequence: 1 MLFWAHLISLQLYCWAFL.....NTEHFQASIDYTRCGCT 840

Scoring table: PAM 150
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: splemb112
1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
9:sp.phage 10:sp.plant 11:sp.rodent 12:sp.unclassified
13:sp.vertebrate 14:sp.virus

Statistics: Mean 52.670; Variance 98.786; scale 0.533

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	6338	100.0	840 11	Q920R8	POTATIVE TASTE RECEPTO	0.00e+00
2	2083	32.9	843 11	Q920R7	POTATIVE TASTE RECEPTO	0.00e+00
3	1455	23.0	868 13	Q73636	PEROMONE RECEPTOR.	3.64e-282
4	1422	22.4	848 13	Q93553	POTATIVE ODORANT RECEPTOR	8.57e-275
5	1385	21.9	864 13	Q73637	PEROMONE RECEPTOR.	1.55e-266
6	1371	21.6	940 13	Q73635	CALCIUM2+ SENSING RECEPTOR	2.06e-263
7	1339	21.1	880 13	Q93552	PEROMONE RECEPTOR.	2.79e-256
8	1295	20.4	844 13	Q93551	POTATIVE ODORANT RECEPTOR	1.74e-245
9	1218	19.2	856 13	Q73638	PEROMONE RECEPTOR.	2.25e-229
10	1192	18.8	875 13	Q73640	PEROMONE RECEPTOR.	1.31e-223
11	1170	18.5	912 11	Q70410	POTATIVE PHEROMONE RECEPTOR	9.87e-219
12	1073	16.9	835 11	Q70409	POTATIVE PHEROMONE RECEPTOR	2.75e-197
13	972	15.3	779 11	Q93269	POTATIVE PHEROMONE RECEPTOR	4.63e-175
14	878	13.9	458 13	Q93555	POTATIVE ODORANT RECEPTOR	1.73e-154
15	844	13.3	850 11	Q93189	POTATIVE PHEROMONE RECEPTOR	4.44e-147
16	830	13.1	983 11	Q92915	METABOTROPIC GLUTAMATE RECEPTOR	4.93e-144
17	827	13.0	408 13	Q93558	POTATIVE ODORANT RECEPTOR	2.21e-143
18	808	12.7	866 11	Q93268	POTATIVE PHEROMONE RECEPTOR	2.97e-139
19	799	12.6	908 4	Q95945	METABOTROPIC GLUTAMATE RECEPTOR	2.56e-137
20	795	12.5	803 11	Q95191	POTATIVE PHEROMONE RECEPTOR	1.96e-136

21	755	11.9	667 11	Q95267	POTATIVE PHEROMONE RECEPTOR	8.88e-128
22	746	11.8	429 11	Q70413	POTATIVE PHEROMONE RECEPTOR	7.80e-126
23	718	11.3	350 13	Q93556	POTATIVE ODORANT RECEPTOR	8.45e-120
24	707	11.2	548 11	Q93265	POTATIVE PHEROMONE RECEPTOR	1.96e-117
25	694	10.9	604 11	Q93195	POTATIVE PHEROMONE RECEPTOR	1.22e-114
26	687	10.8	852 11	Q93192	POTATIVE PHEROMONE RECEPTOR	3.87e-113
27	681	10.7	768 11	Q93266	POTATIVE PHEROMONE RECEPTOR	7.48e-112
28	672	10.6	604 11	Q93194	POTATIVE PHEROMONE RECEPTOR	6.34e-110
29	652	10.6	695 11	Q93272	POTATIVE PHEROMONE RECEPTOR	6.34e-110
30	652	10.3	723 11	Q93193	POTATIVE PHEROMONE RECEPTOR	1.20e-105
31	625	9.9	339 11	Q70411	POTATIVE PHEROMONE RECEPTOR	6.84e-100
32	566	8.9	808 11	Q93190	POTATIVE PHEROMONE RECEPTOR	2.16e-87
33	567	8.9	1267 5	Q93564	F55...4 PROTEIN.	1.33e-87
34	533	8.4	250 13	Q73647	CALCIUM SENSING RECEPTOR	1.87e-80
35	518	8.2	311 11	Q93633	CALCIUM SENSING RECEPTOR	2.57e-77
36	514	8.1	251 13	Q73652	PEROMONE RECEPTOR	1.76e-76
37	515	8.1	301 11	Q93634	CALCIUM SENSING RECEPTOR	1.09e-76
38	508	8.0	251 13	Q73655	PEROMONE RECEPTOR	3.15e-75
39	504	7.9	250 13	Q73645	PEROMONE RECEPTOR	2.15e-74
40	499	7.9	250 13	Q73643	PEROMONE RECEPTOR	2.36e-73
41	495	7.8	251 13	Q73653	PEROMONE RECEPTOR	1.60e-72
42	492	7.8	251 13	Q73656	PEROMONE RECEPTOR	6.73e-72
43	488	7.7	250 13	Q73649	PEROMONE RECEPTOR	4.56e-71
44	488	7.7	250 13	Q73646	PEROMONE RECEPTOR	4.56e-71
45	482	7.6	250 13	Q73651	PEROMONE RECEPTOR	8.00e-70

ALIGNMENTS

RESULT ID	Q920R8	PRELIMINARY	PRT	840 AA
AC	Q920R8			
DT	01-MAY-1999 (T-EMBLrel. 10, Created)			
DT	01-MAY-1999 (T-EMBLrel. 10, Last sequence update)			
DE	POTATIVE TASTE RECEPTOR TR1 (FRAGMENT).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-MISTAR:			
RX	MEDLINE: 99159821.			
RA	HOON M.A., ADLER E., LINDEMEIER J., BATTLEY J.F., RYBA N.J.P., ZUKER C.S.,			
RT	"Putative mammalian taste receptors: a class of taste-specific GPCRs with distinct topographic selectivity."			
RL	Cell 96:541-551(1999).			
DR	EMBL: AF127389; AAD18069.1; -			
KW	Receptor.			
FT	NON_TER	840	840	
SQ	SEQUENCE	840 AA;	93496 MM;	B1FF564 CRC32;
Query Match				
Best Local Similarity 100.0%; Pred. No. 0.00e+00;				
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Db	1	MLFWAHLISLQLYCWAFLSCPTSSPGFLP35FLAGLSLGGDCIQVHRPLVTS	60	
Qy	1	MLFWAHLISLQLYCWAFLSCPTSSPGFLP35FLAGLSLGGDCIQVHRPLVTS	60	
Db	61	CDPDSFNGHYLFLPAMRTVEINSSALPNTILGVLVYCGESAAVATIRVAL	120	
Qy	61	CDPDSFNGHYLFLPAMRTVEINSSALPNTILGVLVYCGESAAVATIRVAL	120	
Db	121	QGPRIHIEIQDLRNNHSSKVAFLGPNTD3AVTTAALGFLPLVSYEASSVLSAKR	180	
Qy	121	QGPRIHIEIQDLRNNHSSKVAFLGPNTD3AVTTAALGFLPLVSYEASSVLSAKR	180	
Db	181	FPFELRIVPSDRHQVEYVQVLOSFGWVSLIGSGIDGLOVQALDELAVRGICVAF	240	
Qy	181	FPFELRIVPSDRHQVEYVQVLOSFGWVSLIGSGIDGLOVQALDELAVRGICVAF	240	


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Db 241 KDIVPSARVGPDRMSMOHQAARTVYVVSNRHLARVFRSVLANITGKVMASE 300
Oy 241 KDIVPSARVGPDRMSMOHQAARTVYVVSNRHLARVFRSVLANITGKVMASE 300
Db 301 DVAISITISVYIGIGIVLCAVVOORVPGLKEFESYRAVYAPASACPESSKSTN 360
Oy 301 DVAISITISVYIGIGIVLCAVVOORVPGLKEFESYRAVYAPASACPESSKSTN 360
Db 361 QLCRECHTFTTRNMPITLGFASMSAARYEAVYANABHLHLLGCTSEICSGVPVPMOL 420
Oy 361 QLCRECHTFTTRNMPITLGFASMSAARYEAVYANABHLHLLGCTSEICSGVPVPMOL 420
Db 421 LQOIKVFLHENTVAADDNDGDIYDIIAMDNGPEWTFEIIIGSASISPHLDINKT 480
Oy 421 LQOIKVFLHENTVAADDNDGDIYDIIAMDNGPEWTFEIIIGSASISPHLDINKT 480
Db 481 KIQWGNKNOVPVSVCTTDCLAGHRRVYVSGHCCFECVCEAGTFLNMSLHICQPCGT 540
Oy 481 KIQWGNKNOVPVSVCTTDCLAGHRRVYVSGHCCFECVCEAGTFLNMSLHICQPCGT 540
Db 541 EEMAPKSTCTCFPTVEFLAMHEPISLVLIANTLLLLVGTAGLFAMHFTPVVRSAG 600
Oy 541 EEMAPKSTCTCFPTVEFLAMHEPISLVLIANTLLLLVGTAGLFAMHFTPVVRSAG 600
Db 601 GRCLFMLGSLVAGSCSFYFSGFPYPAQLLQPLFSLGFAIFLSCLTIRSFQVLIIFK 660
Oy 601 GRCLFMLGSLVAGSCSFYFSGFPYPAQLLQPLFSLGFAIFLSCLTIRSFQVLIIFK 660
Db 661 FSTRKVPFTYTAQONHAGLFTVIVSVTHLLICLTWLVMTPTPTREXORPHVILICT 720
Oy 661 FSTRKVPFTYTAQONHAGLFTVIVSVTHLLICLTWLVMTPTPTREXORPHVILICT 720
Db 721 EVNSVGFLLAFTHNLLISTFVCSYLKELPENNEAKCVTFSLILNFVSMIAFTMAS 780
Oy 721 EVNSVGFLLAFTHNLLISTFVCSYLKELPENNEAKCVTFSLILNFVSMIAFTMAS 780
Db 781 IYOGSLPRAVNVLATLITLISGFSGYFLPKCVIILCRELNNTEHFOASIDYTRRCGTT 840
Oy 781 IYOGSLPRAVNVLATLITLISGFSGYFLPKCVIILCRELNNTEHFOASIDYTRRCGTT 840

```

```

RESULT 2
ID 0920R7 PRELIMINARY: PRT: 843 AA.
AC 0920R7:
DT 01-MAY-1999 (TREMUREL. 10, Created)
DT 01-MAY-1999 (TREMUREL. 10, Last sequence update)
DT 01-MAY-1999 (TREMUREL. 10, Last annotation update)
DE PUTATIVE TASTE RECEPTOR TR2 (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
RN
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR;
RX MEDLINE: 99159821.
RA HOON M.A., ADLER E., LINDEMEIER J., BATTERY J.F., RYBA N.J.P.,
RT ZUKER C.S.;
RT "Putative mammalian taste receptors: a class of taste-specific GPCRs
RT with distinct topographic selectivity.";
RL Cell 96:541-551(1999).
DR EMBL: AF127390; AAD18070.1; -.
KW Receptor.
FT NON_TER
SQ SEQUENCE 843 AA: 95799 MW: 680AEEDE CRC32;

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Query Match 32.9%; Score 2083; DB 11; Length 843;

Best Local Similarity 39.6%; Pred. No. 0.00e+00;

Matches 326; Conservative 188; Mismatches 286; Indels 24; Gaps 22;

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Db 27 NSDFHLAGDYLGGFTLTHANVKSISHSLYQPKCNF-TMKYLGYNLQAMRFAVEEI 85
Oy 27 NSDFHLAGDYLGGFTLTHANVKSISHSLYQPKCNF-TMKYLGYNLQAMRFAVEEI 85

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Db 86 NNCSSILPGLVLYGEMVYCYLSNNIHPLGYFLA-QDDDLLPILKDYQYPRVAVIGP 144
Oy 86 NNCSSILPGLVLYGEMVYCYLSNNIHPLGYFLA-QDDDLLPILKDYQYPRVAVIGP 144
Db 145 DNESEATVNSNLHFLIPQITTSASIDKDRKHFFSMRTVPSATHTHEAMVQMLVHF 204
Oy 145 DNESEATVNSNLHFLIPQITTSASIDKDRKHFFSMRTVPSATHTHEAMVQMLVHF 204
Db 146 DMTDAVNTTALIGFLLPLVSVYASSVLSAKRKFPSFLRTVSDRHQYEVVQLQST 205
Oy 146 DMTDAVNTTALIGFLLPLVSVYASSVLSAKRKFPSFLRTVSDRHQYEVVQLQST 205
Db 205 QMNNIVLVSDDYGRENSHLISQRTFTSDICIAFQEVPIPESSQVMSSEQRLDNI 264
Oy 205 QMNNIVLVSDDYGRENSHLISQRTFTSDICIAFQEVPIPESSQVMSSEQRLDNI 264
Db 266 GWMVWISLIGSYGDYQGLQYQALAE-LAVPRGICVAFADIVP--SARV--GD--PR--MQSM 258
Oy 266 GWMVWISLIGSYGDYQGLQYQALAE-LAVPRGICVAFADIVP--SARV--GD--PR--MQSM 258
Db 265 LDKLRRTSARVYVES--PELSYFHEHVRMNTGEVWJASMSAIDPVILHLETRT 323
Oy 265 LDKLRRTSARVYVES--PELSYFHEHVRMNTGEVWJASMSAIDPVILHLETRT 323
Db 259 MOHLAQARTVYVVSNRHLAR-VFERSVLANITGKVMASEDMAISYITISVYIGIGI 317
Oy 259 MOHLAQARTVYVVSNRHLAR-VFERSVLANITGKVMASEDMAISYITISVYIGIGI 317
Db 324 GTFLGVTIORVSLPGFQFVRDRDKGYPVPTN-TN-LTTTCNODDACLN-TTYSFNNI 380
Oy 324 GTFLGVTIORVSLPGFQFVRDRDKGYPVPTN-TN-LTTTCNODDACLN-TTYSFNNI 380
Db 318 GTVGVAVOORVPGLKEFESYRAVYAPASACPESSKSTNQLCRECHTFTTRNMPITL 377
Oy 318 GTVGVAVOORVPGLKEFESYRAVYAPASACPESSKSTNQLCRECHTFTTRNMPITL 377
Db 381 LILGERVYVSYSAVYAAHAIHRLGCRNVRCTKQKVPQMLREIWHVFTLGNRL 440
Oy 381 LILGERVYVSYSAVYAAHAIHRLGCRNVRCTKQKVPQMLREIWHVFTLGNRL 440
Db 378 GAPS-MSAATRYEAVYAAHAIHRLGCRNVRCTKQKVPQMLREIWHVFTLGNRL 436
Oy 378 GAPS-MSAATRYEAVYAAHAIHRLGCRNVRCTKQKVPQMLREIWHVFTLGNRL 436
Db 441 FPDQGDMPMLDIIQWMDLSQNPQSIASYSPTSKRL-TYINNVSYTPNNTVPSMC 499
Oy 441 FPDQGDMPMLDIIQWMDLSQNPQSIASYSPTSKRL-TYINNVSYTPNNTVPSMC 499
Db 437 AFDDNDGDLGYDIIAMDNGPEWTFEIIIGSASISPHLDINKTKIQWGNKNOVPVSV 496
Oy 437 AFDDNDGDLGYDIIAMDNGPEWTFEIIIGSASISPHLDINKTKIQWGNKNOVPVSV 496
Db 500 SKSCOPGOMKKSGLHPCFCEBLCMDPGTYINRSADENFCLSCPSMSYKNDITCQOR 559
Oy 500 SKSCOPGOMKKSGLHPCFCEBLCMDPGTYINRSADENFCLSCPSMSYKNDITCQOR 559
Db 497 TTIDCLAGHRRVYVSGHCCFECVCEAGTFLNMSLHICQPCGT EEMAPKSTCTCFPT 555
Oy 497 TTIDCLAGHRRVYVSGHCCFECVCEAGTFLNMSLHICQPCGT EEMAPKSTCTCFPT 555
Db 560 PFLENEHVPITVAAILAAGFSTALITF-MRHOTPVARSAGMCFMLVPLLA 618
Oy 560 PFLENEHVPITVAAILAAGFSTALITF-MRHOTPVARSAGMCFMLVPLLA 618
Db 556 VERFLAMHEPISLVLIANTLLLLVGTAGLFAMHFTPVVRSAGRLCFMLGSLVAG 614
Oy 556 VERFLAMHEPISLVLIANTLLLLVGTAGLFAMHFTPVVRSAGRLCFMLGSLVAG 614
Db 619 FGAVPVYGPPTVEFCFROAFFTVCSISLCTITVRSFOIVCFKARLRPSAYPMR 678
Oy 619 FGAVPVYGPPTVEFCFROAFFTVCSISLCTITVRSFOIVCFKARLRPSAYPMR 678
Db 615 SCSTFSGFGEPTVPACLLRQPLFSLGFAIFLSCLTIRSFQVLIIFKSTVPTFTYTAQ 674
Oy 615 SCSTFSGFGEPTVPACLLRQPLFSLGFAIFLSCLTIRSFQVLIIFKSTVPTFTYTAQ 674
Db 679 YHGPVFAFTIAIKVALVGNMGLATINIPGRDPPDPMILSCHPNRNLGNTSM 738
Oy 679 YHGPVFAFTIAIKVALVGNMGLATINIPGRDPPDPMILSCHPNRNLGNTSM 738
Db 675 NHGAGLFVYSSVTHLLICLTWLVMTPTPTREXORPHVILICTEVNSVGFLLAFTH 733
Oy 675 NHGAGLFVYSSVTHLLICLTWLVMTPTPTREXORPHVILICTEVNSVGFLLAFTH 733
Db 739 DLLSYGFSRANKGELPYNNEAKCVTFSLILNFVSMIAFTMASIYOGSLPRAVNVL 798
Oy 739 DLLSYGFSRANKGELPYNNEAKCVTFSLILNFVSMIAFTMASIYOGSLPRAVNVL 798
Db 734 NILLSITFVCSYLKELPENNEAKCVTFSLILNFVSMIAFTMASIYOGSLPRAVNVL 793
Oy 734 NILLSITFVCSYLKELPENNEAKCVTFSLILNFVSMIAFTMASIYOGSLPRAVNVL 793
Db 799 VTIVNLAIGL-GYFGPKCYMILFEYPERNTSAFNSMIGCYTR 841
Oy 799 VTIVNLAIGL-GYFGPKCYMILFEYPERNTSAFNSMIGCYTR 841
Db 794 AG-LTTLISGFSGYFLPKCVIILCRELNNTEHFOASIDYTRR 836
Oy 794 AG-LTTLISGFSGYFLPKCVIILCRELNNTEHFOASIDYTRR 836

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RESULT 3
ID 073636 PRELIMINARY: PRT: 868 AA.
AC 073636:
DT 01-AUG-1998 (TREMUREL. 07, Created)
DT 01-AUG-1998 (TREMUREL. 07, Last sequence update)
DT 01-NOV-1999 (TREMUREL. 12, Last annotation update)
DE PHEROMONE RECEPTOR.
OS CA02.1.
OC Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Perciformes;
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
RN
RP SEQUENCE FROM N.A.
RX MEDLINE: 98226788.
RA NAITO T., SAITO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,
RA NAKANISHI S., BRENNER S.;
RT "Putative pheromone receptors related to the Ca2+-sensing receptor in
RT Fugu.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).

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Db 749 VIGYIGLALICFEFLAFLARLPDNEFAKTFESMLI-FCAYWIAFIPAYVSSPGKFTV 807
 QY 730 AFTHNILLISTFVCSYKRELPENYKACVTFSLINFTVS-WIAFTMASTYQSGYLP 788
 Db 808 AVEVFAI LASTYGMLEPCIFIPKCYIIILKPKDKSKKL 845
 QY 789 AVNVLAGLTLLSGFGSYFLPKCYIILCRPELNTTEHF 826

RESULT 5
 ID 073637 PRELIMINARY: PRT: 864 AA.
 AC 073637;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE PHEROMONE RECEPTOR.
 GN CA09.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
 OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98226788.
 RA NAITO T., SAITO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,
 RA NAKANISHI S., BRENNER S.;
 RT "Putative pheromone receptors related to the Ca2+-sensing receptor in
 RT Fugu.";
 RT Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).
 DR EMBL: AB008859; BAA26124.1; -.
 DR PFAM: PF00003; 7tm_3; 1.
 DR PFAM: PF01094; ANF_receptor; 1.
 DR PRINTS: PR00248; GPCRMRG.
 KW Pheromone.
 SQ SEQUENCE 864 AA; 96216 MW; E26A0114 CRC32;

Query Match 21.9%; Score 1385; DB 13; Length 864;
 Best Local Similarity 30.5%; Pred. No. 1,556-266;
 Matches 250; Conservative 227; Mismatches 299; Indels 45; Gaps 35;

Db 44 PGDVLGGLFQVYVSSV-FPEWTFSEPHOPVCTRPDILGFRIAMTAFVQIENKPNL 102
 QY 34 PGDFLLAGLFLSHGDCQVRHRLVTVSCDRPD-S-FNGHGYHLFQARFVEEINNSSL 91
 Db 103 LPLNLTIGRLYDNCALVYVFGSALALASQEBALFQOG-CAGSPPLVIGVDSLTFT 161
 QY 92 LPLNLTIGRLYDNCSEBANYATLRLVALOGPRHIEQKRLRHSSKVAVFIPGPDTHA 151
 Db 162 IASASVGLTKIPMVSTFATCCLTNRQRPSEFRITPSDDFQVRAMITQILKHFGWTWG 221
 QY 152 VTAAALGLPFLMLVSEYASVLSAKRKPSFLRTVPDRHQVEVWVQLQSGFWWIS 211
 Db 222 LLYSDDDYGLHVARSPQSD-LYSGGOCCLAYLEVLPMDNLSNR-R-IYHVKESTARY 278
 QY 212 LTISSYDYGQGVQALE-ELAVPRGI-CVAFKDIVPSARVGPBMQSMQHLQAQATTV 269
 Db 279 LMFVAFOSHIMHL-EEVYRQKTYGLQMLASEAMTGTTFLOTDFPMYLNGLTIGAIRG 337
 QY 270 VVVFNSR-HLARYFPRSVLANLTKGWVASEDMAISTITSTVGLIGITVIGAVQQR 328
 Db 338 EITGLDFLLR-IRPOSSNNTSYDMVQOFWEYSFOCKFASASSAEACTDENIQOVDAT 396
 QY 329 QVGLKEFESESVRAV-TAAPSACP-EGSM-----CS-TNQLCRE-CHTF-TTRNMT- 376
 Db 397 FLDVSNLRPEYNYKAVYALALDMLQCEPGRGPRSSGSCADIKHLEWQVHYIQHY 426
 QY 377 -LGAFMSAAYRYEAHYAAHGLHQLGC-TS-E-ICS-R-GPVY---PMOQLQOYKYV 427
 Db 457 NETTTFGDOVSPDNGDVLPIYDILNOMQLPDGRTOVQVNGEYKRSRGEELQIHEDIK 516
 QY 428 NELLH-ENYVAFPDNDGLGYDILAMDWNGPEMT-PEIIGSASLSYVH---LDINKTKI 482
 Db 517 FMVESNKPVSHVCSSECPGTRMSRRKKGQVCCFDCLLCSEGRKISNTDTSMECTSCPED 576

QY 483 QWNGKNNQVPAVSCITDCLAGHRRVYVSGSH-CCFECVCEAGTFILNSELHICQPCGTE 541
 Db 577 FWSRPDRDVCVRKTFEFLSYHEPDLGICLTAASLIGVIVVYVGLFIHRRSPVYRANS 636
 QY 542 EWAPKREKTCFPRTEYELAMHEPISLVLIANTLILLVGTAGLFAWFFHPPVYSAAG 601
 Db 637 ELSFLLVSLKFLCISLA-FIGRPRLMTQDRLHAFGIFVLCVSCIVKTMVYLAVER 695
 QY 602 RUCFLMLGSL-VAGSCSFIFGEPVYRACILRQPLFSIGFAIFLSCILTRSFQVYIIFK 660
 QY 661 FSTKVPTFEYRTW-AQNHGAGLFLVIVSSVHLICLTWLMTMPRPRTREYQRPPLVILEC 719
 Db 755 VVSGTGFVNLSTYGLALISFLAFLARNLPDNEAKLTFTSMLI-FCAYWIAFVPA 813
 QY 720 TEVNSVGFLLAFTNHLISITFVCSYGLKELPENNEKCVTFSLINFTVS-WIAFTMA 778
 Db 814 YINSPKRYDAVEVFAILTSFGLVALFPGPKCYIILFRPE 854
 QY 779 ASIIQSGYLPANVNLAGLTLLSGFGSYFLPKCYIILCRPE 819

RESULT 6
 ID 073635 PRELIMINARY: PRT: 940 AA.
 AC 073635;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE CALCIUM2+ SENSING RECEPTOR.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
 OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98226788.
 RA NAITO T., SAITO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,
 RA NAKANISHI S., BRENNER S.;
 RT "Putative pheromone receptors related to the Ca2+-sensing receptor in
 RT Fugu.";
 RT Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).
 DR EMBL: AB008857; BAA26122.1; -.
 DR PFAM: PF00003; 7tm_3; 1.
 DR PFAM: PF01094; ANF_receptor; 1.
 DR PRINTS: PR00248; GPCRMRG.
 KW Pheromone.
 SQ SEQUENCE 940 AA; 105814 MW; 034CB09E CRC32;

Query Match 21.6%; Score 1371; DB 13; Length 940;
 Best Local Similarity 30.8%; Pred. No. 2,066-263;
 Matches 256; Conservative 237; Mismatches 284; Indels 53; Gaps 35;

Db 29 MFGDILLGLFPIHFG-ISSKDNELAARPESTKCVRFNFRGFRWLQAVYFAIEEINNSS 87
 QY 33 LPDFFLLAGLFLSHGDCQVRHRLVTVSCDRPD-S-FNGHGYHLFQARFVEEINNSSA 90
 Db 88 LPLNLTIGRLYDNCSEBANYATLRLVALOGPRHIEQKRLRHSSKVAVFIPGPDTHA 147
 QY 91 LPLNLTIGRLYDNCSEBANYATLRLVALOGPRHIEQKRLRHSSKVAVFIPGPDTHA 147
 Db 148 SAVSTAVANLISLEYPOSYASSSRLSNKQVSEMTITPDEHQAAMADVLEYEPOM 207
 QY 148 TDHAYTTAALLGFLMPLVYSASSVYLSAKKPFSELTFTVSDRHQVEVWVQLQSGFW 207
 Db 208 NMYIAVASDDYGRDGIENKEMERDICIHLNELI--SQYFEDCEIKALVDRIENSTGA 265
 QY 208 VMSILIGYGDYGLQGVQALEELAVPRGICVAFKDIVPSARVGPBMQSMQHLQAQAT 267
 Db 266 KYIYVAFSPDIEPLIKENYRNRITDRILWLEASAMSSLLAKPEYLDVVBGTIGFYKA 325
 QY 268 TVVVFNSRHLARYFPRSVLANLTKGWVASEDMAISTIT-S--VVGIOG-IGTVL-- 321

D	b	683	AHAKRPGWTVYCS--VPLQRTSVACI--TLQVIICVLMLTLPAPRHKKMTAAKERIT	739
O	y	660	KESTVP--T-FYRMAONHGAGLFIIVSSIVTHLLICTLWMPTPRETRFYQEPFLHI	716
D	b	740	LECNIGSPFWMEVVVIGYLGLAVIFLIATFARKPDJDNENAKFTFSMIL-FCVAWTF	798
O	y	717	LECTEVNSVGFLATHNILLISIFVCSYIKELPEPNYNKACVTSLINIFS-WIAF	775
D	b	799	IPAYVSPGKFTVAVEIFAIIASSFGLLFCIFAPKCXYILILPKENKTGH	848
O	y	776	FPMASIVQGSYLPVANVLGLTTLSGGSGVFELPCRVCIILCPRELNTNH	825
 RESULT 10				
ID		073640	PRELIMINARY:	PRT: 875 AA.
AC		073640:		
DT		01-AUG-1998	(TREMBLrel. 07, Created)	
DR		01-AUG-1998	(TREMBLrel. 07, last sequence update)	
DT		01-NOV-1999	(TREMBLrel. 12, last annotation update)	
DE			PHEROMONE RECEPTOR.	
GN		CA15.1.		
OS			Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	
OC			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;	
OC			Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorphia;	
OC			Tetraodontiformes; Tetraodontidae; Tetraodonidae; Fugu.	
RN		[1]		
RP			SEQUENCE FROM N.A.	
RX			MEDLINE: 98226788.	
RA		NALTO T., SAITO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,		
RA		NAKANISHI S., BRENNER S.;		
RT			'Putative pheromone receptors related to the Ca2+-sensing receptor in	
RT			Fugu.'	
RL			Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).	
DR		EMBL: AB008862; BAA26127.1; -		
DR		PFAM: PF00003; TM_3: 1.		
DR		PFAM: PF01094; ANF_Receptor; 1.		
DR		PRINTS: PRO0248; GPCRMR.		
KW			Pheromone.	
SQ			SEQUENCE 875 AA: 94934 MW: 8FC188F2 CRC32:	
 Query Match 18.8%; Score 1192; DB 13; Length 875; Best Local Similarity 29.4%; Pred. No. 1,31e-223; Matches 251; Conservative 221; Mismatches 326; Indels 55; Gaps 44.				
D	b	30	ALTCQMSSTPTEQCFLFOGHVYVGGLEFNLAHYTPPIANFTQOSHAKACTGLENLPLYOI	89
O	y	19	AFSC-QR-TESPGRSLDGFLLAFLFSLHDGDCIQVRNR-PLVTSQCDPSDFNGHGLHF	75
D	b	90	YAMFAVEEINSHALLRGVKIGHIRDSICALHPWTOTALVALYAGBSASCETAPADYS	149
O	y	76	CAMRTVEEINNSSLALPNLTIGELYLVDCBSBA-NVAYALTRLVALQOPR-HIEIQDLR	133
D	b	150	AETSEKGAASYPLLIGASSMAATILIGT-LSPISITYTASCCLSRRNRYPTFFRTMA	208
O	y	134	NHSS--KYVAEFGDPNDTHAYTTA-ALLGPFLMP-VSEYASSVYLSAKRKFPSELRTVP	189
D	b	209	SDIYAQALAOVLRENTWTIGAVYANDDYHVAKVQOEOTQCKGVCLAVEILORETI	268
O	y	190	SDRHOVEVMVOILQSGFMWVISLISYGDYQOLGQAILEELAVRGCIVARKDLYPPSAR	249
D	b	269	VADVARRARTIOASTAR--VILVSWYTDVGHLF-RQLQKINTVDROFLASEANSTSEVL	325
O	y	250	VDDPRMOGMHQHLAQARTTVVVF--NRHLARVFFRSVLANLTIGKWVASSEDMAISTYI	308
D	b	326	LKDPTSTIVASVYVVALIASOHIPFDNFLGLNPSLRPSKFLQEPNEEFEGCSPSPPS	385
O	y	309	TSVIGIQIGGT-VLDVAVAOORVPLKEFE--E-ESYVR-A--VTA--APS-AC-PGWSW	356
D	b	386	SETSDGLANSLAPCGSAESLECQVQRPFDTSHLRVTVWYVAANAALSHLSLSCIHN	445
O	y	357	CSIN-QL-C-RECTHTTT-RKMP-TLAPFS-MSAAIVYDAVVAVAHGLHOLLGC----	405
D	b	446	SESGETSHCTSPKGKITTELLOHLSKVNFTTPDGKHLYFERGADIPAWDYLINWO-SGITGI	504

[illegible]

Oy	155	AALIGPFLMLVSVSEBASSVVLISAKRKPPSEFLRTVPDSRHOYEVNVOVLQSGFWWMISLG	214
Db	226	ADDYQKTKGVKTEFKKMSANLCAVFSSTIP-KV-YSEKKQAKVAVKSTAKVLYLT	283
Oy	215	SYGDGGQGLVQALEELAVPRGICVAFKDIYVESARVDDPRQSMQOHIAQRTVVVF-	273
Db	284	SDIDS-LFVLEMHHNHTDTWTMTAEMITSAIAKPEVFPYGGTIGATPRSVPG	342
Oy	274	SNRHIAARFPFSSVLANLTKGVWAASEDMALSTYTSTGTGGIGTYLGVAVQOQVPG	333
Db	343	KEFLYDVHPNKPDPNDVLITIEFWQPAFNCTWPNSSVPYNVDHRYVMKTEKEDRLYDMSDLC	402
Oy	334	KEFE-ESYV-R-A--V-TAA--PSA-C--PEGS-WCSTQ--LC-RECHTFETRN-MP	375
Db	403	TGEEKLEDLKNMNYLDTSDLRITKQCKAVVVAIAGDHLNSQCDGSGPSPSNQOCAPPT	462
Oy	376	T---LGAP-S-MSAA-YR--Y-EKAVVAHAGHLQGLGCT-SE--ICSRGP-VY-P-	417
Db	463	FDFWQLMATYMEIKERKSHEDKMWVILIDNGDLKNCHYVILNMHLDDGEISFVTVGRENFR	522
Oy	418	WQLLQOIT-K-VNPLHEMT-VAFDONGD-TLGYDIIANDMNGP-EWTFEIIIGSASLS	471
Db	523	STNEFLVLPNTSTIWTMTESSRDPDSFCTQVCPPTKRGINOGPITCPCDPCPADGSYS	582
Oy	472	PVHLD-I-NKTKIOMKRNKNQVPVSVCTTCLLGHNVVWVSHH--CCFEVPEACTFL	577
Db	583	EKSGOREDDPCGEDDMSNAGSKCKVPKVEFLAYGALGFTVLTSIFGALVLAIVVY	642
Oy	528	NKSELHICQPCGTBEAKKESTCTCPPRVELANHEPISLVLIANLILLLLVLGTRGLF	587
Db	643	VIHHTPLVYKANDEFLSLIOMSLVITVLSLFIIGKPCNMSCARQITLALGFCICLSS	702
Oy	588	AMHEFTPVVRSAGKFLCMLGSLVAGSCSFYSEFGEPTVPACILRLPFLSGAIFLSC	647
Db	703	ILGKISLFFPVARSVSKTRLI-S-MHPIFKRLIVCVAGEIGCVAGCAVYLEPPRFEKN	760
Oy	648	LTIRSFQVLIIFKSTKVPPTRTYMAQNHGAGLFVIVSSVHLICLFLMLVMTPTRE	707
Db	761	IE-IQNVKIIIECNE-GSVEFLCSIFGFDVLRALCELTTFVARQOLDPNYEGKCITFGM	818
Oy	708	YORPFL-VILECTEVNSVGF-LAFTHNLLISITFVCSYLAGKELPNEAKCVTFSL	765
Db	819	LVFFIWMISFPAYLSTGKRFKVAVEIPAILASSYGLLGLCFLEPKGTIIILRPKRNTD	877
Oy	766	LNFFSWIAFFTMASITGSGYSLPAPVNLALGLTTLISGSGSGLFKCYVILCRLPNLNTD	824
RESULT	12	PRELIMINARY:	PRT: 855 AA.
ID	070409		
AC	070409		
DT	01-AUG-1998	(TIREMBLrel. 07, Created)	
DT	01-AUG-1998	(TIREMBLrel. 07, last sequence update)	
DT	01-MAY-1999	(TIREMBLrel. 10, last annotation update)	
OS		POTATIVE PHEROMONE RECEPTOR V2R1.	
OC		Mus musculus (Mouse).	
CC		Eutharyota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia;	
NC		Eutheria, Rodentia; Sciurognathi, Muridae; Murinae; Mus.	
RN		(1)	
RP		SEQUENCE FROM N.A.	
RC		TISSUE=VOMERONASAL NEURONS;	
RA		RYBA N.J.P., TIRIDELLI R.,	
RL		Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.	
DR		EMBL, AF053985, AAC08412.1, -	
PFAM		PF00003, 7tm_3, 1.	
DR		PFAM; PF01094; ANF_receptor; 1.	

[illegible]

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

[1]

RN SEQUENCE FROM N.A.

RC STRAIN-SPRAGUE-DAWLEY;

RA MEDLINE; 97433086;

RR HERADA G., DULAC C.;

RT "A novel family of putative pheromone receptors in mammals with a

RT topographically organized and sexually dimorphic distribution.";

RL Cell 90:763-773(1997).

DR EMBL; AF016182; AAC53325.1; -.

DR PFAM; PF00003; 7tm_3; 1.

DR PFAM; PF01094; ANF_receptor; 1.

SO SEQUENCE 779 AA; 88096 MW; B89CE4D5 CRC32;

Query Match 15.3%; Score 972; DB 11; Length 779;

Best Local Similarity 26.3%; Pred. No. 4,63e-175;

Matches 206; Conservative 218; Mismatches 302; Indels 56; Gaps 48;

DB 1 MREAIENSNPHLRLPNTSLGEFINNV-PHGR-VTLVKLFSSLSGSNY-DIPNYISASE 57

78 MRTVEINSSALPLNITLGYELVCSASAVATLRLA-LQPRHLEICKLR-NH 135

58 SNSAVALTPBSWTISECV-GTLIDLYKFPOLTFGPDSLSSEORRSSLQYAPKDTFLT 116

136 SSKVAFVIGPDNDHVAVTALALGPLMLVSYEASSVLSAKRKPPSLTPVSDRHQV 195

117 PGIVSLMLHFHMWVGLFIIDDKGAQTLSDLNEMD-KNGVCTAVEMPVKGSFEFK 175

196 EYVWVLQSGFWYISLISGYDYGOLVOAL-EELAVPGICIVAKDIPV-FSARV-GD 252

176 SWKNHV-QIL-ESSNVIIIGDSDLSLIVIKOKLLTWKVVLIQMDVSKFDDYEM 233

253 PRQSMQMLHQAQRTVVVVFSSRLHARFERRVLANLIGKVVASDEMAISITITSVT 312

234 -VDSLGLAL-ITSHAREEPNFTDEMOKNPS-KIPEDITYLHLMHFNCSYVKDCKI 290

313 GLOGITVGVAAVOQRO-VPLGEFESYVAVTAPASACPEGSW----CS-TNOLCRE 365

291 VHNCELNASLGLPGNIFPDAMSESYNYNAVVAHSHHEMLINOVOPOTHEKKNVY 350

366 CRT-FITRMNPL-GA-F--SKSA-AYRYEAYVAHGHQL-LG-CSEISCRG--V 415

351 FEPWQI-HPFLEROLINONGANEDLCTKSHVEDILNF-WNPFKGLGLNKGVTFSF 408

416 Y-PWQLQIYKKNFLHETVAFD-D-NDITLGYDIIAMDNGE-WTEFL-IGS-AS 469

409 SAPKEOKLISSMIGWATGSTIPQSVCSCHPGFRKTHOEGRYAACFCDCIPCENET 468

470 LSP-VH-LDINKTKIOMHGKNNQVPVSVCTDCLAGHRRVY-VGSHHCCEFCVCEAGTF 526

469 SNETDVOVCCEHYANIEKIHLOKTYETLYDDPLCKTICFSLGSSITAVLVY 528

527 LNNSEIHQPCGTEEMARKESTICPRIVEFLAMHEPISLVIAANTLLLLVLTAGL 566

529 FLKNDPTIKVANNLALSTYLLTLMCEPL-L-FIGRSTASCLIQNIIFLFTVAL 587

587 FAHHFTPVRSAGRLCLMLGSLVAGS-CSFYSPFGERTYACLRQLRLESLGAIFL 645

588 STYLAKTIVIAFKITS--PGIRWMLISRAPNFIPLCTLLQVFLSGIWLTPPT 645

646 SCITIRSFOLVIFKSTIKVPTFYRTMAQNHGAGLFVI-VSSIVHLLICLTMVMTPR 704

646 DKDAHSEHGHIII-CNKSAAVAFHCLNGLGLAL-VSTFM-AFLSRNPPTFNNAKL 702

705 TREYQR-FPHLVLECTEVNSVGL--LAFTHNLLISTFVSGYLKELPENYNAKCV 761

703 AFSMLV-FCSVWTFPLPYVHSTKGMVAMEVSIILASSSTLGIIFAPKCYITLPER 761

762 TPELLNFPVS-WIAFTMASIYOGSLPRAVNLAGLITLSGSGSYFLPRCYVILCRPEL 820

DB 762 NS 763

DB 821 NN 822

RESULT 14 PRELIMINARY; PRT; 458 AA.

ID 093555;

AC 093555;

DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)

DE PUTATIVE ODORANT RECEPTOR (FRAGMENT).

GN GFB7.

OS Carassius auratus (Goldfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Cyprininae; Carassius.

RC TISSUE=OLFACATORY EPITHELIUM;

RX MEDLINE; 98426265.

RA CAO Y., OH B.C., STRYER L.;

RT "Cloning and localization of two multigene receptor families in

RT goldfish olfactory epithelium";

RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).

DR EX3; AF083084; AAC64079.1; -.

DR PFAM; PF00003; 7tm_3; 1.

FT NON_TER 1

SO SEQUENCE 458 AA; 5119 MW; 8CB6FB43 CRC32;

Query Match 13.9%; Score 878; DB 13; Length 458;

Best Local Similarity 31.2%; Pred. No. 1.73e-154;

Matches 140; Conservative 122; Mismatches 172; Indels 15; Gaps 14;

DB 4 YKAVYAAVAAHS-HSLNCKGEOTGCEKSLTIOPKHVYEAALKVNYKVPGDHWPFDSIGA 63

388 VYEAVYAAHGHQLIGCTSEI-CSRG-PYRWQLQIYKKNFLIH-ENTVAFDNGT 444

64 VAHEVYVNMQDSNRSIQPKPVGYEDTSLPPOSEYKXENTVYIAGGQLEKPSVCSGC 123

445 LGYDIIAMDWNG-PEWTEIIG--SASLSPVH-LDINKTKIOMHGKNNQVPVSVCTD 500

124 PRGTRAAKGRPVCCYDIPCAEGEISNETDSINCKOPGEYVPAENKCYLKAVEFL 183

501 LAGHNRVYV-GSHHCCFCEVPCBAGTFELNMSLHICQPCGTEEMARKESTICPRIVEFL 559

184 SFEIMGIVLFPSLPGVCLTVLVAIFYSKKNIPYKANNSELSLFLFSLSICSL 243

560 AMHEPISLVLIANTLLLLVGTAGLFAMHRTPVRSAGRLCLTMGSL-VAGSCSF 618

244 -TFIGRTEMSCMLRHTAFGITFVLICISCIILGKTIVVLAFR-ATLPGSNVKKF-GPAQ 300

619 YSPFGEPTYPACLRQPLSLSGAIFLSCLTIRSPQLVIFKSTKVPPTFYRTMAQNHGA 678

301 QRESVLAETLIOYLCLMLTISPPYPHKNMKYKKEKIIIECSLRSTLCFMAVLGVGL 360

679 GLFVIVSST-VHLLICLTLVMTPTREYORFPHLVLECTEVNSVGLLAFTHNILL 737

361 AVICFLAFLARTLPNENAKFTFESMLI-FCVAWITEIPVYSSPGKTVAVEHATL 419

738 SISTEVCSTLGEKLPENYNAKCVITSLNFPVS-WIAFTMASIYOGSLPRAVNLAGL 796

420 ASFGILFCIFAPKCYIILKSDONTKH 448

797 TILSGGFSGYFLPKCYVILCRPELNTEH 825

DB 420 ASFGILFCIFAPKCYIILKSDONTKH 448

DB 797 TILSGGFSGYFLPKCYVILCRPELNTEH 825

DB 797 TILSGGFSGYFLPKCYVILCRPELNTEH 825

DB 797 TILSGGFSGYFLPKCYVILCRPELNTEH 825

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DB 797 TILSGGFSGYFLPKCYVILCRPELNTEH 825

 WISE (TM)

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MPsrch_pp Protein - protein database search, using Smith-Waterman algorithm
 Run on: Fri Mar 17 13:03:18 2000; MasPar time 44.06 Seconds
 569.357 Million cell updates/sec
 Tabular output not generated.

Title: >US-09-361-652-1
 Description: (1-840) from US09361652.pep
 Perfect Score: 6338
 Sequence: 1 MFWMAHLLLSQLVYCNMF.....NNTHEHQASIDYTRCGTT 840

Scoring table: PAM 150
 Gap 11

Searched: 82229 seqs, 29854866 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot38
 1:swissprot

Statistics: Mean 54.039; Variance 93.294; scale 0.579

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1311	20.7	1085	1	CASR_BOVIN EXTRACELLULAR CALCIUM-	3.56e-271
2	1290	20.4	1078	1	CASR_HUMAN EXTRACELLULAR CALCIUM-	4.19e-265
3	1285	20.3	1079	1	CASR_RAT EXTRACELLULAR CALCIUM-	6.74e-265
4	873	13.8	1203	1	MGR5_RAT METABOTROPIC GLUTAMATE	2.46e-165
5	870	13.7	1212	1	MGR5_HUMAN METABOTROPIC GLUTAMATE	1.26e-165
6	847	13.4	872	1	MGR2_RAT METABOTROPIC GLUTAMATE	3.43e-160
7	843	13.3	912	1	MGR4_RAT METABOTROPIC GLUTAMATE	3.01e-159
8	837	13.2	912	1	MGR4_HUMAN METABOTROPIC GLUTAMATE	7.84e-158
9	821	13.0	1199	1	MGR1_RAT METABOTROPIC GLUTAMATE	4.63e-154
10	819	12.9	872	1	MGR2_HUMAN METABOTROPIC GLUTAMATE	1.37e-153
11	812	12.8	1194	1	MGR1_HUMAN METABOTROPIC GLUTAMATE	6.10e-152
12	808	12.7	877	1	MGR3_HUMAN METABOTROPIC GLUTAMATE	5.33e-151
13	808	12.7	908	1	MGR8_RAT METABOTROPIC GLUTAMATE	5.33e-151
14	806	12.7	908	1	MGR8_MOUSE METABOTROPIC GLUTAMATE	1.57e-150
15	800	12.6	908	1	MGR8_HUMAN METABOTROPIC GLUTAMATE	4.06e-149
16	793	12.5	879	1	MGR3_RAT METABOTROPIC GLUTAMATE	1.79e-147
17	779	12.3	877	1	MGR6_HUMAN METABOTROPIC GLUTAMATE	3.48e-144
18	772	12.2	871	1	MGR5_RAT METABOTROPIC GLUTAMATE	1.53e-142
19	760	12.0	915	1	MGR7_HUMAN METABOTROPIC GLUTAMATE	9.94e-140
20	755	11.9	915	1	MGR7_RAT METABOTROPIC GLUTAMATE	1.47e-138
21	561	8.9	976	1	MGR_DROME METABOTROPIC GLUTAMATE	1.18e-93
22	372	5.9	999	1	MGR1_CAELI PROBABLE METABOTROPIC	1.72e-51
23	145	2.3	938	1	NM21_HUMAN GLUTAMATE [NMDA] RECP	1.16e-06

24	144	2.3	938	1	NM21_RAT GLUTAMATE [NMDA] RECP	1.68e-06
25	148	2.3	1233	1	NME3_HUMAN GLUTAMATE [NMDA] RECP	3.75e-07
26	145	2.3	1237	1	NME3_RAT GLUTAMATE [NMDA] RECP	1.16e-06
27	145	2.3	1239	1	NME3_MOUSE GLUTAMATE [NMDA] RECP	1.16e-06
28	142	2.2	938	1	NM21_MOUSE GLUTAMATE [NMDA] RECP	3.54e-06
29	130	2.1	1125	1	CYGS_STRPU SPERACT RECEPTOR PRECU	2.68e-04
30	125	2.0	986	1	CYGR_ARBP RESACT RECEPTOR PRECU	1.52e-03
31	126	2.0	1323	1	NME4_MOUSE GLUTAMATE [NMDA] RECP	1.08e-03
32	123	1.9	1464	1	NMEL_MOUSE GLUTAMATE [NMDA] RECP	2.99e-03
33	123	1.9	1464	1	NMEL_RAT GLUTAMATE [NMDA] RECP	2.99e-03
34	120	1.9	1482	1	NME2_MOUSE GLUTAMATE [NMDA] RECP	8.19e-03
35	120	1.9	1482	1	NME2_RAT GLUTAMATE [NMDA] RECP	8.19e-03
36	112	1.8	434	1	VC34_HELPY HYPOTHETICAL PROTEIN H	1.10e-01
37	111	1.8	434	1	VC05_VARY PROTEIN G5	1.50e-01
38	113	1.8	532	1	YH37_YEAST HYPOTHETICAL 61.2 KD P	8.00e-02
39	117	1.8	842	1	YH2_TREPA TRANSLATION INITIATION	2.20e-02
40	117	1.8	1108	1	CYGF_RAT RETINAL GRANULYL CYCLA	2.20e-02
41	111	1.8	1108	1	CYGF_HUMAN RETINAL GRANULYL CYCLA	1.50e-01
42	115	1.8	2749	1	IP3R_MOUSE INOSITOL 1,4,5-TRISPO	4.21e-02
43	109	1.7	360	1	CKR4_MOUSE C-C CHEMOKINE RECEPTOR	2.80e-01
44	109	1.7	434	1	VC05_VACCC PROTEIN G5	2.80e-01
45	110	1.7	444	1	CEFG_CEPAC ACETYL-COA--DEACETYLCE	2.06e-01

ALIGNMENTS

RESULT	1	STANDARD	PRT	1085 AA.
ID	CASR_BOVIN			
AC	P35384			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR).			
DE	CASR OR PCAR.			
GN	Bos taurus (Bovine).			
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;			
OC	Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;			
OC	Bovinae; Bos.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PARATHYROID.			
RX	MEDLINE; 94077182.			
RA	BROWN E.M., GAYZA G., RICCARDI D., LOWBARDI M., BUTTERS R., KIFOR O., SUN A., HEDIGER M.A., LYTTON J., HEBERT S.C.;			
RA	"Cloning and characterization of an extracellular Ca(2+)-sensing receptor from bovine parathyroid."			
RT	Nature 366:575-580(1993).			
RL	-1- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.			
CC	*****			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	*****			
DR	EMBL; S67307; AB29171.1; ..			
DR	PIR; S40476; S40476.			
DR	GCDB; GCR_0900; ..			
DR	PROSITE; PS00979; G-PROTEIN_RECP_F3_1; 1.			
DR	PROSITE; PS00980; G-PROTEIN_RECP_F3_2; 1.			
DR	PROSITE; PS00981; G-PROTEIN_RECP_F3_3; 1.			
DR	PFAM; PF00003; 7tm_3; 1.			
DR	PFAM; PF01094; ANF_receptor; 1.			
KW	G-protein coupled receptor; Transmembrane; glycoprotein; signal.			
FT	SIGNAL 1 19			

FT CHAIN 20 1085 EXTRACELLULAR CALCIUM-SENSING RECEPTOR.
 FT DOMAIN 20 613 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 614 636 I (POTENTIAL).
 FT DOMAIN 637 650 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 651 671 II (POTENTIAL).
 FT DOMAIN 672 682 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 683 701 III (POTENTIAL).
 FT DOMAIN 702 725 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 726 746 IV (POTENTIAL).
 FT DOMAIN 747 770 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 771 793 V (POTENTIAL).
 FT DOMAIN 794 806 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 807 829 VI (POTENTIAL).
 FT DOMAIN 830 837 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 838 863 VII (POTENTIAL).
 FT DOMAIN 864 1085 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 91 91 POTENTIAL.
 FT CARBOHYD 131 131 POTENTIAL.
 FT CARBOHYD 262 262 POTENTIAL.
 FT CARBOHYD 288 288 POTENTIAL.
 FT CARBOHYD 401 401 POTENTIAL.
 FT CARBOHYD 447 447 POTENTIAL.
 FT CARBOHYD 469 469 POTENTIAL.
 FT CARBOHYD 489 489 POTENTIAL.
 FT CARBOHYD 542 542 POTENTIAL.
 FT CARBOHYD 595 595 POTENTIAL.
 SQ SEQUENCE 1085 AA; 121170 MW; 501FE6CD CRC32;

Query Match 20.7%; Score 1311; DB 1; Length 1085;

Best Local Similarity 31.9%; Pred. No. 3,566-271; Matches 272; Conservatave 233; Mismatches 275; Indels 73; Gaps 50;

Db 31 GDIIIGGLPIIFHG-VAAKDDDKSPESVEICIRYNGFRMQLQAMIFAEINSSPALL 89
 QY 35 GDFLAGFSLHGDCLQYRHRPLVTSQDRPS-FNGHYHLFQAMRTVEINSSALL 92
 Db 90 PNMIGIPIPTCNTVSALENTLSFVAKNKIDSLNDFPCNSHIFTAVGATGSG 149
 QY 93 PNITGLYELVYCSSESANVY-ATLVLVLAQGRHIEIOK-DLRHSSKVAFAIPDNTD 149
 Db 150 ISTVANLGLFYIPQVYASSRLSNKNOKSFRTIPNDHQATAMADIEFRNMW 209
 QY 150 HAVTIALGLPFLMPLVYEAASSVLSAKRFPFLRTVPSDRHVEYVOLLQSGVWV 209
 Db 210 VGTIAADDDYGRPIEKEEREAEEDICIDSELI--SQSDEKIQOVVEYIOWSTAKV 267
 QY 210 ISLGSYDYGQGLQVQALDELAVPRGICVAFRDYFSAVGDPRMGMHLAARTTV 269
 Db 268 IVFSSGPDLEPLI-KEIVRRNITGRIMLASEFAMASSLIAMPEYHVGGTIGFGLKAG 326
 QY 270 VVVFESN-RHLARVFEFRSVVLANLTKVWVASEDMA---IS-T-YITSVTG-IQ-GI--G 318
 Db 327 QIPGRFELQVHPKRSVHNGFAKFEWETFNCHLOEGAKGSLPDTLRGHEEGAGLS 386
 QY 319 TVLG-----VA-VQQRQ-VP-GI-KEF-BEST--VR-AVTA-P-S--ACPBS-SM-C 357
 Db 387 NSPLAFRLPCLGEENISSVEPYMDYTHLRISYNYLAVYSIAHALQDIYICIPGRGLT 446
 QY 358 -S-IN-Q-LCRECHFTTRNMPTLGAFSMSAARYEAIVANAHLQDLGTSF--I-- 409
 Db 447 NGSCADIKKVAQVYKHLRHLNFTSNMGEQVTEDECDDLGNISIIIMHLSPEDEGSIVF 506
 QY 410 --CS-RGPVYPWOLLQOIYKVNFLH-ENTVAFDNDGDTLGYDIIAMDMNGPE-WT-F 462
 Db 507 KEVGYNYAKKGERLFINDEKILMSGFSREVPFNSCRDCLAGRKIIIESEPCCEC 566
 QY 463 ELIG-S-SLSPVHLINKTKIQHGNNOVPVSVCTDCLAGHRRVYV-GSHHCCEC 518
 Db 567 VECPDGEYSDTDAACDKCPDDFENSNHTSCIAKEIEFTLSWTEPFIALTLFAVLGTF 626
 QY 519 VPCEAGTFLNNSSELHICQPCGEEMAPKRESTTCFPRTEFLAMHPRISLVLIANTLTL 578
 Db 627 LTAFLVGLVFI-KFRNTPIVAKATNELSTLLFSLCCFSSSLF-FIGEPDMTCRLRPA 684

QY 579 LTVAGLFAHHEH-TRVVSAGGRCLCFMLMGLSVAG-SCSFYSFEGEPVPALLRQPL 636
 Db 685 FGISFVLCISQILVTKTRVLVVE--AKIPSEFRKMGKNTLOFLVFLCTFMQIVCAI 742
 QY 637 FSLGFALFSLCITRSFOLVLEIFKSTKVPF-FYRVAONHAGLFYIVSVYHLLCLT 695
 Db 743 WLNTAPSSSYNHELEDEIFITCHEGSLMALGFLIGYTC-LLAALCFFP-AFKSRKLP 800
 QY 696 WLVMYTRPRTEYGRFPHVILLECTEVN--SVGFLAFTHNILLISTFVCSYGLKELPE 753
 Db 801 NFNAKFTLSMLIFFVWISFIPAYASTY-GKVSAREVYALIAASFGLIACIFENKVV 859
 QY 754 NYNBAKCTFSLINFEVSWIAFFTM-ASIVQSYLPVAVNLVAGLTLTSGFSYGFLPKCY 812
 Db 860 IILKPSNTE 871
 QY 813 YILCRPELUNTE 824

RESULT 2

CASR_HUMAN STANDARD; PRT: 1078 AA.

AC P41180; Q163912; Q163912; Q16108; Q16109; Q16110;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR).

GN CASR OR PCARL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homnidae; Homo.

[1]

SEQUENCE FROM N.A.

RA PEARCE S.H.S., THAKKER R.V.;

RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.

[2]

SEQUENCE FROM N.A.

RA TISSUE-PARATHYROID;

RX MEDLINE; 95279439.

RA GARRETT J.E., CAPUANO I.V., HAMMERLAND L.G., HUNG B.C., BROWN E.M.,

HEBERT S.C., NEMETH E.F., FULLER F.;

RT "Molecular cloning and functional expression of human parathyroid

calcium receptor cDNAs.";

RL J. Biol. Chem. 270:12919-12925(1995).

[3]

SEQUENCE FROM N.A.

RA TISSUE-KIDNEY;

RX MEDLINE; 95408281.

RA AIDA K., KOISHI S., TAMAYA M., ONAYA T.;

RT "Molecular cloning of a putative Ca(2+)-sensing receptor cDNA from

human kidney.";

RL Biochem. Biophys. Res. Commun. 214:524-529(1995).

[4]

SEQUENCE FROM N.A.

RA MEDLINE; 96343808.

RA FRICHEL M., ZINK-LORENZ A., HOLLOSCHI A., HAFNER M., FLOCKERZI V.,

RAUVE F.;

RT "Expression of a calcium-sensing receptor in a human medullary

thyroid carcinoma cell line and its contribution to calciumin

secretion.";

RL Endocrinology 137:3842-3848(1996).

[5]

VARIANTS FHH GLU-185; LYS-257 AND TRP-795.

RA POLAK M.R., BROWN E.M., CHOI Y.H., HEBERT S.C., MARX S.J.;

RA STEINMANN B., LEVI T., SEIDMAN C.E., SEIDMAN J.G.;

RT "Mutations in the human Ca(2+)-sensing receptor gene cause familial

hypercalcemic hypercalcaemia and neonatal severe

Cell 75:1297-1303(1993).

[6]

VARIANT ADH ALA-127.

RX MEDLINE: 95179179.
 RA POLLAK M.R., BROWN E.M., ESTEP H.L., MCCLAIN P.N., KIFOR O., PARK J.,
 RA HERBERT S.C., SEIDMAN C.E., SEIDMAN J.G.;
 RT "Autosomal dominant hypocalcemia caused by a Ca(2+)-sensing receptor
 gene mutation.";
 RL Nat. Genet. 8:303-307(1994).
 RN [17]
 RP VARIANTS FHH MET-62; CYS-66; MET-138; GLU-143 AND GLN-227.
 RX MEDLINE: 95243223.
 RA CHOU Y.-H.W., POLLAK M.R., BRANDI M.L., TOSS G., ARNOVIST H.,
 RA ATKINSON A.B., PAPAPoulos S.E., MARK S., BROWN E.M., SEIDMAN J.G.,
 RA SEIDMAN C.E.;
 RT "Mutations in the human Ca(2+)-sensing-receptor gene that cause
 familial hypocalcemic hypocalcemia.";
 RL Am. J. Hum. Genet. 56:1075-1079(1995).
 RN [8]
 RP SEQUENCE OF 1-61 FROM N.A., AND VARIANT FHH ALA-39.
 RX MEDLINE: 95403641.
 RA AIDA K., KOISHI S., INOUE M., NAKAZATO M., TAMURA M., ONAYA T.;
 RT "Familial hypocalcemic hypocalcemia associated with mutation in the
 human Ca(2+)-sensing receptor gene.";
 RL J. Clin. Endocrinol. Metab. 80:2594-2598(1995).
 RN [9]
 RP VARIANTS NSHPT LEU-227 AND TYR-598.
 RX MEDLINE: 96292293.
 RA PEARCE S.H.S., TROMP D., WOODING C., BESSER G.M., CHEW S.L.,
 RA GRANT D.B., HEATH D.A., HUGHES I.A., PATERSON C.R., WHITE M.P.,
 RA THAKKER R.V.;
 RT "Calcium-sensing receptor mutations in familial benign hypocalcemia
 and neonatal hyperparathyroidism.";
 RL J. Clin. Invest. 96:2683-2692(1995).
 RN [10]
 RP VARIANTS ADHP THR-116; HIS-881 AND SER-806, AND VARIANT SER-851.
 RX MEDLINE: 96311554.
 RA BARON J., WINER K.K., YANOVSKI J.A., CUNNINGHAM A.W., LAUE L.,
 RA ZIMMERMAN D., CUTLER G.B. JR.;
 RT "Mutations in the Ca(2+)-sensing receptor gene cause autosomal
 dominant and sporadic hypoparathyroidism.";
 RL Hum. Mol. Genet. 5:601-606(1996).
 RN [11]
 RP VARIANT FHH ARG-174.
 RX MEDLINE: 97442275.
 RA WARD B.R., STUCKEY B.G.A., GUTTERIDGE D.H., LAING N.G., PULLAN P.T.,
 RA RATAJCZAK T.;
 RT "A novel mutation (L174R) in the Ca2+-sensing receptor gene
 associated with familial hypocalcemic hypocalcemia.";
 RL Hum. Mutat. 10:233-235(1997).
 CC -1- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF
 CC CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A
 CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS SEEM TO BE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: FOUND IN KIDNEY, BUT NOT IN BRAIN, LUNG,
 CC LIVER, HEART, SKELETAL MUSCLE, OR PLACENTA.
 CC -1- DISEASE: DEFECTS IN CASR ARE A CAUSE OF FAMILIAL HYPOCALCAEMIC
 CC HYPERCALCAEMIA (FHH) AND NEONATAL SEVERE HYPERPARATHYROIDISM
 CC (NSHPT). TWO INHERITED CONDITIONS CHARACTERIZED BY ALTERED CALCIUM
 CC HOMOEOSTASIS. THE MUTATIONS REDUCE THE ACTIVITY OF THE RECEPTOR.
 CC FHH AFFECTED INDIVIDUALS EXHIBIT MILD OR MODEST HYPERCALCAEMIA,
 CC RELATIVE HYPOCALCAURIA, AND INAPPROPRIATELY NORMAL PTH LEVELS. IN
 CC CONTRAST, NSHPT IS A RARE AUTOSOMAL RECESSIVE LIFE-THREATENING
 CC DISORDER CHARACTERIZED BY VERY HIGH SERUM CALCIUM CONCENTRATIONS,
 CC SKELETAL DEMINERALIZATION, AND PARATHYROID HYPERPLASIA. IN SOME
 CC INSTANCES NSHPT HAS BEEN DEMONSTRATED TO BE THE HOMOZYGOUS FORM OF
 CC FHH.
 CC -1- DISEASE: DEFECTS IN CASR ARE ALSO THE CAUSE OF AUTOSOMAL DOMINANT
 CC HYPOCALCAEMIA (ADH) IN WHICH THE RECEPTOR IS ACTIVATED AT SUBNORMAL
 CC CA(2+) LEVELS.
 CC -1- DISEASE: DEFECTS IN PCAR1 ARE ALSO THE CAUSE OF AUTOSOMAL DOMINANT
 CC HYPOPARATHYROIDISM (ADHP). ADHP IS CHARACTERIZED BY HYPOCALCAEMIA
 CC AND HYPERPHOSPHATEMIA DUE TO INADEQUATE SECRETION OF PARATHYROID

CC HORMONE. SYMPTOMS ARE SEIZURES, TETANY AND CRAMPS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@sib.ch).
 CC -----
 DR EMBL: X81086; CAA56990.1; -
 DR EMBL: U20759; AAA86503.1; -
 DR EMBL: U20760; AAA86504.1; -
 DR EMBL: D50855; BAA09453.1; -
 DR EMBL: S83176; AAB46873.1; -
 DR EMBL: S79217; AAB35262.1; -
 DR EMBL: S68032; AAB29413.1; -
 DR EMBL: S68033; AAB29414.1; -
 DR EMBL: S68036; AAB29415.1; -
 DR GCRDB: GCR_1337; -
 DR GCRDB: GCR_1874; -
 DR GCRDB: GCR_2012; -
 DR GCRDB: GCR_2013; -
 DR GCRDB: GCR_2696; -
 DR GCRDB: GCR_2697; -
 DR MTX: 601199; -
 DR MTX: 145980; -
 DR MTX: 601198; -
 DR PROSITE: PS00979; G-PROTEIN_RECEP_F3_1; 1.
 DR PROSITE: PS00980; G-PROTEIN_RECEP_F3_2; 1.
 DR PROSITE: PS00981; G-PROTEIN_RECEP_F3_3; 1.
 DR PFAM: PF00003; 7tm3.3; 1.
 DR PFAM: PF01094; ANF_receptor; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Disease mutation; Alternative splicing; Polymorphism.
 FT SIGNAL 1 19
 FT CHAIN 20 1078
 FT DOMAIN 20 612
 FT TRANSMEM 613 635
 FT DOMAIN 638 649
 FT TRANSMEM 650 670
 FT DOMAIN 671 681
 FT TRANSMEM 682 700
 FT DOMAIN 701 724
 FT TRANSMEM 725 745
 FT DOMAIN 746 769
 FT TRANSMEM 770 792
 FT DOMAIN 793 805
 FT TRANSMEM 806 828
 FT DOMAIN 829 836
 FT TRANSMEM 837 862
 FT DOMAIN 863 1078
 FT CARBOHYD 90 90
 FT CARBOHYD 130 130
 FT CARBOHYD 261 261
 FT CARBOHYD 287 287
 FT CARBOHYD 386 386
 FT CARBOHYD 400 400
 FT CARBOHYD 446 446
 FT CARBOHYD 468 468
 FT CARBOHYD 488 488
 FT CARBOHYD 541 541
 FT CARBOHYD 594 594
 FT CARBOHYD 536 536
 FT VARSPLIC 39 39
 FT VARIANT 62 62
 FT VARIANT 66 66
 FT VARIANT 116 116
 FT VARIANT 116 116
 /FTId-VAR_003586.
 R -> C (IN FHH).
 R -> M (IN MID FHH AND NSHPT).
 /FTId-VAR_003587.
 A -> T (IN ADHP).
 /FTId-VAR_003588.

FT VARIANT 127 127 E -> A (IN ADH).
 FT /Frid-VAR_003589.

Note: remainder of annotations omitted.

Query Match 20.4%; Score 1290; DB 1; Length 1078;
 Best Local Similarity 32.0%; Pred. No. 4.19e-266;
 Matches 273; Conservative 230; Mismatches 276; Indels 73; Gaps 49;

30 GDILGLFPHFG-VAAKODLKRSPESVCIRNFRGFWMLOAMFALEINSSPLL 88
 35 GDFLAGFESHGDCLOVRRHPLVTSORPDS--FNGHYHLPQMRVTEINSSALL 92
 DB PNLTGRIEDTCTVSKALPATLSFYAOKNIDSLDEFNCSEHPTSTAVGATGSG 148
 89 PNLTGRIEDTCTVSKALPATLSFYAOKNIDSLDEFNCSEHPTSTAVGATGSG 148
 93 PNLTGRIEDTCTVSKALPATLSFYAOKNIDSLDEFNCSEHPTSTAVGATGSG 149
 DB VSTAVANLGLFTYPOVSASSRLLSKNOFKSFLRTIPDEHQATAMADIEYFRMW 208
 149 VSTAVANLGLFTYPOVSASSRLLSKNOFKSFLRTIPDEHQATAMADIEYFRMW 208
 150 HAVTAAALGLFPLPLVSYEASSVLSAKRFPFLRTVPSDRHQVEVMVQLQSGVW 209
 DB VGTIAADDDVRGRIEKRFAEERDIDCELSL--SQYDEEIQHVAVIONSTAKV 266
 209 VGTIAADDDVRGRIEKRFAEERDIDCELSL--SQYDEEIQHVAVIONSTAKV 266
 210 ISLIGSGDVGQGLVQALEELAVPRGICVARKDIVPSARVGDPMOSMQLAQARTV 269
 DB IVVSSGPDLEPL-KEIVRRNITGKIWLASEANASSSLIAMPQYFHVGGTIGFALAG 325
 267 IVVSSGPDLEPL-KEIVRRNITGKIWLASEANASSSLIAMPQYFHVGGTIGFALAG 325
 270 VVVSNS-RHLARVFRSVLVANLGVKVVASEDA---IS-T-YIISVIG-IQ-GI-G 318
 DB QIPEFREFLKVRHPRKSVHNGFAEFWEETFNCHLQEGAKPPLVDFTFLGHESGDRFS 385
 326 QIPEFREFLKVRHPRKSVHNGFAEFWEETFNCHLQEGAKPPLVDFTFLGHESGDRFS 385
 319 TVLDE---VA-VQORQ--VP-GL-KEF-EESY---VR-AVTRA-P-S---ACPE-GSW-- 356
 DB NSSAFRPLCTGDNISSEVPYIDYTLKRSYNYVLAVSIAHALODIYCLGRGLFT 445
 386 NSSAFRPLCTGDNISSEVPYIDYTLKRSYNYVLAVSIAHALODIYCLGRGLFT 445
 357 -CSTN-Q-LCECHFTFTNRPPTLGASMSAAYRYEYVAVAGLHQL--L-GC--T 406
 DB NGSCADIKKRYEAMOVLLKRLHNFNNNGEOTFECGDLVGNYSIIMHLSPEDEGIVE 505
 446 NGSCADIKKRYEAMOVLLKRLHNFNNNGEOTFECGDLVGNYSIIMHLSPEDEGIVE 505
 407 SEIS-RGPVYPMQLDQIYKVNFLH-ENTVAFDNDGDTLGYDIIAMDNNGE-WT-F 462
 DB KEVGYVYNAKGERLFTNEKILMSGFSREVPSSNCRDCLAGTKGIIIEGPTCCFEC 565
 506 KEVGYVYNAKGERLFTNEKILMSGFSREVPSSNCRDCLAGTKGIIIEGPTCCFEC 565
 463 EIIS--SA-SLSPVHLDNKTKIOMHGNNNOVPVSVCTDLAGHRRVYV--GSHHCPEC 518
 DB VECDEGSESDTDSACNCPDPMFMSNNHNSIAKETEFISWTEPREGIATLFAVIGIF 625
 566 VECDEGSESDTDSACNCPDPMFMSNNHNSIAKETEFISWTEPREGIATLFAVIGIF 625
 519 VPCAGTFFLNSEHLICOPCTEEMAPKESTTCPRIVEFLAMHDPISLVLIANTLILL 578
 DB LTAFLVGF-I-KFRNTPIVATNRELSTLLFSLCCFSSSLF-FIGRPDWTCLRQPA 683
 626 LTAFLVGF-I-KFRNTPIVATNRELSTLLFSLCCFSSSLF-FIGRPDWTCLRQPA 683
 579 LVVGTAGLFAHFR-TPVVRASAGRLCFLMGLSLVAG-SCSFYSPFGSPVPAQLLRPL 636
 DB FGISFVLCISITLYKTNVLLVFE--AKIPFSHRKMGMLQDLVFLCTFMOIVICI 741
 684 FGISFVLCISITLYKTNVLLVFE--AKIPFSHRKMGMLQDLVFLCTFMOIVICI 741
 637 FSLQFAFLSCLTIRSLQIIFEFSTKVPF-FYRTAQNHGAGFLVSVTHLILCLT 695
 DB WLYAPSSVYNOLEDELIIFITCHESSIMLGLIGTC-LLAICGF-AFASKRIPE 799
 742 WLYAPSSVYNOLEDELIIFITCHESSIMLGLIGTC-LLAICGF-AFASKRIPE 799
 696 WLYAPSSVYNOLEDELIIFITCHESSIMLGLIGTC-LLAICGF-AFASKRIPE 799
 DB NEFAKEITSMLEFFIYVWISFIPAYASTY-GKFEVSAEVAIILASGLGACIFENKI 858
 800 NEFAKEITSMLEFFIYVWISFIPAYASTY-GKFEVSAEVAIILASGLGACIFENKI 858
 754 NYNAKCVTFLLNFYSWIAFTIM-ASIIYGSLIPAVNVLAGLITLSSGSGIFLPCY 812
 DB IILFKPSRNTIE 870
 859 IILFKPSRNTIE 870
 813 VILCRPEINTE 824
 813 VILCRPEINTE 824

RESULT 3 STANDARD; PRT; 1079 AA.
 ID CASR_RAT
 AC P48442;

DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID
 DE CELL CALCIUM-SENSING RECEPTOR).
 GN CASR OR PCARL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 NC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-KIDNEY OUTER MEDULLA;
 RX MEDLINE; 95116508.
 RA RICCARDI D., PARK J., LEE W., GAMBA G., BROWN E.M., HERBERT S.C.;
 RT "Cloning and functional expression of a rat kidney extracellular
 RT calcium/polyvalent cation-sensing receptor".
 RL Proc. Natl. Acad. Sci. U.S.A. 92:131-135(1995).
 RN [2]
 RP SEQUENCE OF 1-294 FROM N.A.
 RC STRAIN-WISTAR;
 RX MEDLINE; 95241465.
 RA RYAN M., SNOWMAN A.M., SNYDER S.H.;
 RT "Calcium sensing receptor: molecular cloning in rat and localization
 RT to nerve terminals".
 RL Proc. Natl. Acad. Sci. U.S.A. 92:3161-3165(1995).
 CC -1- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF
 CC CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A
 CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL; U10354; AAC52149.1; -;
 CC EMBL; U20289; AAC52195.1; -;
 CC GCRDB; GCR_1449; -;
 CC PROSITE; PS00979; G-PROTEIN_RECP_F3_1; 1.
 CC PROSITE; PS00980; G-PROTEIN_RECP_F3_2; 1.
 CC PROSITE; PS00981; G-PROTEIN_RECP_F3_3; 1.
 CC PRAM; PR00003; 7tm_3; 1.
 CC PRAM; PF01094; ANF_receptor; 1.
 CC G-protein coupled receptor; Transmembrane; glycoprotein; signal.
 CC SIGNAL 1 19
 CC CHAIN 20 1079
 CC DOMAIN 20 612
 CC TRANSSEM 613 635
 CC TRANSSEM 638 649
 CC TRANSSEM 650 670
 CC TRANSSEM 671 681
 CC TRANSSEM 682 700
 CC TRANSSEM 701 724
 CC TRANSSEM 725 745
 CC TRANSSEM 746 769
 CC TRANSSEM 770 792
 CC TRANSSEM 793 805
 CC TRANSSEM 806 828
 CC TRANSSEM 829 836
 CC TRANSSEM 837 862
 CC TRANSSEM 863 1079
 CC CARBOHYD 90 90
 CC CARBOHYD 130 130
 CC CARBOHYD 261 261
 CC CARBOHYD 287 287
 CC CARBOHYD 386 386
 CC CARBOHYD 446 446
 CC CARBOHYD 468 468
 CC POTENTIAL.
 CC EXTRACELLULAR CALCIUM-SENSING RECEPTOR.
 CC EXTRACELLULAR (POTENTIAL).
 CC I (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC II (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC III (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC IV (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC V (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC VI (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC VII (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC POTENTIAL.
 CC POTENTIAL.
 CC POTENTIAL.
 CC POTENTIAL.
 CC POTENTIAL.
 CC POTENTIAL.

FT CARBOHYD 488 488 POTENTIAL.
 FT CARBOHYD 541 541 POTENTIAL.
 FT CARBOHYD 594 594 POTENTIAL.
 SQ SEQUENCE 1079 AA; 120867 MW; 34118BE9 CRC32;

Query Match 20.3%; Score 1285; DB 1; Length 1079;
 Best Local Similarity 31.6%; Pred. No. 6,74e-265;
 Matches 272; Conservative 232; Mismatches 285; Indels 73; Gaps 50;

Db 30 GDIIIGLGFPIHFG-VAAKDDLKSPESVECIIRYNGFRWLQAMIFAIIEINSSPLL 88
 QY 35 GDFLLAGLFSHGDCLOVHRPLVTSRDPDS--FNGHGYHLFOAMRFTVEINNSSL 92
 Db 89 PNMTLGYLFTCNTVSKALEATLSFVAQNKIDSLNDFECSCSHISTIIWVATQSG 148
 QY 93 PNITIGLYLVDCSSANVY-ATLKVLAQGRHIEIOK--DLRHHSSKVVAFFIPDNTD 149
 Db 149 VSTAVANLLGLFYIPQVSYASSSRLSNKNOYKSFRTIPNDHQATAMADIIIEFRNMW 208
 QY 150 HAVTTAALLGFLPLMPLVSEASSVYLSAKRKPSFLRTVPSDRHQVEVYVQLQSGFWW 209
 Db 209 VGTIADDDYGRPGIEKREAEEDIDISFELL--SOYSEEDIQOVVEYIONSTAKV 266
 QY 210 ISLIGSYDYGQLGVQAEELAVPRGICVAFEDIVFSAVGDPMQSMOHLAQARTTV 269
 Db 267 IVFSSGDPLEPLI-KEIYRNRITGRIMVLASAPMASSLIAMPEYFHVGGTIGFGLKAG 325
 QY 270 VVFSN-RHLARVFRSVYLANLTCKVAVASCDMA----IS-T-YITSYTG-IQ-GI--G 318
 Db 336 QIPGREFLQKVHPRKSVHNGFAKEWEETFNCHLOGAKGCPDPVDFVRSHEGGRNL 385
 QY 319 TVLG---VA-VQORQ-VP-GI-KEF-EESY---VR-AVTA-A-P-S-A-CPE--GSM-- 356
 Db 386 NSSIFRRLCTGDEINSEVETPYKMEHLRISYNYLAVYSIAHALODITYCLPRGFLT 445
 QY 337 -CSTN-Q-LCECHTFTTRNMTLGAFSMSAARYEYVAVAHGLHOL---L-CC--I 406
 Db 446 NGSCADIKKVAOYLKELRLHNTNNNGEOYFDECGDLVNGYSIIMWHSPEGSITVF 505
 QY 407 SEICS-RBPVYPMOLLQOYKVNFLH-ENYVAFDNGDTLGYIILAMDNGPE-WI-F 462
 Db 506 KEVGYNYVAKGERLFTNEKILMSGFSREVPFNSCRDCAQTRKGIIEGEPTCCFEC 565
 QY 463 EIIG--SA-SLSPVHLINKTKYIOHGNKNQVPSVCTDCLAGHRRVY--GSHHCCEC 518
 Db 566 VECPRGEISGETDASACKCPDDEFNSNHTSCIAKEIEFLMALTPEFGIALTLFVVLGIT 625
 QY 519 VPCEAGITLNMSELHICQPCGIEEWAPEKRESTICFPRIVEFLAMHEPISLVLIANTLILL 578
 Db 626 LTAFLVAGVFI-KFRNTPIVAKFNRELSTYLLLSLCCFSSSLF-FIGEPDMTCRLQPA 683
 QY 579 LTVGAGLFAHNFH-TPVYRSAGGRCLMLGSLVAG-SCSYFSFGEPTVPACLLRPL 636
 Db 684 FGISFVLICISILVKTNVLVFE--AKIPTSFHRKMWGLNLOFLVLCTFMOIICII 741
 QY 637 FSLGHAIFLSCLTIRHSFOLVIEFKSTKVPF-FYRTWQNHNAGLGVIVSSVHLLICT 695
 Db 742 WLYTAPPSYNNHLEDDITITTCHEGSLMAGSLIGTIC-LLAICCF--AFKSRKLP 799
 QY 696 WLVMVTPRIREYORFPHLVILECEVFN--SVGFLLAFTHNLLISITFVCSYLKELPE 753
 Db 800 NENEAKFTFEMLIFFIYVIFIPAYASTY-GKEVSAVEVIALLAASGLLACIFENNVY 858
 QY 754 NYNEKACTESLNLNFVWIAFFTM-ASIIQGSYLPVAVNLGLTLLSGSGFYLPKCY 812
 Db 859 IILFKPSRNTIEEVRSSATAHA 880
 QY 813 VILCRPELNTHEFOASIDQYT 834

RESULT 4
 ID MGRS_RAT STANDARD; PRT; 1203 AA.
 AC P31424;

DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.
 GN GRMS OR MGLUR5.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN:
 RX MEDLINE: 92317054.
 RA ABE T., SUGIHARA H., NAWA H., SHIGEMOTO R., MIZUNO N., NAKANISHI S.;
 RT "Molecular characterization of a novel metabotropic glutamate
 RT receptor mglur5 coupled to inositol phosphate/Ca2+ signal
 RT transduction.";
 RL J. Biol. Chem. 267:13361-13368(1992).
 RN [2]
 RP SEQUENCE OF 859-923 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE-BRAIN:
 RX MEDLINE: 93343913.
 RA MINAKAWA R., KATSUKI F., SUGIYAMA H.;
 RT "A variant of metabotropic glutamate receptor subtype 5: an
 RT evolutionally conserved insertion with no termination codon.";
 RL Biochem. Biophys. Res. Commun. 194:622-627(1993).
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
 CC CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
 CC CHLORIDE CURRENT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS: 5A (SHOWN HERE) AND 5B; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF
 CC 32 RESIDUES.
 CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN NEURONAL CELLS OF THE
 CC CENTRAL NERVOUS SYSTEM.
 CC -1- MISCELLANEOUS: ACTIVATED BY QUISQUALATE > GLUTAMATE > IBOTENATE >
 CC TRANS-1-AMINOCYCLOPENTYL-1,3-DICARBOXYLATE.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST, TO MGLUR1.
 CC -----
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 CC -----
 DR EXBL: D10891; NOT ANNOTATED_CDS.
 DR EMBL: S64315; AB27666.1; -.
 DR PIR: A42916; A42916.
 DR GCRDB: GCR_0444; -.
 DR GCRDB: GCR_0760; -.
 DR PROSITE: PS00979; G-PROTEIN_RECEPTOR_1; 1.
 DR PROSITE: PS00980; G-PROTEIN_RECEPTOR_2; 1.
 DR PROSITE: PS00981; G-PROTEIN_RECEPTOR_3; 1.
 DR PFMW: PF00003; 7tm_3; 1.
 DR PFMW: PF01094; ANF_receptor; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; signal;
 KW Multigene family; Alternative splicing.
 FT SIGNAL 1
 FT CHAIN 21 1203 METABOTROPIC GLUTAMATE RECEPTOR 5.
 FT DOMAIN 22 578
 FT DOMAIN 579 601
 FT DOMAIN 602 615
 FT DOMAIN 616 636
 FT DOMAIN 637 647
 FT DOMAIN 648 666
 FT DOMAIN 667 692
 FT DOMAIN 693 713
 FT DOMAIN 714 736
 FT TRANSMEM 737 758
 FT TRANSMEM 759 771
 FT DOMAIN 759 771
 FT CYTOPLASMIC (POTENTIAL).

FT	DOMAIN	638	548	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	649	667	III (POTENTIAL).
FT	DOMAIN	668	693	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	694	714	IV (POTENTIAL).
FT	DOMAIN	715	737	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	738	759	V (POTENTIAL).
FT	DOMAIN	760	772	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	773	795	VI (POTENTIAL).
FT	DOMAIN	796	801	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	802	827	VII (POTENTIAL).
FT	DOMAIN	828	1212	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	88	88	POTENTIAL.
FT	CARBOHYD	210	210	POTENTIAL.
FT	CARBOHYD	378	378	POTENTIAL.
FT	CARBOHYD	382	382	POTENTIAL.
FT	CARBOHYD	445	445	POTENTIAL.
FT	CARBOHYD	734	734	POTENTIAL.
FT	VASCPPLIC	877	908	MISSING (IN ISOFORM 5A).
EQ	SEQUENCE	1212	AA: 132468	MISSING; 16E81574 CRC32;

Query Match	13.78;	Score 870;	DB 1;	length 1212;
Best Local Similarity	27.68;	Pref. No. 1.25e-165;		
Matches	231;	Conservative	214;	Mismatches 326;
				Indels 65;
				Gaps 55;

[illegible]

ID	RESULT	6	STANDARD	PT	872	AA
DB	789	-VP-ITFGSNVKITTCFVS-LSATFALCMCPVKYIILAKPERNVRASATTS	840			
QY	776	FTMASIVGSLPAPNVNLAGLTJSSGGS-GY-FLPKRYVILLCRPELNTNTHFOAS	829			
AC	P31421					
DT	01-JUL-1993	(Rel. 26, Created)				
DT	01-JUL-1993	(Rel. 26, Last sequence update)				
DT	15-JUL-1999	(Rel. 38, Last annotation update)				
DE	METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR.					
GN	GRM2 OR MGLUR2.					
OS	Rattus norvegicus (Rat).					
OC	Eukaryota; Metazoa; Chordata; Cnemidota; Vertebrata; Mammalia;					
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
RC	SEQUENCE FROM N.A.					
RN	TISSUE=BRAIN.					
RX	MEDLINE: 92110002.					
RA	TANABE Y., YASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;					
RT	"A family of metabotropic glutamate receptors.";					
RL	Neuron 8:169-179(1992).					
CC	-1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS					
CC	MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLYL CYCLASE ACTIVITY.					
CC	MAY MEDIANTE SUPPRESSION OF NEUROTRANSMISSION OR MAY BE INVOLVED IN					
CC	SYNAPTOGENESIS OR SYNAPTIC STABILIZATION.					
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.					
CC	-1- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS AND PROMINENT					
CC	EXPRESSION IS SEEN IN GOLGI CELLS OF THE CEREBELLUM AND SOME					
CC	PARTICULAR NEURONAL CELLS IN OTHER BRAIN REGIONS.					
CC	-1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.					
CC	STRONGEST, TO MGLUR3.					
CC	-----					
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CC	or send an email to license@isb-sib.ch).					
CC	-----					
DR	EMBL: M92075. -1- NOT_ANNOTATED_CDS.					
DR	PIR: JH0561; J05551.					
DR	HSSP: P06612; IECL.					
DR	GCRDB: GCR_0361; -1-					
DR	PROSITE: PS00979; G_PROTEIN_RECP_F3_1; 1.					
DR	PROSITE: PS00980; G_PROTEIN_RECP_F3_2; 1.					
DR	PROSITE: PS00993; G_PROTEIN_RECP_F3_3; 1.					
DR	PFAM: PF00003; 7tm_3; 1.					
DR	PFAM: PF01094; ANF_receptor; 1.					
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;					
KW	Multigene family.					
FT	SIGNAL	1	18			
FT	CHAIN	19	872			
FT	DOMAIN	19	567			
FT	TRANSSEM	568	590			
FT	DOMAIN	591	604			
FT	TRANSSEM	605	625			
FT	DOMAIN	626	636			
FT	TRANSSEM	637	655			
FT	DOMAIN	656	679			
FT	TRANSSEM	680	700			
FT	DOMAIN	701	725			
FT	TRANSSEM	726	747			
FT	DOMAIN	748	760			
FT	TRANSSEM	761	783			
FT	DOMAIN	784	793			
FT	TRANSSEM	794	819			
FT	DOMAIN	820	872			
FT	METABOTROPIC GLUTAMATE RECEPTOR 2.					
FT	EXTRACELLULAR (POTENTIAL).					
FT	I (POTENTIAL).					
FT	CYTOPLASMIC (POTENTIAL).					
FT	II (POTENTIAL).					
FT	EXTRACELLULAR (POTENTIAL).					
FT	III (POTENTIAL).					
FT	CYTOPLASMIC (POTENTIAL).					
FT	IV (POTENTIAL).					
FT	EXTRACELLULAR (POTENTIAL).					
FT	V (POTENTIAL).					
FT	CYTOPLASMIC (POTENTIAL).					
FT	VI (POTENTIAL).					
FT	EXTRACELLULAR (POTENTIAL).					
FT	VII (POTENTIAL).					
FT	CYTOPLASMIC (POTENTIAL).					

Query Match 13.4%; Score 847; DB 1; Length 872;
 Best Local Similarity 26.6%; Pred. No. 3,436-160;
 Matches 227; Conservative 222; Mismatches 341; Indels 62; Gaps 51;

FT	CARBOHYD	203	203	POTENTIAL.
FT	CARBOHYD	286	286	POTENTIAL.
FT	CARBOHYD	338	338	POTENTIAL.
FT	CARBOHYD	402	402	POTENTIAL.
FT	CARBOHYD	547	547	POTENTIAL.
SO	SEQUENCE	872 AA;	95773 MW;	C3C34676 CRC32;

DB 4 LIGLALLLMG-AVASEPAKVLLEBDVLGGLFPHV---Q-KGSP-AEEGC-PVN-54
 9 LLS-LQVYCAAFSCORTESPGEFLPDPLAGLFLSHGGLVRRHPLVTSDDRPSF-67
 55 EHRGIORLEALFALDRNPRLPGVRLGAHLIDSKDTHLEQALDVPASLSGA-114
 68 NGHGYLFOARKRTVEELINNSALUPITLGYELDYCESANVYA-TL--RV-LA--L-120
 115 DGRHICPDGSYATHSDAPAVTGVIGGSYSVSIQVNLRLPQIPQISYASTAKLSD-174
 121 QGRPHIEIQKDLRMS-S-KVYA-FIGPDNDHVTALLGPFIMPLVSEASSVLSA-177
 175 KSRDYIARYPPDFQAKAMAEILRFNWYVSTVASEGDTGTFAPFLARANNIC-234
 178 KRKPSFLRTVPSDRHOVEVVOLOSGFWISIGSYGQOLGQVQALEELAVPRGIC-237
 235 VATEKRG-RA-MSRAAFEGVVRALLOKPSARVAVLFRSDARELLAATQRLN-ASPFW-291
 238 VAFMDIYFPAKRVDPKRMQMOHLQART-VVAVFSNRHLARFERSVVLANTGKVM-296
 292 VASDGMGALSVASGERAEGAL-TIELASYPISDFASYPOSIDPNNNSHPFERWE-350
 297 VASDMDIASTVITVGTGIGTGLVAVQORVPGLKEFESY-VRAVTAAPSAC-P-353
 351 ERFCSERQ-RDCAASHLAVP-FEDSK-IMFYV-NAVYAMAHLNMRALCPNTH-405
 354 GSW-CSTNOLRECHTFTRMPTLGAESMAARYEAVALVAGHLQQL-G-C--TSE-408
 406 LCDAMRPNGRLKDFLANKFDAPFRADTDEVRDRGDIAGRINIFTYLRAGSGR-465
 409 IC-SRGFYVQQLAQ-IYKVN-L-LH-ENT---VAFDNGDITLGYDITLAMDNGPEW-460
 466 -YRY-QKGVYAEGLTDTSPFIPWASPSAGPLPASRSEPCLONEVKSQGEVOCWLCI-523
 461 TFEIIGSASLSBPHLDIKTKIQMHG-KNNOVPYSVCTDCLAGHRRVYVSHHOCCECV-519
 524 PCQYER-RLDEF-TCADCGIGY-PNASLTGCELPQETIRMGDAVGVTTIACIGAL-580
 520 PCEAGTFLNSELHICQPCGTEEMAPKES-TTCEPRIVEFLAMEPILSLVLIANTLILL-578
 581 ATLEVLGVFVHNATPYKASGREICYLLGGVFLCYCMTEVFETAKPSTAVCTLRIGL-640
 579 LLVOTAGLFAHNEFTPVKRSAGRLCEMLSLVAGSCSYSPFEGEPVPCLLRQPLS-638
 641 TAFSVCSALTCTNRJARING-GAREGA-ORPREISPAVOALCLALISQILLIVAML-698
 639 LGFAIFLSCULIRSFQVILFKFSKVTFTFRMAQNNGALLFVYS-STVHLLICLTLWL-697
 699 VVEAPGTGKETAPRREYVTLRCNHRDA-SMUGSLAVVLLIACLT-YAFTRKCPENF-756
 698 VMMPRPTREVORPH-LVILECTEVNSVGLAFTHNILL-SISTEVCYSLGKELPENY-755
 757 NEAFIGTWTTCIIMLAPIFYVNSSDYRVOITTCVSVSVGLCLAPAKLHI-816
 756 NEACVTFSLINLFVSWIAFTMASITOGSYLPAVNVLAGLTTISGGFS-GY-FLPKCYV-813
 DB 817 ILFOPKRVSH-828
 QY 814 ILCRPELNTEH-825

ID	MGR4_RAT	STANDARD;	PRT;	912 AA.
AC	P31423;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.			
GN	GRM4 OR MGLUR4.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISUE-BRAIN;			
RC	TISUE-BRAIN;			
RA	TANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;			
RT	"A family of metabotropic glutamate receptors."			
RL	Neuron 8:169-179(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISUE-BRAIN;			
RC	MEDLINE: 93332699.			
RA	O'HARA P.J., SHEPPARD P.O., THOGERSEN H., VENEZIA D., HALDEMAN B.A.;			
RT	"The ligand-binding domain in metabotropic glutamate receptors is related to bacterial periplasmic binding proteins."			
RL	Neuron 11:41-52(1993).			
CC	- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.			
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINANT EXPRESSION IS SEEN IN THE GRANULE CELLS OF THE CEREBELLUM.			
CC	- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS. STRONGEST, TO MGLUR6.			
CC	-----			
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CC	-----			
DR	EMBL: M92077; ; NOT ANNOTATED_CDS.			
DR	EMBL: M90518; AAA33190.1; ;			
DR	PIR: JH0563; JH0563.			
DR	GCRDB: GCR_0352; ;			
DR	GCRDB: GCR_0363; ;			
DR	PROSITE: PS00979; G_PROTEIN_RECP_F3_1; 1.			
DR	PROSITE: PS00980; G_PROTEIN_RECP_F3_2; 1.			
DR	PROSITE: PS00981; G_PROTEIN_RECP_F3_3; 1.			
DR	PFAM: PF00003; 7tm_3; 1.			
DR	PFAM: PF01094; ANF_receptor; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;			
KW	Multigene family.			
KW	STGNL	1	32	
FT	CHAIN	33	912	
FT	DOMAIN	33	587	
FT	TRANSSEM	588	610	
FT	DOMAIN	611	624	
FT	TRANSSEM	625	645	
FT	DOMAIN	646	656	
FT	TRANSSEM	657	675	
FT	DOMAIN	676	699	
FT	TRANSSEM	700	720	
FT	DOMAIN	721	750	
FT	TRANSSEM	751	772	
FT	DOMAIN	773	785	
FT	TRANSSEM	786	808	
FT	DOMAIN	809	821	
FT	TRANSSEM	822	847	
FT	DOMAIN	848	912	
FT	CARBOHYD	98	98	

POTENTIAL.
 METABOTROPIC GLUTAMATE RECEPTOR 4.
 EXTRACELLULAR (POTENTIAL).
 I (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 II (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 I (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 IV (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 V (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 VI (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 VII (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 POTENTIAL.

FT TRANSMEM 751 772 V (POTENTIAL).
 FT DOMAIN 773 785 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 786 808 VI (POTENTIAL).
 FT DOMAIN 809 821 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 822 847 VII (POTENTIAL).
 FT DOMAIN 848 912 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 98 98 POTENTIAL.
 FT CARBOHYD 301 301 POTENTIAL.
 FT CARBOHYD 454 454 POTENTIAL.
 FT CARBOHYD 484 484 POTENTIAL.
 FT CARBOHYD 569 569 POTENTIAL.
 SQ SEQUENCE 912 AA: 101867 MW: 740D9054 CRC32;

Query Match 13.28; Score 837; DB 1; Length 912;
 Best Local Similarity 26.5%; Pred. No. 7.84e-158;
 Matches 211; Conservative 222; Mismatches 300; Indels 63; Gaps 50;

75 GHRLEAMLEALRINNDPDLNLTGARIIDTSCRDHALBOSLTFVQALIEKDTEV 134
 71 GYLLFQAMRTVEINSSALPNITLIGELYDVCESANVA-TLR-VLAL-Q-GP-- 123
 135 RCGSGPPITTKPERVYVAGSGSSVIMVANIILRFKIPQISYASTADLSNRYDF 194
 124 RHEIOLKDRNHSKVAEFGPNDTHAVTALLGPFLMPLVSYASSVYSAKRKPS 183
 195 FSRVPSDYYQAMVDIYALKANVSTVASEGSGESGEAEATQKSRDEGVCAOSV 254
 184 FLRTVPSDHQVEVMYVOLLQSGFWWISLIGSYGDYQGLQVQALBELAVPRG-ICVAFND 242
 255 KIPREKAGE--FDKILRLLETSNARAVIIPANEDIRVLEAARANQGHFPMGSD 312
 243 IVPFSARVDDPRMSMQLAQART-VVVFSSNHLAVFRSYVALNLGKV-WVASE 300
 313 SWG-SK-IAPVHLBEVANG-AVTLLPKRMS-VRGFDRTYSSRTLDNNRNITWEAEFED 368
 301 DVAISTYITVYVIGIGIVGVAAYOORVPGIKKEFEESYV-RAVTAAPSAC--PE--G 354
 369 NFHCLSRHALKKGSHVKCTNRERIGODSAEKGXQVYIDAYANGHALHMHRLC 428
 355 SW-CS-TNG-LORECHT--FTTRNPTL-GAFMSAAYR-YEAVYAAHGHOLL-G-C 405
 429 PGRVGLCPMDVDGTOLIKYIRANVFSGIAGNPVTENENGADAPRYDIYQOLRNSA- 487
 406 TSEI--CSR-GRVYPMQLQIQYKVNFL-LHNTVAFDNDNTLGYDILMD-WNGPEW 460
 488 EYKVGSWT-DHLHLRIER--MHWPSSGOQPRISCSLPQCPGERRKTVKGMPCWCEP 544
 461 TFEITGSASLSBVLHDIKTKTIQMHGKNNOVSVCTTDCLAGHRRVYVSGHCCFECVP 520
 545 C-TG-YOYVDRYCTCKCPYDMRPTENTGCRPIPIIKLEWSPMAVLPFLAVVGIAT 602
 521 CEAGTFLMSELHICOPCGTEEMAPKRESTICFPTVEFLMHNP-ISLVL-IAANTLLL 578
 603 LEVYIT--FVAYNDTPYKASGRELSYVLGIFLCATTFFLMAEDLGTCSLRITLG 660
 579 LVTAGTGAFAHHTPVVRSAGRLCLMLGSLVAGSSFEFGEPVPAICLLRQLFS 638
 661 LGMISYAAALTKTNRIYRIFEGOKRSASAPRISPAQSALITSLSS--LQLLGIV-W 717
 639 LGFALIFSLCLIRSFQVLIIFKESTKPTPYR-TWAONHGGGLFVIVSVTHLL-ICLLW 696
 718 FVYDPSISVVDQDRTLDPRFARGVLC-DISDLSLCLIGYSMLMTCTVYAIKTRG 776
 697 LVMTPTPTREYQ--R-F-PHLV--ILECTEVNSVGLLAFTHNILLISTEFCSTYIGKE 750
 777 VPENENAKRIGETMYTTCIWMALFIPFGTSSADKLYIQTTLTVSVSLASVSLG 836
 751 LPEYVNAKCVTSLINFSWIAFTMA-SIYQGSY-L-PAVNVLAGLTLLSGGS-G- 805
 837 LYMKYVILLFHEON 852
 806 YFLPKCVIILCREPN 821

RESULT 9
 ID MGR1_RAT STANDARD; PRT: 1199 AA.
 AC P23385;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 1 PRECURSOR.
 GN GRI1 OR MGLR1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPAGUE-DAWLEY; TISSUE-BRAIN;
 RX MEDLINE; 91156047.
 RA MASU M., TANABE Y., TSUCHIDA K., SHIGEMOTO R., NAKANISHI S.;
 RT "Sequence and expression of a metabotropic glutamate receptor.";
 RL Nature 349:760-765(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 92022526.
 RA HOUAMAD K.M., KUIJPER J.L., GILBERT T.L., HALDEMAN B.A., O'HARA P.J.,
 RT MDLVIRHIL E.R., ALMERS W., HAGEN P.S.;
 RL "Cloning, expression, and gene structure of a G protein-coupled
 glutamate receptor from rat brain.";
 RL Science 252:1318-1321(1991).
 RN [3]
 RP ALTERNATIVE SPLICING (1B).
 RC TISSUE-BRAIN;
 RX MEDLINE; 92110002.
 RA TANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;
 RT "A family of metabotropic glutamate receptors.";
 RL Neuron 8:169-179(1992).
 RN [4]
 RP ALTERNATIVE SPLICING (1C).
 RC TISSUE-BRAIN;
 RX MEDLINE; 93066232.
 RA PIN J.-P., WAEBER C., PREZENTU L., BOCKAERT J., HEINEMANN S.F.;
 RT "Alternative splicing generates metabotropic glutamate receptors
 inducing different patterns of calcium release in Xenopus oocytes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10331-10335(1992).
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
 MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
 CALCIUM SECOND MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL
 ACTION OF GLUTAMATE IN THE CNS, SUCH AS LONG-TERM POTENTIATION IN
 THE HIPPOCAMPUS AND LONG-TERM DEPRESSION IN THE CEREBELLUM.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ARE PRODUCED BY ALTERNATIVE SPLICING. 1B AND 1C ARE C-TERMINALLY
 TRUNCATED FORMS OF 1A.
 CC -1- TISSUE SPECIFICITY: IS PREDOMINANTLY EXPRESSED IN CEREBELLAR
 PURKINJE CELLS, CA2-CA3 PYRAMIDAL CELLS OF THE HIPPOCAMPUS, AND
 MITRAL AND TUFTED CELLS OF THE OLFACTORY BULB.
 CC -1- MISCELLANEOUS: ACTIVATED BY QUISOULATE > GLUTAMATE > IBOTENATE >
 TRANS-1-AMINOCYCLOPENTYL-1,3-DICARBOXYLATE; INHIBITED BY
 2-AMINO-3-PHOSPHONOPROPIONATE.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST, TO MGLR5.
 CC
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 CC
 CC EMBL; X57569; CAA40799.1; -
 CC DR EMBL; M61099; AAA19497.1; -
 CC DR EMBL; S48085; AAB24138.1; -
 CC PIR; S15362; S15362.

GCRDB: GCR_1983; -
 DR PROSITE: PS00979; G_PROTEIN_RECP_F3_1; 1.
 DR PROSITE: PS00980; G_PROTEIN_RECP_F3_2; 1.
 DR PROSITE: PS00981; G_PROTEIN_RECP_F3_3; 1.
 DR PFAM: PF00003; 7tm_3; 1.
 DR PFAM: PF01094; ANF_receptor; 1.
 KW G-protein coupled receptor; Transmembrane; glycoprotein; signal;
 MultiGene family: Alternative splicing.
 FT SIGNAL 1 18
 FT CHAIN 19 1194
 FT DOMAIN 19 592
 FT TRANSMEM 593 615
 FT DOMAIN 616 629
 FT TRANSMEM 630 650
 FT DOMAIN 651 661
 FT TRANSMEM 662 680
 FT DOMAIN 681 706
 FT TRANSMEM 707 727
 FT DOMAIN 728 750
 FT TRANSMEM 751 772
 FT DOMAIN 773 785
 FT TRANSMEM 786 808
 FT DOMAIN 809 814
 FT TRANSMEM 815 840
 FT DOMAIN 841 1194
 FT DOMAIN 1014 1035
 FT DOMAIN 1067 1081
 FT DOMAIN 1095 1130
 FT DOMAIN 1142 1194
 FT CARBOHYD 98 98
 FT CARBOHYD 223 223
 FT CARBOHYD 397 397
 FT CARBOHYD 515 515
 FT VARSPLIC 887 906
 FT VARSPLIC 907 1194
 FT VARSPLIC 887 906
 FT CONFLICT 593 593
 FT SEQUENCE 1194 AA; 132376 MW; 6ACDFEC3 CRC32;
 Query Match 12.8%; Score 812; DB 1; Length 1194;
 Best Local Similarity 26.6%; Pred. No. 6,10e-152;
 Matches 211; Conservative 210; Mismatches 315; Indels 56; Gaps 48;
 Db 80 EAMFHLIDINADPVLPTLLCSFIRDSQWHSVALEDSIFRISLSIRKQGINR 139
 QY 76 QAMRFIVEINSSALLPNTLTGLVYDVCESA-VNY-AT-LR-VL-ALQPRH-IE- 127
 Db 140 CLPDGSLPPGRTKRPVAGVIGPSSSVAIOVNLQLPDIPOIAYSATSIDSKTLTK 199
 QY 128 -I-Q-KDLR-NHSSKYVA-FIGPDNDHATVTAALLQPLFLVSTFASVVSARKEP 182
 Db 200 YELRVVPSDTLQARALDIVKRYNMTVSAVHTEGNYESGMDAFKELAAQEGCIAHSD 259
 QY 183 SEFLRTVPSRHQVEVAVQLQSEGMWVWISLIGSYGQGLQVQALBELAVPRGICVAFKD 242
 Db 260 KTYSN-AEKSVDRLKIRKIRLPKARYVVCCEGMIVAGLSAKRRGLGVSEFLIGS 317
 QY 243 IYFESRVADDPWQSMQOH-AQ-ARTTVVYVSNRHLAVFRSVYLANLTLSKV-VAS 299
 Db 318 DGMADDEVIEGVEVANGCI-TIKLOSPEVRFDDYFLK-LRLDNTNRPMFPE-FWQH 374
 QY 300 EDMAISTYITSTGIGTIGLVANVQOQRPVPLKFEFEYVAVAYTAAPSA-CPESSWCS 358
 Db 375 RFO-CRLPGHLENPFRKICTGNESLEENYVODSKMGVINAIVAMHGLQNMHHALCP 433
 QY 359 TIVOLCR-ECHITFTTR-MPT-LGAFMSAAV---RV-Y--EAVYVAHGLHQLL-G-CT 406
 Db 434 GHVGLCDAAKPIDGSKLLDFLTKSSFIVSGEVEWDEKGDAGRDIMKLQTEANR-Y 492
 QY 407 SEI--C-SRGPVYPMWLQOQIVKVNFL-LHENTVAFDNDGTLGYDIDIAMWNGGEWTF 462

Db 493 DYVHGTWHEGVLNIDYKIQ--YKSGVVR-SVCESEPCIKQIKVIRKGEVSCQWICAC 550
 QY 463 EILGSSLSYVHDIDIKTIQIMQKXNQVPSVCTICDLAGHRRVYV-GSHHCCEPCVPC 521
 Db 551 KENEIVQ-DEF-TCKACDILGMWPNADLTGCEPIPVARYLEMSNIEPIAIAVSCGLIVTL 608
 QY 522 EAGTFLNMSLHICQPCGEEMAPRKESTICFPRTVEFLAMHEBISILVIANITLLILLV 581
 Db 609 FVTLIVLVRDPPVYKSSSRELCTIILAGIFLGYVCF-TLAKPTTSCYIQRLVGLS 667
 QY 582 GTGLAMHHPVYVSAAGRLCFLVGLSVAG-SCSEYVSFEPEVPVACILKQPLFSIG 640
 Db 668 SAMCYALVTKTRIRAIAGSKKICTRKPMSAMAQVIAIISILVQLFTVLILIM 727
 QY 641 FAFVLSCLLIRSQVLIIRKFSK-VPTFYRMAQNHGAGLEVYVSTVHLICLTLWVM 699
 Db 728 EPPMPLSPSIKE-VYLIC-NTSNGVAVAPLGYNGLIMSCY-YAEFTRVPAVFEN 784
 QY 700 WTRPRTREVQRFPHVILCTEYVNSVGFLLAEFTN-LLSIS-TFVCSYLKELPENYND 758
 Db 785 KYIAFTMYTCIIMAF--VP-IYFSNKKIITTCVAVSLSVYALGCMFTPMYIILK 841
 QY 759 KCVTSLLINFSWIAEFTMASLYQGS-YLZAVNVLAGJTLUSGFSGYFLPCYVILCR 817
 Db 842 PERNVSAFTTS 853
 QY 818 PELNTEHFOAS 829

RESULT 12
 ID MGR3_HUMAN STANDARD; PRT: 877 AA.
 AC Q14832;
 DT 01-NOV-1997 (rel. 35, Created)
 DT 01-NOV-1997 (rel. 35, Last sequence update)
 DT 01-NOV-1997 (rel. 35, Last annotation update)
 GN METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR.
 GN GRM3 OR MGLUR3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE: 96437205.
 RA MAKOFF A., VOLPE F., LELCHUK R., HARRINGTON K., EYSON P.;
 RT "Molecular characterization and localization of human metabotropic
 RL glutamate receptor type 3.";
 RL Brain Res. Mol. Brain Res. 40:55-63(1996).
 CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
 CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
 CC ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST, TO MGLUR2.
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: X77748; CAAS4796.1; -.
 DR GCRDB: GCR_2070; -.
 DR MIM: 601115; -.
 DR PROSITE: PS00979; G_PROTEIN_RECP_F3_1; 1.
 DR PROSITE: PS00980; G_PROTEIN_RECP_F3_2; 1.
 DR PROSITE: PS00981; G_PROTEIN_RECP_F3_3; 1.
 DR PFAM: PF00003; 7tm_3; 1.
 DR PFAM: PF01094; ANF_receptor; 1.
 KW G-protein coupled receptor; Transmembrane; glycoprotein; signal;
 MultiGene family.

FT	DOMAIN	844	908	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	95		POTENTIAL.
FT	CARBOHYD	298		POTENTIAL.
FT	CARBOHYD	452		POTENTIAL.
FT	CARBOHYD	480		POTENTIAL.
FT	CARBOHYD	565		POTENTIAL.
50	SEQUENCE	908 AA:	101866 MM:	5043FFB1 CRC32:

Query Match	12.7%;	Score 808;	DB 1;	Length 908;
Best Local Similarity	25.3%;	Pred. No. 5.33e-151;		
Matches	201;	Conservative	228;	Mismatches 305;
			Indels	60;
			Gaps	49

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Db 72 GIREAMLVAMIDQINPKRBDLNTLGLRILDDCSPTALLESOSTVQALIEKDA5D 131
OY 71 GYHLEAARFVEEELNNSSALLPITLLELYDVS--ESANYAYLR-VLW-Q-GPHI 126
Db 132 KCANDPEIFTRPKDISCVIGAA5SVSIVMANILRLKRIQI5YASTAPELSDNTRDF 191
OY 127 EIQR-D--LRNHSKVVAFIGPNDTHAVITLALGLPLMLPEVSEASVYLSAKRKPS 183
Db 132 FSRVYPPSYQAQAVDLYTALGNVYSTLASSENGISGVEAFQIRLETIGVCIAOQ 251
OY 184 FLRIYPSRHOVEVYVOLLQSGFWWIELISGYQGLQVQALELVPVPG-ICVAKED 242
Db 252 KIPREPRGE--FEKIKRLETPARAVIPEANDDJRRILEAAKKNOSGHFIMIGD 309
OY 243 IYFESARQDPRMOSMOHLQART-VVYVFSNHLARVFRSVYLANLTGK-VWVASE 300
Db 310 SWG-SK-IAPVYQOEIEAG-AVTLPRK-ASIDGDFRYFSRSLANRRWVAFEM-E 364
OY 301 DWAISTYITVTLGIGITVLGVAQOQVRGPKLEFESEY-VRAVTAAPSAC-PEGSWCS 358
Db 365 ENFGCKLSHGKRNHIIKCTGLEFIADSSVEQCGKQVQYIDAVYSAVYALHNNHKRC 424
OY 359 TNOQLR-ECH-TFTTR-WMPT-LGAFSSAAV---RV-Y--EAAYVAHOLHOLL-G-C 405
Db 425 PGYIGLCPRMWTIDGKELLYGIRAVENGSAGTPVTENGDAPGRYDIFOQIYNKSTE 484
OY 406 TSEI--GCR-GVYRWOLLQDIYKNFLLHENT-VAFDNDGDTLCYDIIAMDANGPEWT 461
Db 485 YKIGHMT-NOIHLKVED--MOMANREHTHPASVCSLPCKRGERRKTVKGVPCWHCERC 541
OY 462 FEIISASLSPVHLINIKTKIOWHGKKNQVSVCTTCLLGNHRVWVSGHCCFEQVPC 521
Db 542 EGYNV-QVDELS-CELCGLDORPNINRRCQRIPIKLEWSPMAUVVFAIIGIANT 599
OY 522 EAGTILNSELHIQCPQCTEEMAKREKSTCPPRVTEFLAMEHPSILVLIANTLLELV 581
Db 600 FVIVFVRVNDPIYRASGRELSVYLLGIFLCSYITFL-MIAAPDTICSFRRFIELG 658
OY 582 GJAGLFAMHFIHVVRASAGRCFLML-GSLVAGSCSYSPFGDETPYACLLRPLSELG 640
Db 659 MCFSTALLTNRHRIFFEOGKKSVA-PKFI-SPASOLVITSLSIVOLLGVFWFV 715
OY 641 FAIFLSCLTIRSFOLVILIFESTKVPYRTWAOHNGGLEVIYS-STVHLLICITLWYM 699
Db 717 DPHHTIIDYGBORTDPENAGVUKC-DISDLSLCSGSLMLVCTVYAKIRGPE 775
OY 700 WTPRRTREY--OR-F-P-HL-VILECTVNSVGFLLATHNHLISITFVCSYICKELPE 753
Db 776 TENEAKPIGTYTITCIILMAFIPFIFFGTAQSAEKMYIQTITLTVSMS-LSASVSLGLY 834
OY 754 NYNEAKCYFESLLNFVSWIAFTWA-STYOGS--YLPANVLAGLTLGSGFS-G-YF 807
Db 835 MPKYVILIFHPQN 848
OY 808 LPKCYVILCRPELN 821

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RESULT	14		
ID	MGR8_MOUSE	STANDARD;	PRT; 908 AA.
AC	P47743;		
DT	01-FEB-1996	(Rel. 33, Created)	

DT	01-FEB-1996 (Rel. 33, last sequence update)
DT	15-JUL-1998 (Rel. 36, last annotation update)
DE	METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
GN	GPR8 OR MGLUR8.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
CC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6; TISSUE=RETINA;
RX	MEDLINE: 95293344.
RA	DVOJISIN R.M.; ZHANG C.; RAMONEIL K.;
RT	"A novel metabotropic glutamate receptor expressed in the retina and olfactory bulb."
RL	J. Neurosci. 15:3075-3083(1995).
CC	-1 FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.
CC	-1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC	-1 TISSUE SPECIFICITY: STRONGLY EXPRESSED IN OLFACTORY BULB, ACCESSORY OLFACTORY BULB, AND MMILLARY BODY. WEAKER EXPRESSION IN THE RETINA, AND IN SCATTERED CELLS IN THE CORTEX AND HINDRAIN.
CC	-1 SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; U17252; AAA68149.1; ..
DR	GCRDB; GCR_1172; ..
DR	MGI; MGI:109500; GRM9.
DR	PROSITE; PS00979; G_PROTEIN_RECPE_F3_1; 1.
DR	PROSITE; PS00980; G_PROTEIN_RECPE_F3_2; 1.
DR	PROSITE; PS00981; G_PROTEIN_RECPE_F3_3; 1.
DR	Pfam; PF00003; 7tm_3; 1.
DR	Pfam; PF01094; ANF_receptor; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW	Multigene family; Olfaction.
FT	SIGNAL
FT	1
FT	33
FT	CHAIN
FT	34
FT	583
FT	DOMAIN
FT	584
FT	608
FT	TRANSMMEM
FT	609
FT	620
FT	DOMAIN
FT	621
FT	TRANSMEM
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FT	647
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FT	818
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FT	908
FT	CARBOHYD
FT	95
FT	95
FT	CARBOHYD
FT	298
FT	CARBOHYD
FT	452
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FT	480
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FT	565
FT	565
FT	POTENTIAL.
QO	SEQUENCE
QO	908 AA; 101413 MW; 255B10EF CRC32;

	Query March	12.7%	Score 806;	DB 1; length 908;
	Best Local Similarity	25.2%;	Pred. No. 1,57e-150;	
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Dd	32 HSQYAHSHRIDGDIILGGFVPHA--KG-ERG-V-PCG-DLKKRGIHLEAMLYAI	83		
	: :			
yy	23 QRTSESPFSAPPGGFLAGLSFGDGLCVNHRPLVSCRPDSFNQGHILPFAMFTY	82		

QY 71 GYHLFOAMRFVEEINNSSALLPNITIGELYDVCS-ESANYATLR-VLAL-Q-GPRHI 126
DB 132 KCANGDPPIFKDKISGVIGAAASSVIMVANILRLEFKIPOISYASTAPELSDNTRYDE 191
QY 127 EIOK-D-LRNHSSKVAFAFGPNDTHAVTIALLPFLMPLVSYEASSVYLSAKRRFPS 183
DB 192 FSHVPPDSYOAQAMVDIYALGMYSTLASENGYSGEVEAFQISREIGVCIAQSQ 251
QY 184 FLRTVPSDRHQVEVMVQLQSFQWIMSLIGSYDYGQGLCVQALELAVPRG-ICVAFKD 242
DB 252 KIPREPRGE--FEKIKRLETPNARAVIMFANEDDIRILEAKKLNQSGHFLWIGSD 309
QY 243 IVPFSARVGDPRQSMOHLAQART-VVVVFSNRHLARFFERSVLANLTKR-VWVASE 300
DB 310 SMC-SK-IAPVYQOEIEIAG-AVTILPKR-ASIDGDRYFRSRTLANNRRNWFAEFW-E 364
QY 301 DMAISTYITSVIGIQIGIVLGAVOOROVPGIKEFEEST-VAAYTAAPSAC-PEGSWCS 358
DB 365 ENFGCKLGSRGKRNHKKCTGLERIARDSYEOEGKVOFVIDAVYSMAAYALHMHKDLQ 424
QY 359 TQOLCR-ECH-TETTR-NMPT-LGAFSMAAY---RV-Y--EAYAVAHGLHQLL-G-C 405
DB 425 PGYIGLCPKMSITDCKELLGYIAVNFNGSAGTPVTFNENGDAFGXYDIPQOITNKSTE 484
QY 406 TSEI--CSR-GPYPMOLLQOIKVNFLEHNT-VAFDNGDITLGYDIIAMDMNGPEWT 461
DB 485 YKVIQWMT-NOLHAKVED--MOMAHREHTHPASVCSLPCPKGERKKTGVGPCMHCERC 541
QY 462 FELIGSASLSPVHLINKTKIOMHGKNNOPVSVCTTDLAGHHRVYVGSHHCCFECVPC 521
DB 542 EGVNY-QVDELS-CELCPLDORPNMNRGCOLPIIKLEHSPWAVVPVFAILGIAT 599
QY 522 EAGTEFLNSELHICQPCGHEMAPKRESTICFPRTVEFLAMHEPISLVLIANTLILLLV 581
DB 600 FYIVTVRINDPIVASGRELSTVLLGFLCYSTFL-MIAPDTIICSEFRVFLG 658
QY 582 GTAGLEFAMHFTPVVASAGRLCFML-GSLVAGSCSFYSFGEPTVPACLLRQPLFSIG 640
DB 659 MCFSAALLTKTNRHRIFEQKKSVTA-PKEI-SPASQVITFSLISVOLGVEFWFVY 716
QY 641 FAIFLSCLTIRSFQVLIIFKFSKVPFTFRIMQONHAGLFVIVS-STVHLILCLTLWLVN 699
DB 717 DPPHIIIDYGEORTLDPKARGVLC-DISDLSLCSLGSILMAYCTVYANKTRGVPE 775
QY 700 WTPRPTREY--QR-F-PHLY--ILECTEVNSVGFLAFTHNILLSTFVCSYLKELPE 753
DB 776 TENEAPITGFTMYTTCIIMLAFIPFFGTAQSAEKMYIOTTLTVSKS--LSASVSLGMLY 834
QY 754 NYNEACVTFESLILNFVSWIAFFTMA-SIYOGS--YLPVAVNLAGITLISGGSF-G-YF 807
DB 835 MPKVYIIIFHPDON 848
QY 808 LPRCIVILCRPELN 821

Search completed: Fri Mar 17 13:05:03 2000
Job time : 105 secs.

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Utters

50
50

2

149

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209

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325

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QY 319 TVLG---VA-VQORQ-VP-GL-KEF-EESY---VR-AVTAA-P--S--ACPEG-SW-C 357
Db NSPTAFRLCGEENISSEVTPYMDYTHLRISYNYVLAVYSIAHALODIYICPGRLFT 446
QY 358 -S-IN-Q-LCBECHFTTRNPTLGAFSMAIYRYEAVYAHGLDGLGCTG--I-- 409
Db 447 NGSCADIKKVEAMOVLAHLRLNFTSNMGEQVTEDECDLGNYSIIMHLSPEDGSIVF 506
QY 410 --CS-RGPVYPMQLDQIYKYNFLH-ENTVAFDDNDGDTLGYDIIAMDMNGPE-WT-F 462
Db 507 KEVGYINYAKGGERLFINDEKILMSGFSREVPSCSRDCLAGTRKGIIEGPTCCFEC 566
QY 463 EITG--SA-SLSPVHLIDNKTIRIOMHGKNNQVPSVCTDCLAGHRRVY--GSHHCPEC 518
Db 567 VECPDGEYSDETDASACDCKPDDEFSNMNHTSCIAKEIEFLSWTEPFGIALTLFAVLGIF 626
QY 519 VPCEAGTFLNMSLHICPCGTEEMARKESTTCPRVYEFLAMEHPISLVLIANTLLL 578
Db 627 LTAFLVLGVFI-KFRNTPIVKATNRELSTYLLFSLCCFSSSLF-FIGEPDWTCLRLQPA 684
QY 579 LTVGAGLGFAMHFI-TPVRSAGRLCFMLGSLVAG-SCSFYSFSGEPYPAQLRLQPL 636
Db 685 FGISFVLCISCIIVKTNVLLVEF--AKIPTSFHRKMGMLNQLFLVFLCTPMQIVICAI 742
QY 637 FSLGFAIFLSCLTIRSFQVLIIFKFSYKVPF-FYRTWAQNHGAGLFVIVSSVHLILCLT 695
Db 743 WLNTAPSESYNNHELEDFITFHEGSLMALGLIGYTC-LLAICEFF-AFKSRKLE 800
QY 696 WLWMTPTPEYQRFPLVILIECEVN--SVGLIATHTNHLISITFVCSYLCKEPE 753
Db 801 NFNEAKFTFSMLFFIYVWISFIPAYASTY-GKEVSAVEVIAIILASGLLACIFENKY 859
QY 754 NYNEAKCVTFSLNLFVSWIAFETW-ASLYOGSYLPAVNVLAGLTLTSGSGYFLPCY 812
Db 860 IILFKPSKNTIE 871
QY 813 VILCRPELNTE 824

RESULT 2
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ORGANISM Homo sapiens #common_name man
DATE 16-Feb-1995 #sequence_revision 12-May-1995 #text_change
ACCESSIONS S49341; A49419; B49419; C49419
REFERENCE S49341
#authors Pearce, S.H.S.; Thakker, R.V.
#submission submitted to the EMBL Data Library, August 1994
#accession S49341
#status preliminary
#molecule_type DNA
#residues 1-1078 #label PEA
#cross-references EMBL:X81086
REFERENCE A49419
#authors Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levl, T.; Seidman, C.E.; Seidman, J.G.
#journal Cell (1993) 75:1297-1303
#title Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalcemic hypercalcemia and neonatal severe hyperparathyroidism.
#cross-references MUID:94094324
#accession A49419
#status preliminary
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#residues 178-180, 'K', 182-192 #label POL
#experimental_source family N
#note sequence inconsistent with nucleotide translation
#note sequence modified after extraction from NCBI backbone
#note 186-Arg mutation is associated with familial hypocalcemic hypercalcemia and neonatal severe hyperparathyroidism
#note sequence extracted from NCBI backbone (NCBIN:142453)

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#accession B49419
#status preliminary
#molecule_type DNA
#residues 289-303 #label P02
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#note sequence modified after extraction from NCBI backbone
#note 298-Lys mutation is associated with familial hypocalcemic hypercalcemia and neonatal severe hyperparathyroidism
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#accession C49419
#status preliminary
#molecule_type DNA
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#experimental_source family J
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#note sequence extracted from NCBI backbone (NCBIN:142457)
SUMMARY ##note
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Query Match 20.4%; Score 1293; DB 2; Length 1078;
Best Local Similarity 32.0%; Pred. No. 1,51e-225;
Matches 273; Conservative 230; Mismatches 276; Indels 73; Gaps 49;

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Db 89 PNLLIGRIEPTCTVSKALEATLSFYAONKIDSLNDEFNCSEHISTAVVAGATGSG 148
QY 93 PNILGRIELDVCSANVY-ATLRVALAQPRRIEIQK--DLRNHSSKYVAFIGPNTD 149
Db 149 VSTAVANLGLFPIYQVSYSSSRLLSNKNOFGLTIPRDEHQATAMADIIYFPMW 208
QY 150 HAVTTAALLGFLMPLIVSYEASVYLSAKRKFPEFLTRVPSDRQVEMVOLLQSPFW 209
Db 209 VGTIAADDYGRPGIEKFEAREBERDICIPESELI--SQYSDEEIOHVVEIIONSRKY 266
QY 210 ISLIGSGDVGQLCVQLEELAVPRGICVAFKDIYPSARVAGDRMOSMQLAQATTV 269
Db 267 IVFSSGPDLLEPLI-KEIVRNITGKIWLASEAWASSLIAMPQYFHVGGTIGFALKAG 325
QY 270 VVVESEN-RHLARVFRSVLVANLUGKVMASDEDA----IS-T-YIISVIG-ID-GI- 318
Db 326 QIPGFREFLKVHRKSVHNGFAKEWETPNCHLQGAGPLDVTFTLGHESGDRFS 385
QY 319 TVLG---VA-VQORQ-VP-GL-KEF-EESY---VR-AVTAA-P--S--ACPE-GSM-- 356
Db 386 NSTAFRLCTGDENISSEVTPYDTHLRISYNYVLAVYSIAHALODIYICPGRLFT 445
QY 357 -CSIN-Q-LCBECHFTTRNPTLGAFSMAIYRYEAVYAHGLDGLGCTG--I-- 406
Db 446 NGSCADIKKVEAMOVLAHLRLNFTSNMGEQVTEDECDLGNYSIIMHLSPEDGSIVF 505
QY 407 SEIS-RGPVYPMQLDQIYKYNFLH-ENTVAFDDNDGDTLGYDIIAMDMNGPE-WT-F 462
Db 506 KEVGYINYAKGGERLFINDEKILMSGFSREVPSCSRDCLAGTRKGIIEGPTCCFEC 565
QY 463 EITG--SA-SLSPVHLIDNKTIRIOMHGKNNQVPSVCTDCLAGHRRVY--GSHHCPEC 518
Db 566 VECPDGEYSDETDASACDCKPDDEFSNMNHTSCIAKEIEFLSWTEPFGIALTLFAVLGIF 625
QY 519 VPCEAGTFLNMSLHICPCGTEEMARKESTTCPRVYEFLAMEHPISLVLIANTLLL 578
Db 626 LTAFLVLGVFI-KFRNTPIVKATNRELSTYLLFSLCCFSSSLF-FIGEPDWTCLRLQPA 683
QY 579 LTVGAGLGFAMHFI-TPVRSAGRLCFMLGSLVAG-SCSFYSFSGEPYPAQLRLQPL 636
Db 684 FGISFVLCISCIIVKTNVLLVEF--AKIPTSFHRKMGMLNQLFLVFLCTPMQIVICAI 741
QY 637 FSLGFAIFLSCLTIRSFQVLIIFKFSYKVPF-FYRTWAQNHGAGLFVIVSSVHLILCLT 695

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DB	742	WYTPAPSSYNOELEDJIIITTCHEGSLMGLIYTC-LLAICOFF-ARKSKLE	799
QY	666	WLYMPTPTPRYQYQFPHLVILECTEVN--SVGLLAFTHNILLISTFPCSYGLKEDE	753
Db	800	NENAEKFTFSKLIFFIWMISFIPAVASTY-GKFSVAEVEIALIILASFGIACIFPNKTY	858
QY	754	NNNEAKCTFELLNFVSMIAFFIM-ASIVGSLPLAVNNVLGITLISGFSOFCYLPKCY	812
Db	859	ILFKFSKRNTE 870	
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ORGANISM	#formal_name Homo sapiens #common_name man		
DATE	19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-1999		
ACCESSIONS	A56715		
REFERENCE	A56715		
authors	Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.		
#journal	Brown, E.M.; Hebert, S.C.; Nemeth, E.F.; Fuller, F.		
#title	J. Biol. Chem. (1995) 270:12919-12925		
#cross-references	Molecular cloning and functional expression of human parathyroid calcium receptor cDNAs.		
#accession	M0UD:95279439		
#status	preliminary		
#molecule_type	mRNA		
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Best Local Similarity	32.0%; Pred. No. 6,16e-225;		
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QY	35	GDPLAGLFPSLHGCLQYRHRRLPITSCDRPDS--FNGHGHLQOAMFTVEEITNNSALL	92
Db	89	PNLTIGYIPEDCNVSKALEATISLPAQKNKIDSLDECCNCESEHPISTIAVNGATGG	148
QY	93	PNITIGYILVYCSASAWY-ATLRVATLQCPRIETQK--DLRNSKVVATIGDNTD	149
Db	149	VSTAVANLGLFIPOVSYASSSRLLSNKNOFKSFLTIPNDEHOATAMADIEFRMM	208
QY	150	HAVTAAALGLFLMPDIVSYEASSVYLAKRFRPFLNTPSDRHQVEYVMQLOSGCW	209
Db	209	VGTIADDDYRPGIEKREFAERDIDCFSEIT--SQYSEDEIOHVEVIONSTAKV	266
QY	210	ISLISYDYDQOLGOALEELAVRGICVAFKDIVPFSASVGPDRMSMOHILQARTIV	269
Db	267	IIVFSSGDEPLI-KEIVRENIIGKIMLASEMASSSLAMPQYEVVGGITGFALXAG	325
QY	270	VVVEN-RLRLARVFRSRVLANLIGKAVVASDEMA---IS-TYIISVTG-IQ-GI-G	318
Db	326	QIPGREFLKVHPRKSYHNGFAKEFEETFNCHLOGAGKPLPVDTFLGHESGDRFS	385
QY	319	TVLG---VA-VQORQ-VP-GL-KEF-EESY---VR-AVTA-P-S--ACEE-GSW--	356
Db	386	NSTAFRLCTGDENISSVEPIYDIHLRLSYNYVLAVISIAHALODITYCLPGGLT	445
QY	357	-CSTN-Q-LCEECHTFTRNMPITGASMSAAVYVAYVAVAHGHQL--D-GC--T	406
Db	446	NGSCDIKKVAMQILKRLRLTNNGDEVTDECGDVGKYSIIMHLSSEDSIYE	505
QY	407	SLTCS-RGPYVPMQLOQIYKYNLLH-ENTVAADDNGDITGLYDITLAMDMPPE-WT-F	462
Db	506	KEVGYVNYAKGERLFINEEKIIMSGFSREVPFNSRDLQAGTRKGIIEGPTCCFEC	565

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QY      463  ELIG--SA-SLSPVHLDINKRIKIOHGKKNVOVPVSVCTTDCLAGHAKVAV--GSHHCFCFEC 518
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QY      519  VPCGAGTFLNNSSELHICQPCGTGEEMAKRESITCPR7VEFLAMHEP7SLVLIANTLILL 578
Dd      526  LTAFLVGLFT7KFRNP7PVKATNELSYLL7SL7LCCFSSSL7F7EPODWTICRLQPA 663
QY      579  LLVGTAQFLAMFH7TPVRSAGR7L7CFLM7LS7VAG7SC7F57FECE7PVPA7CL7LOPL 636
Dd      684  FGISV7L7DIS7LI7K7TN7V7LL7VE7--K7IP7SR7K7W7G7NL7Q7FL7V7EL7CT7FO7IV7CVI 741
QY      637  FSLG7A7FL7SCL7L7IS7F7OL7V7I7EF7ST7K7VP7-F7RT7AQ7NH7AG7L7F7V7SV7VH7L7CL7T 695
Dd      742  W7Y7A7P7SS7Y7NO7E7DE7E7D7I7IT7HE7G7L7MA7L7G7Y7TC7-L7A7L7A7FF7-A7FR7SK7L7PE 799
QY      696  WL7YMT7P7R7ET7RE7YQ7R7FL7V7L7I7B7E7TV7N7--SV7G7L7A7FT7IN7L7IS7T7F7VC7SL7G7K7L7PE 753
Dd      800  N7EN7AK7FIT7SM7L7IF7FI7W7IS7FI7PA7V7AST7Y7-G7K7V7AS7V7E7V7A7I7A7S7F7GL7L7AC7I7F7EN7K7I7Y 858
QY      754  NY7NE7AK7CV7F7E7LL7L7NF7V7SW7I7F7FT7M7-A7SI7OG7SY7L7P7V7N7L7AG7L7TL7L7SG7F7SG7F7L7PK7CY 812
Dd      859  I7L7F7R7S7R7N7T7IE 870
QY      813  V7IL7C7R7P7EL7N7T7E 824

RESULT      4
ENTRY      159362      #type complete
TITLE      calcium/polyvalent cation-sensing receptor precursor - rat
ORGANISM   formal_name Rattus norvegicus #common_name Norway rat
DATE      02-Jul-1996 #sequence_revision 02-Jul-1996 #-ext_change
REFERENCES
#authors   I59362; A55594
#journal   Proc. Natl. Acad. Sci. U.S.A. (1995) 92:3161-3165
#title     Calcium sensing receptor: molecular cloning in rat and
            localization to nerve terminals.
#cross-references MIMD:95241465
#accession I59362
#status    translated from GB/EMBL/DBJ
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#residues  1-1079 #label RES
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REFERENCE
#authors   Riccardi, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.;
            Hebert, S.C.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1995) 92:131-135
#title     Cloning and functional expression of a rat kidney
            extracellular calcium/polyvalent cation-sensing receptor.
#cross-references MIMD:95118508
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#molecule-type mRNA
#residues  1-133, 'X', 135-1079 #label RIC
#cross-references GB:U10354
#experimental_source kidney
KEYWORDS    calcium; glycoprotein; phosphoprotein; transmembrane protein
FEATURE
1-20      #region signal sequence #status predicted #label SIG\
187-212   #domain hydrophobic\
613-635   #domain transmembrane #status predicted #label TM1\
650-670   #domain transmembrane #status predicted #label TM2\
683-700   #domain transmembrane #status predicted #label TM3\
725-744   #domain transmembrane #status predicted #label TM4\
770-790   #domain transmembrane #status predicted #label TM5\
806-828   #domain transmembrane #status predicted #label TM6\
841-860   #domain transmembrane #status predicted #label TM7\
90,261,287,386,466, #binding_site carbohydrate (Asn) (covalent) #status
488,594,893,1005 predicted\

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	#binding_site phosphate (Ser)	(covalent)	(by protein)
794	kinase C) #status predicted		
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SUMMARY	kinase A) #status predicted		
	#length 1079	#molecular-weight 120867	#absorbance 0.72

Query Match	20.3%	Score 1285;	DB 2;	Length 1079;
Best Local Similarity	31.6%	Prod No 648	334	

Db 30 GDILIGLFLPHFC-VAAKODLKSRESVECDIRYNFRGFWLOAMFALEINSSPIL 88
QY 35 GDFLLAGLFLSHGCOLQVRHRPLVTSODRPS--FNGHGHLMAFYEELINSSALL 92
Db 89 PNMILGRIPGTCVTYSKALENTISFPAOKKIDSLNDEFONCSERIPSTIAVATGSG 148
QY 93 PNILGELIHDVCSSESNVY-ATLRVATLALOGPHRIEIOK--DLRNHSSKVAFIEGPDNT 149
Db 149 VSTAVANLGLFLYIPQVSYASSRSLNSKNQKYSFLETIPNDEHOATAMADIEYFRNM 208
QY 150 HAVTATALLPFLMPLVSYSEASSVLSAKRKFSFLRTVSDRHOVEVMQILQSGWVA 209
Db 209 VGTIADDDVGRGCIIEKFRREABERDIDFSELI--SOYSDEEIQOAVVEYIONSTAKY 266
QY 210 ISLIGSGDQGOJGOVQALELAVPRGICVAFKDIYFSPASVGDPRBMQMOHLAQTIV 269
Db 267 IVFSSGPDLEPLI-KEIYARNITGRITMIASEMASSLIAMDEYHHVGGITIGRLAKG 325
QY 270 VVVFESN-RHLARVEFRSVLANLIGVAVASEMA-----IS-T-YTSTG-TQ-GI-G 318
Db 326 QIDGFEFLQKVPKRSYANGKFAKEWEETFNCHLOEGAKGRLPYDTEFRSHEEGNRL 385
QY 319 TVLG----VA-VQQRQ-VP-GL-KEF-EBSSY--VR-AVTAA-P-S-A-CPE-GSM-- 356
Db 386 NSSTAERPLCTGDENINSYETPYMDEEHIRISYNYIAYASTAHNLODYTOLPBRGLFT 445
QY 357 -CSTN-Q-LCRCHPTTNMPTLGAFSMAIYRYEAVYAVABELHOL--L-GC--T 406
Db 446 NSSCADIKVEYMOVLKHLRLNFTNNNGEOVTDECGDVGNTSIIIMHLSPEDEGSIVF 505
QY 407 SGTCS-RGQVYWMOLLOQIYKVNFLH-ENTVAFDNDGDTIGYDIIAMDNNGPR-W-F 462
Db 506 KEVGYNYVAKKGERLFINEEKILMSGSRHEVFNCSRDQAGRKQITIGEPTECFEC 565
QY 463 ELIG--SA-SLSPVHLDINKTIQMHGKNNOVPASVCTTDLAGHRRVY--GSNHCCFEC 518
Db 566 VECPRGEISETDASACKCPDDEFSNENHSCIAKEIETLATEEPFIALTLFVAGIGF 625
QY 519 VPCEAGTILNMSELHICOPCETEEVAPRESTQCPREYVEFLAMEHPISIVLIANTLILL 578
Db 626 LTAFLVGYFI-KFRNTPYVAKATNRELSTLFLILLCCSSSLF-FIGEPDOWTCRLROPA 683
QY 579 LTVAGAGLFAHHFH-TPVYRSAGGRCLTCLMAGSLVAG-SCSEYFEEBPVPYALLOPL 636
Db 684 FGISFVLCISGILVKNVLLVEE-AKIPTSFRKMWGMLQFLVFLCTFMOILICII 741
QY 637 FSLIGFAFLFISCLTIRSOVLVYIEFKSRTKVP-FYRTMAQNHGAGLFIYVSYTHLILCT 695
Db 742 WLTPYAPSSYRNHLEDEIIFITCHESMALGSLGYTC-LLAALCFEF-AFKSRKPE 799
QY 696 WLVMYMRPRFREVORFHLVILCTEVN--SVGLAFLTNIIILISTFVCSYLGELEPE 753
Db 800 NFNEAKTITSMLEFIWVISFIPAVASY-GRKFSVAEYIALIASFGILACIFENKYY 858
QY 754 NYNEAKCVTISLILNFYSWIAFLFM-ASIVQGSILPVRVNLADLITLSSGFSYTFPKCY 812
Db 859 IILFKPRNITIEERSTAAHA 880
QY 813 VILCRPELANTHEROASIDOTY 834

TITLE	ORGANISM	DATE
calcium receptor (clone pPCAR-5.2) - human	#formal_name Homo sapiens #common_name man	19-Oct-1995
	#sequence_revision 19-Oct-1995	#text_change 17-Mar-1999

REFERENCE	#authors	ISSN	Year	Journal	Volume	Page
A56715	1	0000-0000	1999	Journal of the American Medical Association	281	1000
Garraat	1	0000-0000	1999	Journal of the American Medical Association	281	1000

U. Biol. Chem. (1995) 270:12919-12925
 #title Molecular cloning and functional expression of human
 parathyroid calcium receptor cDNAs.
 #cross-references NCID:95279439
 #accession B56715
 ##status Preliminary
 ##molecule_type mRNA
 ##residues 1-1088 ##label GAR
 ##cross-references GB:020760; NID:G683746; PID:G683747
 keywords glycoprotein; receptor; transmembrane protein
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 #length 1088 #molecular_weight 121799 #checksum 5263
 Query Match 18.9%; Score 1198; DB 2; Length 1088;
 Best Local Similarity 31.8%; Pred. No. 3,29e-206;
 Matches 274; Conservative 231; Mismatches 274; Indels 83; Gaps

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627 VPACILRQLEPESLGRAITFELSCITIRSEQLVIIIEKFSRKVPT-FYRTWAQHAGAGLVPIYS 685
       :||| |::: |: ||: ::::: ::::: |: ||| |::: ||::: ||::: |::: |::: |
742 TFMQIVICIMLYTAPSSRYNRQLEDIITITHESLSNALGFLIGYTCL-LIAAICPFPP 800

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QY	686	STVHLLICLTMVYKMTPTREYQRFPRVLLECTEVN--SVGLLAFTHNILLISTFV	743
Db	801	-AFSRKLPENFNEAKFTFSMLFFIWFISFIPAYASTY-GKFSVAVEYAIATIASGFL	858
QY	744	CSYLKELPENYNEAKCYTFSLINFVSMIAFFTM-ASLYGSLPAVNVLAGLHTLSG	802
Db	859	LACIFENKIIYILFKPSRNITE	880
QY	803	FSGIFLPKCYIVLCRPELNMTE	924

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TITLE	metabotropic glutamate receptor mGluR5 - rat
ORGANISM	metabotropic glutamate receptor mGluR5 - rat
DATE	04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 29-Jan-1999
ACCESSIONS	A42916
REFERENCE	A42916
authors	Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakaniishi, S.
#journal	J. Biol. Chem. (1992) 267:13361-13368
#title	Molecular characterization of a novel metabotropic glutamate receptor mGluR5 coupled to inositol phosphate/Ca2+ signal transduction.
#cross-references	MUJID:92317054
#accession	A42916
#status	preliminary
##molecule_type	mRNA
##residues	1-1171 ##label ABE
##cross-references	GB:DI0891; NID:9220813; PID:d1002186; PID:g220814
##experimental_source	brain
#note	sequence extracted from NCBI backbone (NCBIN:107749, NCBIPI:107750)
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Query Match	13.8%	Score 873;	DB 2;	Length 1171;	
Best Local Similarity	27.7%;	Pred. No. 1,21e-140;			
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Db	31	MPGDIITALLSVYHQP-TV-DKHERKCG-AVR-EQYIGIRVYAMLTLEIRINSPTLL	86		
QY	33	LPQDFLLGLGSLSHQDCLQVRRPLVTSQDRPDSFNGHGYLFQAMRFTEIINSSALL	92		
Db	87	PNITLGGCIRPSCHMSAAVLEQSIETFRDLSISSEEEGGLVRCVDSSSPRSKPIYGY	146		
QY	93	PNITLGYELLYVCSBSANVA-TLR-VL-AIQGRPHIE--IQ-KD-IRN-HSSK-VVAFT	143		
Db	147	GGSSSVAYIQVONLQLPILNIPQIAYASITMDLSKTFIKYEMRYVPSDAQARAMDIVK	206		
QY	144	GPNDNDAVHTAALLGPLMLPLVEYKASVYLAKRKFPSTLRTVPDRDROVEVMVQLQ	203		
Db	207	RYNMITYSAVHTEGNYGSGMEAFKDKMSAKGICITIAHSYKI-VSN-AGEQSFDKLLKLR	264		
QY	204	SFGWMIWISLISYSGYGGQLGQVALEELAVPRGICVAFKDIYFESARAGDPRMOSMGNL	262		
Db	265	SHLPARVVAQFCGMYTRGGLMMRRIRGLAGELLGSDGWA--DRDYV--DGYQ-REAV	321		
QY	263	AO-KATTVYVVFNSNHLARVFRSVLVANLLGK--VWASDEMAISTYITSTGTGIGIGIV	320		
Db	322	GGITIKL-QSPDYWFMDYVYKLRPEPTMLRNPMFOEFMORHFOQLGFAQENSKYKTC	380		
QY	321	LGVAAVQKQVQGLKFEFESSY--RAVIAAPACGEGSM-----CSTNQLCRECHTF--TR	372		
Db	381	NSSLTLRTHVQDSKMGFVIAINATYSMAVGLHNKMSLCPGYAGLCDAKMPIDGRKLDSL	440		
QY	373	NMP-TLGAFFSMAAYRVV--EAVYVAVAHGLHQL-LG-CIS-E-IC-SRGPYVPMQLLOQI	424		
Db	441	MKTNTGSGGMILPDEGDSRGEYIENFKEMKDY-FQVINGSMWMDNGELKMDDEV--	428		
QY	425	YKVNPL-LHENTVADDDGDTGLGIDIIAMDMPPEMTFELIGSASLSPVHLIDNKTQIQ	483		

Db	499	MSKKNIRF-SVSGEPCKGKGIKYRRNGEVSOCMTCTCPCKENEV-FDE-VTCAQOLGS	555
Oy	484	WHGKNVPVSVCTICDLAGHHRVV-GSHHCCEPCPACENGATFLNSELHIPOCSTEE	542
Db	556	WPTDDLITCCDLIPDYLRMGDPDEPIAAVVEFCILCLLALTEFY-TVIFIIYR-DTPVRSSS	613
Oy	543	WAPKESTICFRRYEPLAW-H-ETISLVLIANLLLLLLVGTLGLAMHHHPVVASG	600
Db	614	RELCTIILAGICLGLYTFC-LIAKPQIYCYLORIS-CGSPASISALVTKTIRIARIL	672
Oy	601	GRLCFMLGMS-VWAGS-CSFYSEFEPEPTVPACILLROP-FSIGFAIFLSCLTIKRSOLFVIIF	659
Db	673	AGSKKKICTK-KPRFMSCAQVLVIAFILICIQIGIIVALTMEPPDIIMHOYSIRE-VYL	730
Oy	660	KFTSR-VTFEYRTWAQNNGAGLEV-IYSSIVHLICITLVMWTMPRTREYORPHVLIL	717
Db	731	ICNTTN-LGVVTPPLGYNNLLISTCF-YAEKTRAVPANENAKYAIFTNYTCIIMLAF-	787
Oy	718	ECHENVNSGFLLATHTNLIS-TFVOSYIGKRLEPNYNNAKVTSLLNFPSWLAF	776
Db	788	-VP-IYEGSNKITTMCFESV-LSAIVALGCMFPVKYIILIAKERVNRSASFITS	839
Oy	777	TMASIQGSYLPAYNAVIALGTLLSGFS-gx-FLPKCIVILCRBELNTERFOAS	829
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ENTRY			metabotropic glutamate receptor 5 A - human
TITLE			#formal_name Homo sapiens #common_name man
ORGANISM			28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change
DATE			05-Jan-1996
ACCESSIONS		JC2132	
REFERENCE		JC2131	Minkami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Authors			Biochem. Biophys. Res. Commun. (1994) 199:1136-1143
#journal			Molecular cloning and the functional expression of two
#title			isoforms of human metabotropic glutamate receptor subtype
			5.
#cross-references		MUTID:94197696	
#accession		JC2132	
#molecule_type		mRNA	
#residues		1-1180	#label MIN
COMMENT			This protein is coupled to guanine nucleotide binding proteins.
KEYWORDS			glycoprotein; neurotransmitter; receptor; transmembrane protein
FEATURE			
580-604			#domain transmembrane #status predicted #label TM1\
617-637			#domain transmembrane #status predicted #label TM2\
644-664			#domain transmembrane #status predicted #label TM3\
694-714			#domain transmembrane #status predicted #label TM4\
738-759			#domain transmembrane #status predicted #label TM5\
773-794			#domain transmembrane #status predicted #label TM6\
803-827			#domain transmembrane #status predicted #label TM7
SUMMARY			#length 1180 #molecular_weight 129053 #checksum 237
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Best Local Similarity	27.6%;	Pred. No. 4,82e+140;	
Matches 231;	Conservative 214;	Mismatches 326;	Indels 65; Gaps 55
Db	31	MPGDIIIGALFVSHOP-TV-DYHERKG-AVR-EQYGIORYEAMLTIERINSDPTLL	86
Oy	33	LPGDFLLAGLFSLHGDCQVARRPLVYSCNDPDSFNHGHTQLPMAMFTYEIINNSSL	92
Db	87	PNITGCIIRDSCMHAVALAEQSIEFIKDSLISEESEGLRVCDVGSSSSFRSKPIIVG	146
Oy	93	PNITGELYLYDVCESSAVVA-TLR-VL-AAGGRHIE--IQ-KDLNHS--SK--VVAE	142
Db	147	IGPSSSAIIOVNULLDFNIPOIAYSATSMDSDKLTFFXEMVYVSDAQARAMDIV	206
Oy	143	IGPDTHAVITTAALLGPFLLKPLVSYENSVDLSAKKXKPSFELEFTVPSDRHOEVNWOLL	202

Db	207	KRYNNTYSAVTEEGYGGSGGEAFEDMSAKNGKICIAHSYKI-YSN-AEGSGFDKLTKL	264
Oy	203	OSFGWWTSLISYSGDYGLGVQVQLDELLVPRGICAFKQDIYFESKRVSDPPRMOSQHL	262
Db	265	TSHLKRVAVACFCGEMTGRGLMMRRRLGLAGEFELLGSDQWA-DRYDVT-DGYO-REA	321
Oy	269	A-Q-ARTTVVVVFNRRHLARVEFRSVYLVANLIG-K-VWASDEMALSTIYTSVIGIGIST	319
Db	322	VGGITIKL-QSGDVYKWFDDYLYKLRPETHRRNPWFQEHFRQCHLSEGFPOENSKYNT	380
Oy	330	YGVGVAVOORQVGLKEFEESYVRATYAPASCP--EGSW-----CSTNOLCRECHFT-T	371
Db	381	CNSLTLTKHHODSMGCVINAIYMSMAIGLNMOSLPGYAGLDAKPPIDGRKLIES	440
Oy	372	RMP-TLGFASFSAARVY--EAYIAVANGHLQ-LG-CTS-E-IC-SAGPYPMQLLQ	423
Db	441	LMKTNFTGVSGDTLLFEDENGSDPGREYINFNKEMGKDY-FDYINNGSMNGELKMDDEY	499
Oy	424	IKYVNF-L-HEHTVAFDNGDGLGYDILAMOMNGEWMFEIIGSLSLPHLIDIKTKI	482
Db	500	-WKSRSNIR-SVGESEPCERGOIKVIYKRGVSCCMTCPCKENEYV-FDE-YTCAACQLG	555
Oy	483	QMHGKNQVPVSVCTCDLAGHRRVYV-GSHHCCECVACEGATFLMSELHICOPCGTE	541
Db	556	SMPTDGLGCDLIPQYLWMSGPREPIAAVYFPCGLIATLNF-TVYFIYR-DTPVYKS	613
Oy	542	EAPKESTCEPRTYVEFLAM-H-EPLSLVLANTLTLTLVLGTAGLFMHHTVPRVRA	599
Db	614	SRELCTYIILAGICLGYLCTFC-LIAKPKOICYLORIGIGLSPMSYSALVTKTNRIARI	672
Oy	600	GGRLCFLMGLSVAS-CSFYSPFGSPYTPACLLRPLSLGPAIFLSCGLTIRSPQLVII	658
Db	673	IAGSKKIKCTK-KPRMSACQADLVAFILICIQGLIYALFTMEPPDINHDPISIRE-VY	730
Oy	659	FFFSFK-VPTFRTMAONHAGLFFV-IYSSVHLICLTWLMWMPRPRTREYORFPHLYI	716
Db	731	LICNTNT-LGVYTPGLGYNNLLISCF-YAFTRNPAFNPNKAYLAFTMYTICILWAF	788
Oy	717	LECTEVSNGVFLAFTLHNLLISLS-TEVCSYIGKELEPENYNEAKCTVFSLLINFSWIAF	775
Db	789	--VP-IYFGSNKIITMCFSVS-LSATVALGCMFVKKVYIIIAKPERNARSFAFTS	840
Oy	776	FTMASIYGSYSLPANNVLAGLTLTSSGFS-GY-FLPKCVIILCRPLNTEHPQAS	829
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TITLE		metabotropic glutamate receptor 5 B - human	
ORGANISM		#formal_name Homo sapiens #common_name man	
DATE	28-Aug-1985	#sequence_revision 07-Oct-1994	#text_change
ACCESSIONS	JC2131		
REFERENCE	JC2131		
#authors	Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.;		
#journal	Sugiyama, H.		
#title	Biophys. Res. Commun. (1994) 199:1136-1143		
	Molecular cloning and the functional expression of two		
	isoforms of human metabotropic glutamate receptor subtype		
	5.		
	#cross-references MUID:94197696		
	#accession JC2131		
	#molecule_type RNA		
COMMENT	##residues 1-1212	#label MIN	
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	glycoprotein; neurotransmitter; receptor; transmembrane		
	protein		
FEATURE			
560-604	#domain transmembrane	#status predicted	#label TM1\
617-637	#domain transmembrane	#status predicted	#label TM2\
644-664	#domain transmembrane	#status predicted	#label TM3\
694-714	#domain transmembrane	#status predicted	#label TM4\
738-759	#domain transmembrane	#status predicted	#label TM5\
773-794	#domain transmembrane	#status predicted	#label TM6\

803-827	#domain	transmembrane	#status	predicted	label	TM7
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Best Local Similarity	27.6%	Pred. No.	4,82e+140:			
Matches	231;	Conservative	214;	Mismatches	326;	Indels 65; Gaps 55;
Db	31	MPGDIIGALFSVNHQF-TV-DKVENKCG-ANR-EQYIGQRYEAMHLLEKINSDPILL	86			
QY	33	LPDGFLLAGLESLHGDGLQVRHNRPLVTSQDRPDSFGHGYHLEQARFTVEEINNSALL	92			
Db	87	PNTLGCIRDSCHSAVALEOSIEFIRDLISEEPEGJVRCDSSSFRRKPIYGV	146			
QY	93	PNTLGLLELDVCGESANVYA-TLR-VL-ALQSPRIE--IQ-KDLRINS--SK--VYAF	142			
Db	147	IGPSSSVAIOVONLQLEFNIPQIAYSATSMDSKTDLTLEKRYMRVNSDAQARAVDITV	206			
QY	143	IGPDNDHAATVTAALLGPEFLMPVSYSEASSVLSAKRKPPSLRTVPSDRHQVEVMQDL	202			
Db	207	KRYMNTYSAVHTGNTAGSGEMAFKDMASKKEICIAHSYKI-YSN-AGEQSFDKLLKL	264			
QY	203	QSFGWVYISLIGSGDYGOLGVALLEELAPRNCICVAFDIVPFSARVDPDPMQSMQHL	262			
Db	265	TSHLPRKRVYACEEGMTVGLMAMRRGLAGEFLLISDGMN-DRYVYT-DGYO-RRA	321			
QY	263	A-Q-ARTIVVYVYSNRHLAVFRSVLANLTK-VWASEDMALISTYTSYTGIGIGCT	319			
Db	322	VGGITIKL-OSPDVKMFDDYYLKLREPETHNRNWFQEFQHRFOCRLEGFPOENSKYNT	380			
QY	320	VLGVAVGQROQVPGLKEEESYVAHVTAAPACG--EGSN----GSTNOLGCECHTFT-T	371			
Db	361	CNSSLITLTKTHVODSKSGEYINAIYSNAYSLHMQMSLCPGATGLCDAMKPIDGRKLES	440			
QY	372	RNMP-TLGAFSMAAYRVY--EAVYVAHGHOL-LG-CTS-E-IC-SRGPIYPMQLOQ	423			
Db	441	LMKTFEYVSGSDTLTPENGDSPGREYIMFKMGKDY-FDYINVSWMNGELKMDDEY	499			
QY	424	LYKNFEL-LHENYAFDNDNGDTLGYDILIAMDNQGEWTFEILIGSASLSPVHDIKRTI	482			
Db	500	-WSKSNRIIR-SVQSECEGQIKIVIRKGEVSCWCWCTCKENEVY-FDE-YTKRACOLG	555			
QY	483	QWGHKNNQVPSVSCVTCTCLAGHHRVYV-GSHCCFCFPCVCEAGTFLMSELHICQPCGE	541			
Db	556	SMFIDDLTGCDLIPVQYLRMGDPEPIAAVYFACGLLATLV-TVVFITTY-DTPYVSS	613			
QY	542	EWAPKESTCTPRTVEFLAW-H-EPISLYVLIANTLLHLLVGTAGLFAMHETPTVYRSA	599			
Db	614	SRELCTIILGICLGYCTEC-LIARKQIYCOLRIGLGLSPAMSYSLVTKIRIARI	672			
QY	600	GGRLCTFLMLGSLVAGS-CSFYSEFGEPTYACLLRPLTSLGLAIFLSCLTIRSFQVLI	658			
Db	673	LASGAKKICTC-KRFMSACAOQVIAFIIICLQIGIYALFIMEPDIHNDPSIRE-VY	730			
QY	659	EKFSIK-VPTTYKRWAOHNGAGLFV-IVSSTVHLLICLIMLVMTTRPREQORPHLYI	716			
Db	731	LICNTNT-LGVVTPDLYGNLLISCTF-YAKTRVNPANFNEAKYIAFTMYTTCIIWIAF	788			
QY	717	LECTEVNSVGLFLAFTHNILLIS-TEVCSYLKELPENYNEAKCYTFSLINFWSMIAF	775			
Db	789	--VP-IYEGSYKIKITMCFSV-LSATVALGCFVRYKVIYLIILAKPRNVRSAFTS	840			
QY	776	FTMASIYQGSYLPVAVNYALAGLITLLSGGFS-GY-FLPKCYVILCRPELNTNTEHFQAS	829			
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ENTRY	JH0561	#type	complete			
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ORGANISM	metab_name Rattus norvegicus #common_name Norway rat					
DATE	30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998					
ACCESSIONS	JH0561					
REFERENCE	Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S					
Authors						

GENETICS	GLUR4	
#gene		
CLASSIFICATION	#superfamily metabotropic glutamate receptor 4	
KEYWORDS	neurotransmitter receptor	
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Query Match	13.3%	Score 841: DB 2: Length 912:
Best Local Similarity	26.5%	Pred. No. 2,976-134:
Matches	211: Conservative 222: Mismatches 301: Indels 61: Gaps	
Db	75 GIHLEMLFALDRINDPDLRNPITLGLARILDTCSDRTHALQSTLFKALIEKDGTEV	13
OY	71 GYHLEQAMRETVBEINNSALPNIITLGEYELDYCESANAYVA-TLR-VIAL-Q--GP--	12
Db	135 RCGSGGCPITTEKEERYGVAGSGAGSSVSIMVNNILRLEKPIQISASTAPDLSDNSRDF	19
OY	124 RHIEIQDLNNHSSKYVAFIGPNDTHATTYALIGPLMLPVSTEAASVYLSAKRFP	18
Db	195 FSRVPSDIYQAOAMVDIVALKMNVSTSLASEGSYGSGVEAFIOKSRENGVCIAOSV	25
OY	184 FLRTVPDRQYQVVMYVOLLQSGFWWISLIGSGYGGYQVQALBELAVPRG-ICVAFK	24
Db	255 KIREPKTEGFEDK-IKRLLETSSNAGIIIFNEDDIRVLEAARNAQOHHFTMGSDS	31
OY	243 IYFSAVADPDRQSMQMLAARTTVYVVSNNRLAVFRFSVYVLAULTKV-VWASED	30
Db	314 WG-SK-SAPVLRLEEVAAES-AVTILPKRMS-VRGEDRYFSRTILDNNRNWIAFEFEDN	36
OY	302 WALSTYITSTVIOGIGTVLGAAYOORVPGLKEFEESYV-RAVTAAPSAC--PE---GS	35
Db	370 FHCLSLRHALKKGSHKCTKNERIGDQSAVEDEQSKQVFI DAYYAGMGLHMHNRDLP	42
OY	356 W-CS-TNQ-LGECRCH--FTTNMPTL-GATSMASAPV-YEAVYVAHGHOLL-G-CT	40
Db	430 GRVGLCPDRDPDVGQQLKYLRNVNFSGIAGNPVTENGDAPGRYDIYQYOLNCSA-E	48
OY	407 SET--CSR-GPYVPMQLLOQIYKVFLLHENTVAFFDNGDITLGYDIIMD-WNGPEWT	46
Db	489 YKVGSGWT-DHLHLRIER--WOMPGSGOGLPRISICLPCPGEGEKTKYVGMACCWHCEPC	54
OY	462 FELIGSASISPYHLDINKTKIQMHGKKNQVYVSCITDCLAGHRRVAVGSHHCCFECPVC	52
Db	546 -TG-YQYQVDRTYCTCPYDMRPFENRTSCQPIPVKLEWDSWAVLPFLAVAGIATL	60
OY	522 EAGTLNMSSEHLICPGCGTEMAKESYCTCPRTVEFLAMHEP-LSVL-IAANTILLLL	57
Db	604 EYVYV--EVRVNDPPIYVASGREGSLVYLAGIFLCYATTTMLMAEPDLGICSRIRFLGI	66
OY	580 LVGTAGLPAHFHHPYVASAGRCFLCFLMGLSVAGSCSFSPFGEPLVPACILRQPLFSL	63
Db	662 GMSISYALLKTKNRKIYKIFEQGRKVSADRFISPAQSLATPFLIS--LQILGICV-WF	71
OY	640 GAFLPLSCLTIRSPQVLIIFEFSTKVPTEYR-TWAOHNGAGLEFVIYVSRVHLL-IDLTWL	69
Db	719 VDPESHVAVDEQDQRTDPRPARGVLCG-DISLSITLICLGSMLNLMVTCYATITKRV	77
OY	698 VMMPREPRREXQ--R-F-PHYV--ILECTEVSNGFLPAFTNHLISITFCOSYIGKEL	75
Db	778 PETENKAPICFTMYTTCIYWLAFIPFECTSOSADKLYIQTTTLTVSVLSASVIGML	83
OY	752 PENNEAKCVYFSLILNFVSMIAFFTWV-SIYGSY-L-PAVVNLAGLITLISGGRS-G-Y	80
Db	838 YMPKYVILLFHPEDN 852	
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TITLE	glutamate receptor homolog - cherry salmon	
ORGANISM	#formal_name Oncorhynchus masou #common_name cherry salmon	
DATE	11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change	

	ACCESSIONS	S71376	
	REFERENCE	S71376	
	#authors	Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.	
	#journal	EBS Lett. (1995) 392:71-76	
	#title	Cloning and characterization of a bifunctional metabotropic receptor activated by both extracellular calcium and glutamate.	
	#cross-references	MUID:96354880	
	#accession	S71376	
	#status	not compared with conceptual translation	
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	640-660	##domain transmembrane #status predicted #label TM2\	
	672-690	##domain transmembrane #status predicted #label TM3\	
	717-737	##domain transmembrane #status predicted #label TM4\	
	761-782	##domain transmembrane #status predicted #label TM5\	
	796-817	##domain transmembrane #status predicted #label TM6\	
	826-850	##domain transmembrane #status predicted #label TM7\	
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	757	##binding_site phosphate (Ser) (covalent) (by protein kinase C) #status predicted\	
	636,699,961	##binding_site phosphate (Thr) (covalent) (by protein kinase C) #status predicted\	
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Db	226	LDIYKRYWTVVSVAHTPGNGYGESEGMFKFLAQEGICINHDKI-YSN-AGEKHEDRL	283
Oy	199	VOLLDFGWVISLIGSGIDGIGLVQLLEFLAVPRGICVAFKQITPPSARVGSPRMOSM	258
Db	284	LRLERLERPKARVVVFCEGTIVGLILAMKRLLVAGFEILLISGDGAADREVEGYEOE	343
Oy	259	MQHLL-AQ-ARTTYYVVFNSRHLLAVFPFSVVALNLTKR-VWVASBDAIASTYIIISVICIQ	315
Db	344	AVGGI-LYKLHSEVTSDDYFLK-LRLINTNRMPERE-FWQHRFO-CRIPIGHLENMN	399
Oy	316	GIGTYLVGVAAVOORVPGIKKEFEESYVRAVTIAPSA-CREGSWCSTNOLCREC-HTFTRN	373
Db	400	YRKNGSGESLEDNYVDOSKMGFINATLYMAOGIHDMHSILCGNHGLCKAMPIDISOQ	459
Oy	374	MPYL-GAF-SKSAAY---RV-Y-EAAYAAGHGHLQG--CRSET-C-SRPVYPWO	419
Db	460	LLEFLMRTSFTEGVSGEDVFDENCDTGRCYIMNLQYEPG-AEDYINVGSHEGOISID	518
Oy	420	LLQQIYKNEL-LHENITYAFDNODLTGYDLIAMDMNKPMPTTEIIGSASLSVYHLDIN	478
Db	519	DYMAO-INRSDMY-LSVCSEPCSKGEIKVIRKGEVSCWCICTACKDEIYO-DEF-TCTA	574
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Db	575	COLGWMPRELGEGERILTRYLEMGNPESIYQVVFACGLIVTSFYFIPLYLYNDTPYVK	634
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Db	635	SSSRSLCYIIAGLFIFIGCFP-LLIAQPIYASCYLOLRLLVLSATMCYSALVKTIRIA	693
Oy	598	SAGRGTCGLMGSLVAG-SCSFYSFEGFPPTYPAOLLNQPLFLSGLFAFLSCLTIRSQLY	656
Db	654	RILAQSKKICTRKPRESAMAOLVIAGL-LVS-VQILTLEVTLILEPMPVKSYPSI	749

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TITLE	G protein-coupled glutamate receptor - rat		
ORGANISM	#formal_name Rattus norvegicus #common_name Norway rat		
DATE	04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998		
ACCESSION	A41939; S15362		
REFERENCE	A41939		
#authors	Houamed, K.M.; Kujiper, J.L.; Gilbert, T.L.; Haldeman, B.A.; O'Hara, P.J.; Mulvihill, E.R.; Almers, W.; Hagen, F.S.		
#journal	Science (1991) 252:1318-1321		
#title	Cloning, expression, and gene structure of a G protein-coupled glutamate receptor from rat brain.		
#cross-references	MOID:92022526		
#accession	A41939		
#status	preliminary: not compared with conceptual translation		
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##experimental_source	cerebellum		
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REFERENCE	S15362		
#authors	Masu, M.; Tanabe, Y.; Tsuchida, K.; Shigemoto, R.; Nakanishi, S.		
#journal	Nature (1991) 349:760-765		
#title	Sequence and expression of a metabotropic glutamate receptor		
#cross-references	MOID:91155047		
#accession	S15362		
##status	preliminary		
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QY	76	QAMFTVEELINSSALPNTLIGELYDYDCESA-NVY-AT--LR-VL-ALDGPRI-IE-	127
Db	140	CLPDGQTLPPGRKRPPIAGVIGSSSSVAIOYONLLQLFDFOIAVSATSIDLSDTKTK	199
QY	128	-IQK-D-LR-NHSSKYVA-PIGPDNDHVAITTAALLGPLPLPVSEASVYLSAKRKP	182
Db	200	YFLRWPSDTLQARAKMLDIYKRYNMTTVYSAVHTEGNIGSGMDAFKELAAQSGLCIASHD	259
QY	183	SFLRTVPSDHOEYVAMVOLLOSGFGWVWISLIGSGYDGLGVALLETLAVPRGICAFKD	242
Db	260	KI-VSN-AGEKSPDRLLRKLRELRKARVAVVCCCEMTYRGLLSANRRRGVVGESFLIGS	317
QY	243	IVPSASVAGPROMSKMQL-AP-ARTTVVVVFSNRHLRVFPRSVYLANLIGKYV-VAS	299
Db	318	DGMADREVELEGVEAVANGI-TIKLOSEVVSFDYFEK-LRLDTRNPMFPE-FMOH	374
QY	300	EDMAISTYIISVYIGIGITVLGVANQQVQNPOLKRFEESEYRAYVAASA-CPGSGMS	358
Db	375	RFQ-CRLPGLLENPNFKKVCYTGNSLEENYVQDSKXGVFINATYAMAHGLONMHA-CP	433


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QY 359 TNOLCR-ECHFTTTRNMTPL--GAFSMSAY----RV-Y--EAYVAVAHGLHOLL-G-CI 406
Db 434 GHVGLCDLMDKPIIDGRKLLDELFIKSEFVSGSEVWEDEKGDAPGRYDMLNLOYTEANR-Y 492
QY 407 SEI--C-SRGPVPMOLLQOIKYVFL-LHENTVAFFDDGDLTGTYDIAMDNGPEWTF 462
Db 493 DYVHVGVHGVGLNIDYKIQ-MNKSQWVR-SVCSEPCLGKQIKYIRGEVSCCMICTAC 550
QY 463 ELIGSASISPVHLDINKRIQWGNKNNQVPVSVCTDCLAGHRRVYV-GSHHCCEVCPC 521
Db 551 KENEVQO-DEF-TCRACDLGMPNMLGCEPIPRYLEMSIESIILAFSCLGILVTL 608
QY 522 EAGFLNSELHICQPCGTEWAPKESTCEPRTEFLAMHEPISLVLAATLTLILLY 581
Db 609 FVTLIFVLRDPVYKSSRELCTYIILAGIFGYVCPF-TLAKPTTSCYQRLVGLS 667
QY 582 GTAGLFAHHEHTPVYRSAGRGCFMLGSLVAG-SCSFYSFGEPTVACLLROFLSGL 640
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QY 641 FAIFSLCTLINSFOLVILFKFESTK-VPTFYRTMAQNHGAGLEVIYSVHLLICLTLMVM 699
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QY 818 PELNTEHFOAS 829

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ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Sep-1998
ACCESSIONS 149142
REFERENCE 149142
#authors Duvolsin, R.M.; Zhang, C.; Ramonell, K.
#journal J. Neurosci. (1995) 15:3075-3083
#title A novel metabotropic glutamate receptor expressed in the retina and olfactory bulb.
#cross-references MUID:95239344
#accession 149142
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
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KEYWORDS #neurotransmitter receptor
SUMMARY #length 908 #molecular_weight 101413 #checksum 2996

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Best Local Similarity 25.2%; Pred. No. 2,78e-127;
Matches 212; Conservative 241; Mismatches 322; Indels 66; Gaps 52;

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Db 204 QAMVDIYALCMNVSTLASGNTGSEGVFAFQDISREIGSVCIQAQOKIPREPRGE-- 261
QY 196 EVWQVLQDSFGWVWISLGSIGDYGQLGVQALDELAPRG-TCVAFKQIYFFSARVSDPR 254
Db 262 FEKIKRLETPNARAVIMFANEDDIGILEAAKLNQSHFLIGSDSMG-SK-IAPVY 319
QY 255 MQSMWQHLAQART-VYVVFENRHLARFFRSVLANLTGR-VVAVSEDMALISYIISVT 312
Db 320 QOEELABE-AVITLIPKR-ASIDGDFRFRSTLANNRANVFAFSEGNCGCKSGSKR 377
QY 313 GIGQIGVLGVAQOQVPPGKEFEESY-VAVVAAPSACPEGSCSTNOICRE-CH-TF 369
Db 378 NSHIKCTGLERIRADSSEYDEGVQOFYIDAVYMAVALNHMHRELPGYIGLPPRVYTI 437
QY 370 TTR-NMPT-LGAFSMSAY----RV-Y--EAYVAVAHGLHOLL-G-CTSEL--CSR-GPV 415
Db 438 DGEKELGIRAVNNGSAGTPVTEENGDAFGRYDFOYQINNKSTYKIGWT-NQLH 496
QY 416 YPMQLQOIKYVNFLLHENT-VAFDDNDGLGYDIIAMDNGPEWTFEILIGSASISPVH 474
Db 497 LKVED--MQANREHETHPASCSLPCKRGERKTKYKGVPCMHGCRDEGNYV-QYDELS- 552
QY 475 LDINKTKIQWGNKNNQVPVSVCTDCLAGHRRVYVGSRHCCFECVPCBAGTFILMSELHI 534
Db 553 CELCPDLDORPINRNGCORPIIKLEWSPWAVPVILAILGITATFVITFVRYNDTP 612
QY 555 COPGTEPMAREKSTCTCPRTVEFLANHEPISLVLIANTLILLLVGTAGLFMNHHTP 594
Db 613 IVRASGRELSTVLTGIFLCYSTFL-MIAPDTIISFRIRIFGLMCESYAALLTKTN 671
QY 595 VYRSAGRLCFLML-GSLVAGSCSFYSFGEPTVPACILRQPLSLGPAIFLSCLTIRSF 653
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QY 654 QLVITFKSTVPFTFYRTMAQNHGAGLEVIYV-STVHLLICLTLMVMTPTPTREY--QR 710
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Db 789 TTCIIMLAFIPFEGTASAKMTIQTTTLVSNLSASVSLGMLYMPKVIITIFHEPQ 847
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QY 821 N 821

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ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998
ACCESSIONS JH0562
REFERENCE JH0561
#authors Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
#journal Neuron (1992) 8:169-179
#title A family of metabotropic glutamate receptors.
#cross-references MUID:92110002
#accession JH0562
#molecule_type mRNA
#residues 1-879 #label TAN
#experimental_source brain
COMMENT This protein is coupled to a G protein and evokes a variety of functions by mediating intracellular signal transduction.
CLASSIFICATION #superfamily metabotropic glutamate receptor 4
KEYWORDS G protein coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
FEATURE

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MUSE (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MSEARCH protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:09:42 2000; MasPar time 14.57 Seconds

Tabular output not generated. 766,385 Million cell updates/sec

Title: >US-09-361-652-1
Description: (1-840) from US09361652.pep
Perfect Score: 6338
Sequence: 1 MLFWAAHLLSLQLVYCAWF.....NTEHFQASIDYTRCGTT 840

Scoring table: PAM 150
Gap 11

Searched: 134018 segs, 13297625 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:5_COMB 4:PCR9_COMB 5:backfiles1

Statistics: Mean 36.328; Variance 178.464; scale 0.204

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description	Pred. No.
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2	1311	20.7	1085	1 US-08-485-Sequence 5, Applicatio	3.70e-99
3	1311	20.7	1085	2 US-08-480-Sequence 5, Applicatio	3.70e-99
4	1311	20.7	1085	2 US-08-943-Sequence 5, Applicatio	3.70e-99
5	1311	20.7	1085	3 US-08-353-Sequence 5, Applicatio	3.70e-99
6	1290	20.4	1078	2 US-08-943-Sequence 7, Applicatio	2.40e-97
7	1290	20.4	1078	3 US-08-353-Sequence 7, Applicatio	2.40e-97
8	1290	20.4	1078	1 US-08-485-Sequence 7, Applicatio	2.40e-97
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18	1198	18.9	1088	3 US-08-480-Sequence 6, Applicatio	2.04e-89
19	1198	18.9	1088	2 US-08-943-Sequence 6, Applicatio	2.04e-89
20	1198	18.9	1088	1 US-08-485-Sequence 6, Applicatio	2.04e-89
21	1045	16.3	1219	2 US-08-687-Sequence 6, Applicatio	2.87e-76
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32	848	13.4	912	4 PCT-US91-0 Sequence 19, Applicati	1.98e-59
33	821	13.0	906	4 PCT-US91-0 Sequence 17, Applicati	3.93e-57
34	825	13.0	1056	2 US-08-687-Sequence 7, Applicatio	1.79e-57
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41	815	12.9	906	3 US-08-367-Sequence 2, Applicatio	1.27e-56
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ALIGNMENTS

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XX	Sequence 5, Application US/08484565			
CC	Sequence 5, Application US/08484565			
CC	Patent No. 5763569			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Edward M. Brown			
CC	APPLICANT: Steven C. Hebert			
CC	APPLICANT: James E. Garrett, Jr.			
CC	TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE			
CC	TITLE OF INVENTION: MOLECULES			
CC	NUMBER OF SEQUENCES: 20			
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESSEE: Lyon & Lyon			
CC	STREET: First Interstate World Center			
CC	STREET: Suite 4700			
CC	STREET: 633 West Fifth Street			
CC	CITY: Los Angeles			
CC	STATE: California			
CC	COUNTRY: USA			
CC	ZIP: 90071			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage			
CC	COMPUTER: IBM PC compatible			
CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC	SOFTWARE: FASTSEQ			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: US/08/484,565			
CC	FILING DATE: 7 June, 1995			
CC	CLASSIFICATION: 435			
CC	PRIOR APPLICATION DATA:			
CC	PRIOR APPLICATION DATA: including application			
CC	PRIOR APPLICATION DATA: described below: 9			
CC	APPLICATION NUMBER: 08/353,784			
CC	FILING DATE: 9 December, 1994			
CC	APPLICATION NUMBER: PCI/US/94/12117			
CC	FILING DATE: 21 October, 1994			
CC	APPLICATION NUMBER: U.S. 08/292,827			
CC	FILING DATE: 23 August, 1994			
CC	APPLICATION NUMBER: U.S. 08/141,248			
CC	FILING DATE: 22 October, 1993			

CC APPLICATION NUMBER: U.S. 08/009,389
CC FILING DATE: 23 February, 1993
CC APPLICATION NUMBER: U.S. 08/017,127
CC FILING DATE: 12 February, 1993
CC APPLICATION NUMBER: U.S. 07/934,161
CC FILING DATE: 21 August, 1992
CC APPLICATION NUMBER: U.S. 07/834,044
CC FILING DATE: 11 February, 1992
CC APPLICATION NUMBER: U.S. 07/749,451
CC FILING DATE: 23 August, 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Heber, Sheldon O.
CC REGISTRATION NUMBER: 38,179
CC REFERENCE/DOCKET NUMBER: 213/006
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1085 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1085 AA; 121170 MW; 6189757 CN;

Query Match	20.7%;	Score 1311;	DB 1;	Length 1085;
Best Local Similarity	31.9%;	Pred. No. 3.70e-99;		
Matches	272;	Conservative	232;	Mismatches 275;
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Db 90 PMNLGIYIFDTCNTVSKALEATLSFVAONKIDSLNDEFCNSEBHPTIAVVGATGSG 149
Qy 93 PNITGELYELDYCSSANVY--ATLEVLMLQGPRIHEIQR--DLNHSKVAFAFGPNTD 149
Db 150 ISTAVANLLGLFEYIQVYVYASSRLLSKNKFSLRTIPNDEHQATAMADIIIEYFRMN 209
Qy 150 HAVTTHALLGFLMLVSTYEASSVYLSKKRFPSLRTKVPDRHROYEVMVOLLDSFGW 209
Db 210 VGTIADDDYGRPGIEKREAEERDIDISELI--SOYSDERIKOQVEYVIONSTAKY 267
Qy 210 ISLISYDYGOLQVQALEELAVPRGICVAFEDIVFSARVGDDPRMQMHNQARTV 269
Db 268 IYVESSGDLEPLI--KELYRNITGRIMLASFMASSLLIMPEYFNHYGSTITGFLKAG 326
Qy 270 IYVFEN--RLHARVFRSVLANLTKEVVAEDMA---IS-T-YITSVT-IO-GI--G 318
Db 327 QIPGREFLOKHPRKSVHNGFPAKEFMEETFNCHIOEGAKPLPYDTPLRGHEGGARLS 386
Qy 319 TYLG----VA-VQOQO-Vp-GI-KEF-BESY---VR-AVTMA-P-S---ACPEG-SW-C 357
Db 387 NSPLAFRLCTGEEINISSEVETPYMDYTHLRISYNYVLAISIAHALODIYTCIFGRGLT 446
Qy 358 -S-TN-Q-LCECHFTTRNMTPLCAFMSAARYEYVAVVAAGLHOLLCTSE--I-- 409
Db 447 NGSCDIKKVEMOVLKRLHLNFTSNNGEQVTPREGDLAGNSIIMWHLSPDGSLVF 506
Qy 410 ---CG-RKPYVPMOLLQOITYKNVLLH--ENTVAFEDNDDTLGYDIIILAMDNGPE-WT-F 462
Db 507 KEVGYNYNYAKGERLTFENDERILMSGFSREVPFNSGRDCLAGTRKGIIEGEPYCCFEC 566
Qy 463 ELIG--SA-SLSPVHLIDNKTRIQWGNNGNOYRVSVCVTTDCLAGHRRVY--GSHHCCEC 518
Db 567 VECPEGYSDETDASACOKCPDDEFSNNHNSCIAKEIETLSWTEPFGIALTLFAVLGIT 626
Qy 519 VPCEAGTFLNMSLHICOPCGTEEMAPRESSTCEPRYEFLAMHEPIDISLVLIANTLILL 578
Db 627 LNAFLGVFI--KERTNPIYKANRRLSTLLEFSLCLCCSSSLF--SIGEPQWOTRLOPA 684
Qy 579 LTVGTAGLPAWHEH--TPVVRASGGLCTCLMIGSLVAG--SCGFYSFEGEPVPAQLLOPL 636

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Db	685	FGISEFVLCISCIILKTRKRVLLVFE--AKIPTSFRKRWGNGLQELVFLCTFMQIYCAI	742
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Db	743	WLNTAPSSSYNNHLEDELIIFITCEGSLALGFLIGYTC-LLAALICEFF-AFRSRRLPE	800
Qy	696	MLVMMTPRTPREYGRPFHVLIDECTEVN--SVGLLAFNTINILLISTFVCSYLKRELP	753
Db	801	NFNENAKFTISMLIFLFWMSFLPAVAST--GKRVSAVEVIALIAMSFGLLACTFENKY	859
Qy	754	NYNENAKCTFESLLINFVSWIAFFTM-ASIQSGSYLPAVAVNLAGLTITSGGSGFYLPKCY	812
Db	860	IILFRPSRNTIE	871
Qy	813	VILCRPELNTIE	824

RESULT	2		
ID	US-08-485-588-5	STANDARD;	PRT; 1085 AA
XX			
AC	xxxxxx		

Sequence 5, Application US/08485588

Sequence 5, Application US/08485588
Patent No. 5688938

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01  GENERAL INFORMATION:
02  APPLICANT: Edward M. Brown
03  APPLICANT: Steven C. Hebert
04  APPLICANT: Forrest H. Fuller
05  APPLICANT: James E. Garrett, Jr.
06  TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
07  TITLE OF INVENTION: MOLECULES
08  NUMBER OF SEQUENCES: 20
09  CORRESPONDENCE ADDRESS:
10  ADDRESSEE: Lyon & Lyon
11  STREET: First Interstate World Center
12  STREET: Suite 4700
13  STREET: 633 West Fifth Street
14  CITY: Los Angeles
15  STATE: California
16  COUNTRY: USA
17  ZIP: 90071
18  COMPUTER READABLE FORM:
19  MEDIUM TYPE: 3.5" diskette, 1.44 Mb storage
20  COMPUTER: IBM PC compatible
21  OPERATING SYSTEM: PC-DOS/MS-DOS
22  SOFTWARE: FASTSEQ
23  CURRENT APPLICATION DATA:
24  APPLICATION NUMBER: US/08/485,588
25  FILING DATE: 7 June, 1995
26  CLASSIFICATION: 435
27  PRIOR APPLICATION DATA:
28  PRIOR APPLICATION DATA: including application
29  PRIOR APPLICATION DATA: described below: 9
30  APPLICATION NUMBER: 08/353,784
31  FILING DATE: 9 December, 1994
32  APPLICATION NUMBER: PCT/US/94/12117
33  FILING DATE: 21 October, 1994
34  APPLICATION NUMBER: U.S. 08/282,827
35  FILING DATE: 23 August, 1994
36  APPLICATION NUMBER: U.S. 08/141,248
37  FILING DATE: 22 October, 1993
38  APPLICATION NUMBER: U.S. 08/009,389
39  FILING DATE: 23 February, 1993
40  APPLICATION NUMBER: U.S. 08/017,127
41  FILING DATE: 12 February, 1993
42  APPLICATION NUMBER: U.S. 07/934,161
43  FILING DATE: 21 August, 1992
44  APPLICATION NUMBER: U.S. 07/834,044

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149 VSTAVANLGLFPIPOYVASSSRLLSNKQKSFRTIPNDEHOATAMADIIEFRMW 208
150 HATYTAALLGFLPLPLVSYASSVLSAKRPFSLTVPSDROVEVMQLOSGW 209
209 VGTIADDDYGRPGIEKFEAEERDIDFSELI--SQVSEDEEIOHVEVIONSTAKV 266
210 ISLIGSYDYGQGLGVALELAVPRGICVAFKDIIVFSARVGDPRMQSMQHIAQARTTV 269
267 IIVFSSGPDLEPLI-KIIVRNITGKIMLSEAMASSLLAMPQYFHVGGTIFALKAG 325
270 VVVFSSN-RHLARVFFRSVLANLGLKVAASEDA---IS-T-YITSVG-ID-GI--G 318
326 QIDGFEFLKKVPRKSVHNGFAKEWEETFNCLQAGKPLPVDTLRCHESGGRFS 385
319 TVLG---VA-VOOR-V-P-GL-KEF-EES---VR-AVTA-P-S---ACPE-GSM-- 356
386 NSSTAPPLCTGDNISSEVETPYIDYTHLRISYVYLAVYSIAHALODIYTCPLGRGLFT 445
357 -CSIN-Q-LCRECTFTTRNPTIGAFMSAAVYEAVALAHQL---L-GC---T 406
446 NGSCADIKKKEANOVKLHLNLTNNMGEOVTDECGDLVGNSTLNMHSPDSGIVF 505
407 SEICS-RGPVPMQLQOIKVNFLLH-ENTVAEDDGDITLGYDITIAMWNGPE-WT-F 462
506 KEYGVYVYAKKGERLFINKEKILMSGFSREVPFNSCRDCLAGTRKGIIEGPTCCFEC 565
463 EITG--SA-SLSPVHDINKTKIOMHGKNNOVPSVCTTDLACHHRYV-GSHCCFEC 518
566 VECPDGEYDETDASACNKPDPFWSNENHTSCIAKEIEFLSWTEPGIALTLFVAVLIGIF 625
519 VPCEAGTFLLNMSLHICQPCGTBEWAKESITCPRTEVEFLAMHEPISVLIAANTLILL 578
626 LTAFLVGLVF-KRNTPIVATNBSLYLLFLCLCFSSSLF-FICEPQDWTCLRLOPA 683
579 LVTAGLFLAMHFR-TPVVSAGGRLCFLMGLSLVAG-SCSFYSFGEPTVPACILROPL 636
684 FGISEVVICISLIVKINRVLVE--AKIPTSFHKWGLNQLFLVLELCTFPMOIVCIV 741
637 FSLGFAFLSCLTIRSOVLIIFFRSTKVPT-FRTAQNHGAGLFIYVSTYVALLCLT 695
742 WLVTAPSSRYNOLEDELIIFITCHEGSLMALGFLIGTC-LLAICFFP-AFKSRKLP 799
696 WLVMVTRPRTRQRPRLVILECTEVN--SVGFLAFTNHILISTFVCSYGRKLP 753
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RESULT 7
ID US-08-353-784-7 STANDARD: PRT: 1078 AA.
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XXXXXX
Sequence 7, Application US/08353784
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CC Sequence 7, Application US/08353784
CC Patent No. 6011068
CC GENERAL INFORMATION:
CC APPLICANT: Edward F. Nemeth, Edward M.
CC APPLICANT: Brown, Steven C. Hebert,
CC APPLICANT: Bradford C. Van Wagener, Manuel
CC APPLICANT: F. Balandrin, Forrest H. Fuller,
CC APPLICANT: Eric G. DelMar, and Scott T. Moe
CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
CC TITLE OF INVENTION: MOLECULES

CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: First Interstate World Center
CC STREET: Suite 4700
CC STREET: 533 West Fifth Street
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: FASTSEQ
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/353,784
CC FILING DATE: 9 December, 1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC PRIOR APPLICATION DATA: including application
CC APPLICATION NUMBER: PCT/US/94/12117
CC FILING DATE: 21 October, 1994
CC APPLICATION NUMBER: U.S. 08/292,827
CC FILING DATE: 23 August, 1994
CC APPLICATION NUMBER: U.S. 08/141,248
CC FILING DATE: 22 October, 1993
CC APPLICATION NUMBER: U.S. 08/009,389
CC FILING DATE: 23 February, 1993
CC APPLICATION NUMBER: U.S. 08/017,127
CC FILING DATE: 12 February, 1993
CC APPLICATION NUMBER: U.S. 07/934,161
CC FILING DATE: 21 August, 1992
CC APPLICATION NUMBER: U.S. 07/834,044
CC FILING DATE: 11 February, 1992
CC APPLICATION NUMBER: U.S. 07/749,451
CC FILING DATE: 23 August, 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Heber, Sheldon O.
CC REGISTRATION NUMBER: 38,179
CC REFERENCE/DOCKET NUMBER: 209/069
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1078 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1078 AA; 120573 MW; 6153012 CN;
SQ
Query Match 20.4%; Score 1290; DB 3; Length 1078;
Best Local Similarity 32.0%; Pred. No. 2,40e-97;
Matches 273; Conservative 230; Mismatches 276; Indels 73; Gaps 49;
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OY 35 GDFLAGLFLSHDCLQVRRRPLVTSQDRPDS--FNGHGHLFQAMRFTVEELINSSALL 92
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OY 93 PNLTIGELIDVCSSESANVY-ATLRVALAOGPRHIEIOK--DLRNHSSKVAVFAGDPND 149
Db 149 VSTAVANLGLFPIPOYVASSSRLLSNKQKSFRTIPNDEHOATAMADIIEFRMW 208
OY 150 HATYTAALLGFLPLPLVSYASSVLSAKRPFSLTVPSDROVEVMQLOSGW 209
Db 209 VGTIADDDYGRPGIEKFEAEERDIDFSELI--SQVSEDEEIOHVEVIONSTAKV 266
OY 210 ISLIGSYDYGQGLGVALELAVPRGICVAFKDIIVFSARVGDPRMQSMQHIAQARTTV 269

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CC      ZIP: 90071
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: FASTSEQ
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/485,588
CC      FILING DATE: 7 June, 1995
CC      CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:
CC      PRIOR APPLICATION DATA: Including application
CC      PRIOR APPLICATION DATA: described below: 9
CC      APPLICATION NUMBER: 08/353,784
CC      FILING DATE: 9 December, 1994
CC      APPLICATION NUMBER: PCT/US/94/12117
CC      FILING DATE: 21 October, 1994
CC      APPLICATION NUMBER: U.S. 08/292,827
CC      FILING DATE: 23 August, 1994
CC      APPLICATION NUMBER: U.S. 08/141,248
CC      FILING DATE: 22 October, 1993
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CC      FILING DATE: 12 February, 1993
CC      APPLICATION NUMBER: U.S. 07/934,161
CC      FILING DATE: 21 August, 1992
CC      APPLICATION NUMBER: U.S. 07/834,044
CC      FILING DATE: 11 February, 1992
CC      APPLICATION NUMBER: U.S. 07/749,451
CC      FILING DATE: 23 August, 1991
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Heber, Sheldon O.
CC      REGISTRATION NUMBER: 38,179
CC      REFERENCE/DOCKET NUMBER: 213/005
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (213) 489-1600
CC      TELEFAX: (213) 955-0440
CC      TELEX: 67-3510
CC      INFORMATION FOR SEQ ID NO: 7:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 1078 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 1078 AA; 120573 MW; 6153012 CN;
SQ
Query Match          20.4%; Score 1290; DB 1; Length 1078;
Best Local Similarity 32.0%; Pred. No.2,40e-97;
Matches 273; Conservative 220; Mismatches 276; Indels 73; Gaps 49;
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Dh   89 PNLLGYRIPTCTYVSKALEATISPAFAOKKDIDSLNIDECNCESEHISTLAIVVGARGSG 148
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Qy   150 HAVTTAALLGFELMPLYSVSEASSVLAKRKRPSELTPVSDRQIVEMVOLLQSPGMW 209
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Dh   209 VGTLAADDDYRPGIEKFREFAEERDICIDISELT--SQSDEBEILOVVYEVIQNSTAKV 266
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Qy   210 ISLGISGDYDQLVOALEELAVPRGICVAFKDIIVPSARVGPDRMOSMOQHAAQTTV 269
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DB 446 NGSCADIKKVEAMOVHLRLHNLFTNNNGEOVTEDECGLDGNYSIIMHLSPEDEGSIVF 505
QY 407 SEIS-RGPVPMQLLOOIVKVNLLH-ENTVAFDNDNDITGYDIITAMDNGE-WT-F 462
DB 506 KEVYINYVAKKGRRLPINEKILMSGFSREVPSNCSRDCLAGRIIEGPTCCREC 565
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DB 566 VECDDGEYSDTDASACNKCDDEDFMSNNHTSCIAKEIEEFTSWTEPRGIALTLRAVLGIF 625
QY 519 VPCAGIFLNKSELHIQPCGTEEMAPRESTCEPRIVEFLAMEHPISLVLIANTLL 578
DB 626 LTAFLVGF1-KFRNPIVAKATNELSYLLFSLCCFSSSLF-FIGEPQDWTCLROPA 683
QY 579 LVVGTAGLFAMH-FTVVRASAGRLCEFLMGLSLAG-SCFYSFPGPTVPACLLRPL 636
DB 684 FGISFVLCISCLVKNRVLVEF-AKIPTSFRKMMGLNLFVLFLCTEQIVTCVI 741
QY 637 FSLGFATFLSCLTIRSFQLVIIKFSTKVPT-FYRTMAQNHGAGLFVIVSSTVHLLCLT 695
DB 742 WLYAPSSYRNQDELEIIFITCHEGSLMAGLIGTCL-LLAICFF-AFSRKRIPE 799
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QY 754 NYNNAKCVTSLLNFYSWIAFFTM-ASIVGSLPRAVNYLAGLITLSGSGIFLPCY 812
DB 859 IILKPSRNITE 870
QY 813 VILCRPELNTE 824

RESULT 9
ID US-08-484-565-7 STANDARD: PRT: 1078 AA.
XX
AC xxxxxx
XX
DT
Sequence 7, Application US/08484565
XX
CC Sequence 7, Application US/08484565
CC Patent No. 5763569
CC GENERAL INFORMATION:
CC APPLICANT: Edward M. Brown
CC APPLICANT: Steven C. Hebert
CC APPLICANT: James E. Garrett, Jr.
CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
CC TITLE OF INVENTION: MOLECULES
CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: First Interstate World Center
CC STREET: Suite 4700
CC STREET: 633 West Fifth Street
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: FASTSEQ
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/484,565

CC FILING DATE: 7 June, 1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC PRIOR APPLICATION DATA: including application
CC PRIOR APPLICATION DATA: described below: 9
CC APPLICATION NUMBER: 08/353,784
CC FILING DATE: 9 December, 1994
CC APPLICATION NUMBER: PCT/US/94/12117
CC FILING DATE: 21 October, 1994
CC APPLICATION NUMBER: U.S. 08/292,827
CC FILING DATE: 23 August, 1994
CC APPLICATION NUMBER: U.S. 08/141,248
CC FILING DATE: 22 October, 1993
CC APPLICATION NUMBER: U.S. 08/009,389
CC FILING DATE: 23 February, 1993
CC APPLICATION NUMBER: U.S. 08/017,127
CC FILING DATE: 12 February, 1993
CC APPLICATION NUMBER: U.S. 07/934,161
CC FILING DATE: 21 August, 1992
CC APPLICATION NUMBER: U.S. 07/834,044
CC FILING DATE: 11 February, 1992
CC APPLICATION NUMBER: U.S. 07/749,451
CC FILING DATE: 23 August, 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Heber, Sheldon O.
CC REGISTRATION NUMBER: 38,179
CC REFERENCE/PACKET NUMBER: 213/006
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ. ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1078 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1078 AA; 120573 MW; 6153012 CN;
SQ

Query Match 20.4%; Score 1290; DB 1; Length 1078;
Best Local Similarity 32.0%; Pred. No. 2,40e-97;
Matches 273; Conservative 230; Mismatches 276; Indels 73; Gaps 49;

DB 30 GDILGLFPIHFG-VAAKQDILKSRESVEICIRYNERGFRMLOAMFAEETINSSPALL 88
QY 35 GDFLLAGLFSLHGDCLQVRRHPLVTSQDRPDS--FNGGGLHFOAKFTVEETINSSALL 92
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DB 326 QIPGREFELKKVHRKSVHNGFAKEFMEETFNCHLOGAGKPLPVDITFLRGHEESGDRFS 385
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QY 407 SEICSGPYVPMQLOOIKYKVNFLH-ENTVAFDNDGDTLGYDIIAMDMNGPE-WT-F 462
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 DT
 XX
 De Sequence 7, Application US/08480751
 CC Patent No. 5858684
 CC GENERAL INFORMATION:
 CC APPLICANT: Edward F. Nemeth
 CC APPLICANT: Edward M. Brown
 CC APPLICANT: Steven C. Hebert
 CC APPLICANT: Forrest H. Fuller
 CC APPLICANT: James E. Garrett, Jr.
 CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
 CC TITLE OF INVENTION: MOLECULES
 CC NUMBER OF SEQUENCES: 20
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Lyon & Lyon
 CC STREET: First Interstate World Center
 CC STREET: Suite 4700
 CC STREET: 633 West Fifth Street
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90071
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: FASTSEQ
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/480,751
 CC FILING DATE: 7 June, 1995
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC PRIOR APPLICATION DATA: including application
 CC PRIOR APPLICATION DATA: described below: 9
 CC APPLICATION NUMBER: 08/353,784

CC FILING DATE: 9 December, 1994
 CC APPLICATION NUMBER: PCT/US/94/12117
 CC FILING DATE: 21 October, 1994
 CC APPLICATION NUMBER: U.S. 08/292,827
 CC FILING DATE: 23 August, 1994
 CC APPLICATION NUMBER: U.S. 08/141,248
 CC FILING DATE: 22 October, 1993
 CC APPLICATION NUMBER: U.S. 08/009,389
 CC FILING DATE: 23 February, 1993
 CC APPLICATION NUMBER: U.S. 08/017,127
 CC FILING DATE: 12 February, 1993
 CC APPLICATION NUMBER: U.S. 07/934,161
 CC FILING DATE: 21 August, 1992
 CC APPLICATION NUMBER: U.S. 07/834,044
 CC FILING DATE: 11 February, 1992
 CC APPLICATION NUMBER: U.S. 07/749,451
 CC FILING DATE: 23 August, 1991
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Hebert, Sheldon O.
 CC REGISTRATION NUMBER: 38,179
 CC REFERENCE/DOCKET NUMBER: 213/004
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (213) 489-1600
 CC TELEFAX: (213) 955-0440
 CC TELEX: 67-3510
 CC INFORMATION FOR SEQ ID NO: 7:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 1078 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQ ID: 1078 AA; 120573 MW; 6153012 CN;
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 Best Local Similarity 32.0%; P-ident. No. 2,40e-97;
 Matches 273; Conservative 230; Mismatches 276; Indels 73; Gaps 49;
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 QY 35 GDFLGLGFLSLHQDCIQVHRPLVYSCDRPDS-FNGHGYHLFOAMRPTVEINSSALL 92
 Db 89 PNLTLGRIPTICNTVSKALENTLSFVAQNKIDSLNLEFCSCSHISTIAVNGATSG 148
 QY 93 PNTLIGELYDYCESANY-ATLRVIALQGRHLEIQ--DLRHSKVAFAFGPDWTD 149
 Db 149 VSTAVANLIGLYIPOVSYASSRLLSKNKFSEPLRTIPNDEHQATAMADIIEYFRWN 208
 QY 150 HAVTTAALGPFLMPLVSEASVYLSAKRKPSFLRTVPDSRQVEMVQGLSFGVW 209
 Db 209 VGTIADDYGRGRTEKREAEEDICIDISELI--SQYDEDEIQVVEYIONSTAKV 266
 QY 210 ISLISGYDYGQVQALBELVAPRGICVAFKRDIVFSAFVGDPRMOSMOMHLQAARTV 269
 Db 267 IYVFGSDPLEPLI-KEIVRNITGKIWLASEAWASSSLIAMPQYFHYVGGTIFALKAG 325
 QY 270 VYVFSN-RHLARVFRSVYLANLTKSVVASEDMA---IS-T-YITSYG-IG-GI-G 318
 Db 326 QIPGFREFLAKYHPKSVHNGFAKEFMEETFNCHLQEGCAKPLEVDFTLRGHESGDRFS 385
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 QY 407 SEICSGPYVPMQLOOIKYKVNFLH-ENTVAFDNDGDTLGYDIIAMDMNGPE-WT-F 462
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ID	US-08-353-784-8		
AC	xxxxxx		
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XX			
DE	Sequence 8, Application US/08353784		
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CC	Sequence 8, Application US/08353784		
CC	Patent No. 6011068		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Edward F. Nemeth, Edward M.		
CC	APPLICANT: Brown, Steven C. Hebert,		
CC	APPLICANT: Bradford C. Van Wageningen, Manuel		
CC	APPLICANT: F. Balandin, Forrest H. Fuller,		
CC	APPLICANT: Eric G. Delmar, and Scott T. Moe		
CC	TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE		
CC	TITLE OF INVENTION: MOLECULES		
CC	NUMBER OF SEQUENCES: 20		
CC	CORRESPONDENCE ADDRESS:		
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CC	COUNTRY: USA		
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CC	COMPUTER READABLE FORM:		
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CC	COMPUTER: IBM PC compatible		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	SOFTWARE: FASTSEO		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/08/353,784		
CC	FILING DATE: 9 December, 1994		
CC	CLASSIFICATION: 514		
CC	PRIOR APPLICATION DATA:		
CC	PRIOR APPLICATION DATA: including application		
CC	PRIOR APPLICATION DATA: described below: 8		
CC	APPLICATION NUMBER: PCT/US/94/12117		
CC	FILING DATE: 21 October, 1994		
CC	APPLICATION NUMBER: U.S. 08/292,827		
CC	FILING DATE: 23 August, 1994		
CC	APPLICATION NUMBER: U.S. 08/141,248		
CC	FILING DATE: 22 October, 1993		
CC	APPLICATION NUMBER: U.S. 08/009,389		
CC	FILING DATE: 23 February, 1993		
CC	APPLICATION NUMBER: U.S. 08/017,127		
CC	FILING DATE: 12 February, 1993		
CC	APPLICATION NUMBER: U.S. 07/934,151		
CC	FILING DATE: 21 August, 1992		
CC	APPLICATION NUMBER: U.S. 07/834,044		
CC	FILING DATE: 11 February, 1992		
CC	APPLICATION NUMBER: U.S. 07/749,451		
CC	FILING DATE: 23 August, 1991		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Heber, Sheldon O.		
CC	REGISTRATION NUMBER: 38,179		
CC	REFERENCE/DOCKET NUMBER: 209/069		
CC	TELECOMMUNICATION INFORMATION:		

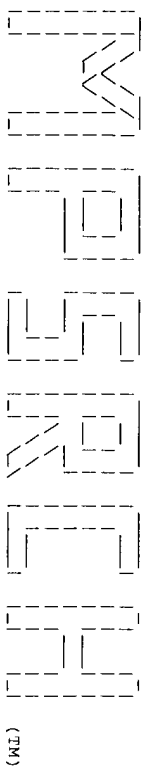
CC	TELEPHONE: (213) 489-1600
CC	TELEFAX: (213) 955-0440
CC	TELEX: 67-3510
CC	INFORMATION FOR SEQ ID NO: 8:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 1079 amino acids
CC	type: amino acid
CC	TOPOLOGY: linear
CC	MOLECULE TYPE: protein
CC	SEQUENCE 1079 AA: 120867 MW; 6054255 CN;
Query Match	20.3% Score:1285; DB 3; length 1079;
Best Local Similarity	31.5% Pred. No.6,48e-97;
Matches 212; Conservative 232; Mismatches 285; Indels 73; Gaps 50.	
Db	30 GDIIIGLGFPIHFQ-VAAKDODLKSREVEECIHYNRGRFMIQAMIFAIEE-NSPSLL 88
Qy	35 GDPLIAGLFSIHGOCLOQRHRRPITISCDRDS--FNHGHTLQAMFTYDELINNSALL 92
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Db	149 VSTAAANLGLFIIPQVSYASSSSLLSNKQYKFFLTINDEHQRAAMDIEYFRMMW 208
Qy	150 HAVTTAALLGLFIMPLIVSYEASVYLAKRKFPELITVPSDRQVEVKNQLQSPGW 209
Db	209 VGTIADDDYDRPGIEKFEAEERDIDIPSELI--SYSDSEIIOQVEVIONSTAY 266
Qy	210 ISLIGSYDIDYQLGVALLELAVVRGICVAFKDIVPFSARVGDPRMSMQHQAQITV 269
Db	267 IVFSSGDEPLI-KEIVRRNITGRIMLASEAWASSLLIAMEYFHVGGITGFGIKAG 325
Qy	270 VVFEEN-RHLARVFEFRSVLANITGKWWASEDA---IS-T-YRSTVG-IO-GI--G 318
Db	326 QIPGRRELQVHRKSYHNGFAKEFMEETPNCLQSGAGPLVPDTFVASHDEGGRL 365
Qy	319 TVLG---VA-VQQRQ--VP-GL-KEF-EESY---VR-AVTA-P-S-A-CPE--GSM-- 356
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Qy	357 -CSTN-Q-LCECHTFTTRNPTIGATSMASNAVYIAVVAHGHQL---L-GC---T 406
Db	446 NGSCADIKKVEAMOVLEHLRLNFTNMKGQVTFDECCDVGANSYLSNMHLSPEDSIVF 505
Qy	407 SEIOS-RGPVYPQMLIQIYKVNFLH-EMTVARDNGDTLGYDIIAMOMNPE-WT-F 462
Db	506 KEVGYNNYAKKGERLTINEKILMSGFSREVPFSNCSRDCQATRKGITIEGPTCCFEC 565
Qy	463 EIIG--SA-SLSPHLDINKKILCWGCKNNQVPVSVTICLGNHVVV--GSHCCFEC 518
Db	566 VECPDGEVSGEETASACDKCPDDFSWSENHTSCIAETEFLEMTAREGIMLLEFVIGIF 625
Qy	519 VPCEAGTFLNWSLEHIDOPGTEEMAKESTGCPKRVETLAMEHPISLVLIANTLLLL 578
Db	626 LTAFLVGLFY-KFRNTPIVAKTNRELTYLLFLSLCCFSSSLF-FIGEPQDTCRLROPA 683
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Db	684 FGISFVLCISCTILVKNRVLVEF--AKIPTSFRRKMGINLOFLVFLDCTEMOILCIT 741
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Qy	696 WLVMPTPEPTIEYQRPFLVILDETEVN--SVGLLFTINILISTSTFCSTVIGELPE 753
Db	800 NFNKAFTFESMLFFIIVMISFIPAVASTY-GKFSVAEVIALLAASFGILACIFPNKY 858
Qy	754 NYNKAQVTSFLLNLFVSMIAFFIM-ASIVQGSILPRAVNVLAGITITSGFSQIFLPKC 812
Db	859 ILFRPSRNTIEVRSSTAHA 880

DT
XX
DE
XX
Sequence 8, Application US/08485588
CC
CC
Sequence 8, Application US/08485588
CC
Patent No. 5686938
CC
GENERAL INFORMATION:
CC
APPLICANT: Edward M. Brown
CC
APPLICANT: Steven C. Hebert
CC
APPLICANT: Forrest H. Fuller
CC
APPLICANT: James E. Garrett, Jr.
CC
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
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TITLE OF INVENTION: MOLECULES
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NUMBER OF SEQUENCES: 20
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CORRESPONDENCE ADDRESS:
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ADDRESSEE: Lyon & Lyon
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STREET: First Interstate World Center
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STREET: Suite 4700
CC
STREET: 633 West Fifth Street
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CITY: Los Angeles
CC
STATE: California
CC
COUNTRY: USA
CC
ZIP: 90071
CC
COMPUTER READABLE FORM:
CC
MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
CC
COMPUTER: IBM PC compatible
CC
OPERATING SYSTEM: PC-DOS/MS-DOS
CC
SOFTWARE: FASTSEQ
CC
CURRENT APPLICATION DATA:
CC
APPLICATION NUMBER: US/08/485,588
CC
FILING DATE: 7 June, 1995
CC
CLASSIFICATION: 435
CC
PRIOR APPLICATION DATA:
CC
PRIOR APPLICATION DATA: including application
CC
PRIOR APPLICATION DATA: described below: 9
CC
APPLICATION NUMBER: 08/353,784
CC
FILING DATE: 9 December, 1994
CC
APPLICATION NUMBER: PCT/US/94/12117
CC
FILING DATE: 21 October, 1994
CC
APPLICATION NUMBER: U.S. 08/292,827
CC
FILING DATE: 23 August, 1994
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APPLICATION NUMBER: U.S. 08/141,248
CC
FILING DATE: 22 October, 1993
CC
APPLICATION NUMBER: U.S. 08/009,389
CC
FILING DATE: 23 February, 1993
CC
APPLICATION NUMBER: U.S. 08/017,127
CC
FILING DATE: 12 February, 1993
CC
APPLICATION NUMBER: U.S. 07/934,161
CC
FILING DATE: 21 August, 1992
CC
APPLICATION NUMBER: U.S. 07/834,044
CC
FILING DATE: 11 February, 1992
CC
APPLICATION NUMBER: U.S. 07/749,451
CC
FILING DATE: 23 August, 1991
CC
ATTORNEY/AGENT INFORMATION:
CC
NAME: Hebert, Sheldon O.
CC
REGISTRATION NUMBER: 38,179
CC
REFERENCE/DOCKET NUMBER: 213/005
CC
TELECOMMUNICATION INFORMATION:
CC
TELEPHONE: (213) 489-1600
CC
TELEFAX: (213) 955-0440
CC
TELEX: 67-3510
CC
INFORMATION FOR SEO ID NO: 8:
CC
SEQUENCE CHARACTERISTICS:
CC
LENGTH: 1079 amino acids
CC
TYPE: amino acid
CC
TOPOLOGY: linear
CC
MOLECULE TYPE: protein
CC
SEQUENCE 1079 AA: 120867 MW: 6054255 CN:
SO

Query Match 20.3%; Score 1285; DB 1; Length 1079;
Best Local Similarity 31.5%; Pred. No. 6,48e-97;
Matches 272; Conservative 232; Mismatches 285; Indels 73; Gaps 50;

Db
30 GDILGLGFPFIHFG-VAAKDQDKSRPSEVCEIRNFRGRLQAMIFAELIINSSPSLL 88
QY
35 GDFLLACLFLSHGDCLOVRRHRPLVTSQDRPDS--FNHGTHLQAMFTVEELINSSALL 92
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89 PNMTLGRIFDTCNTVSKALEATISFYAOKKIDSLNIDFCNCSSEHIFPSTIAVATGSG 148
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149 VSTAVANLLGFIYIPQVSYASSSSRLSNKNOYKSFRTIINDENQOARAMDIEYFPMW 208
QY
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Db
209 VGTIAADDDYGRPGIEKFESEAEERDICIIDFSEII--SQYSDEEIQOQVEVIONSTAKY 266
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859 IILFKPSRNTIEVRSSTAAHA 880
QY
813 VILCRPELNTEHFOASIDQYT 834

Search completed: Fri Mar 17 13:10:13 2000
Job time : 31 secs.



(TM)

Release 3.1A John F. Collins, Bioinformatics Research Unit.
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Msearch_dp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:00:08 2000; Maspar time 39.94 Seconds

Tabular output not generated.

Title: >US-09-361-652-1

Description: (1-840) from US09361652.pep

Sequence: 1 MLFMAHLLSLQLVYCAAF.....NNTFFQASIDYTRCGCT 840

Scoring table: PAM 150

Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-geneseq36

1:geneseqp

Statistics: Mean 38.602; Variance 175.356; scale 0.220

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1311	20.7	1085	1	W89563	1.79e-106
2	1311	20.7	1085	1	W54844	1.79e-106
3	1311	20.7	1085	1	W38272	1.79e-106
4	1290	20.4	1078	1	W54846	1.61e-104
5	1290	20.4	1078	1	W89565	1.61e-104
6	1290	20.4	1078	1	W11889	1.61e-104
7	1290	20.4	1078	1	W38273	1.61e-104
8	1285	20.3	1078	1	W94928	1.71e-104
9	1285	20.3	1079	1	W54847	4.71e-104
10	1285	20.3	1079	1	W89565	4.71e-104
11	1285	20.3	1079	1	W38275	4.71e-104
12	1230	19.4	1026	1	W32059	6.16e-99
13	1199	18.9	1088	1	W38273	4.68e-96
14	1198	18.9	1088	1	W54845	5.80e-96
15	1198	18.9	1088	1	W89564	5.80e-96
16	1198	18.9	1088	1	W11888	5.80e-96
17	1045	16.5	1219	1	W25763	8.87e-82
18	1030	16.3	1058	1	W25762	2.16e-80
19	972	15.3	779	1	W94921	4.92e-75
20	861	13.6	1180	1	W64253	8.15e-65
21	862	13.6	1212	1	R64254	6.10e-65
22	855	13.5	877	1	R64255	2.90e-64
23	844	13.3	850	1	W94901	2.96e-63

24	838	13.2	872	1	R95052	Human metabotropic glu	1.05e-52
25	837	13.2	912	1	R82658	Human mglur4.	1.30e-62
26	834	13.2	912	1	R72092	Human mglur4.	2.45e-62
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30	819	12.9	872	1	R89580	Metabotropic glutamate	5.82e-61
31	815	12.9	906	1	R64250	Human mglur1B.	1.35e-60
32	812	12.8	1194	1	R42199	Hmglur1.	2.55e-60
33	808	12.7	866	1	W94920	Rat pheromone receptor	5.92e-60
34	808	12.7	877	1	R82657	Human mglur3.	5.92e-60
35	804	12.7	879	1	R64252	Human mglur3.	1.38e-59
36	805	12.7	1056	1	W25765	Amino acid sequence of	1.12e-59
37	800	12.6	908	1	W41568	Human metabotropic glu	3.20e-59
38	799	12.6	908	1	W49928	Human metabotropic glu	3.95e-59
39	795	12.5	803	1	W94903	Muscle pheromone recept	9.18e-59
40	779	12.3	877	1	W01099	Metabotropic glutamate	2.67e-57
41	760	12.0	867	1	R72093	Human mglur7 clone cmr	1.46e-55
42	758	12.0	915	1	R72097	Human mglur7A.	2.22e-55
43	760	12.0	922	1	R72098	Human mglur7B.	1.46e-55
44	755	11.9	667	1	W94919	Rat pheromone receptor	4.17e-55
45	755	11.9	915	1	R80479	Rat metabotropic gluta	4.17e-55

ALIGNMENTS

RESULT 1
ID W89563 standard; Protein: 1085 AA.

AC W89563;

DT 19-MAR-1999 (first entry)

DE Bovine parathyroid calcium receptor BopCar 1.

KW Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;

KW calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;

KW spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;

KW neonatal distress; neurodegenerative disease; Alzheimer's disease;

KW Huntington's disease; Parkinson's disease; dementia; muscle tension;

KW depression; anxiety.

OS Bos sp.

PN US5858684-A.

PD 12-JAN-1999.

PF 07-JUN-1995; US-480751.

PR 07-JUN-1995; US-480751.

PR 23-AUG-1991; US-749451.

PR 11-FEB-1992; US-834044.

PR 21-AUG-1992; US-934161.

PR 12-FEB-1993; US-017127.

PR 23-FEB-1993; US-009389.

PR 22-OCT-1993; US-141248.

PR 19-AUG-1994; US-292827.

PR 21-OCT-1994; WO-012117.

PR 08-DEC-1994; US-353784.

PA (BGM) BRIGHAM & WOMENS HOSPITAL.

PA (NPSP) NPS PHARM INC.

PI Balandrin MF, Brown EM, Del Mar EG, Garret JE,

PI Hebert SC, Nemeth EF, Van Wageningen BC;

DR WPI: 99-119871/10.

DR N-PSDB: V82483.

PT Screening for calcium receptor-active compounds - by recombinant

PT expression of nucleic acid encoding calcium receptor and determining

PT the effect of compounds on calcium receptor activity

PT Claim 1: Fig 47: 175pp; English.

CC A method has been developed of screening for a compound able to affect

CC one or more activities of a calcium receptor (CR) comprises: (A)

CC contacting a recombinant cell with a test compound, where the

CC recombinant cell comprises a recombinant nucleic acid expressing from

CC provided that the cell does not have functional CR expression from

CC endogenous nucleic acid; (B) determining the ability of the test

CC compound to affect one or more activities of the calcium receptor; and

CC (C) comparing the ability with the ability of the test compound to

CC affect the one or more CR activities in a cell not comprising the

CC recombinant nucleic acid. The present sequence represents bovine

CC parathyroid CR, designated a BopCar 1. The nucleic acid sequence of

CC BopCar 1 can be used as part of the recombinant nucleic acid in the

method described above. The compounds identified can be used to treat diseases or disorders characterized by abnormal calcium homeostasis, e.g. hyperparathyroidism, osteoporosis and other bone and mineral-related disorders. They can also be used for the treatment of diseases and disorders associated with disrupted Ca²⁺ responses, e.g. seizures, stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in cardiac arrest or neonatal distress, epilepsy, neurodegenerative diseases such as Alzheimer's disease, Huntington's disease and Parkinson's disease, dementia, muscle tension, depression, and anxiety. Sequence 1085 AA;

Query Match 20.7%; Score 1311; DB 1; Length 1085;

Best Local Similarity 31.9%; Pred. No. 1.79e-106; Matches 272; Conservative 232; Mismatches 275; Indels 73; Gaps 50;

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Db 31 GDIIIGLGFPIHFG-VAVKDDDKSRPESVCIRYNGFRWQAMFAIEINSSPALL 89
QY 35 GDFLLAGLFLSHGCLQVRRHPLVTSQDRPDS--FNGHGHLQAMFTVEINSSALL 92
Db 90 PNMTLGRIIDTCNTVSKALEATLSFYAOKNIDSLNIDFNCSEHPISTIYAVGATGSG 149
QY 93 PNITLGEYLIVGSESAVNY-ATLRVLAQGPRIHEIOK--DLRNHSSKVAFIIGPONTD 149
Db 150 ISTVANILGLFYIPQVSYASSSRLSKNOKSFLEITPDEHOATAMADIIEYFRMNM 209
QY 150 HAVTTAALLGFLPLVSYEASSVYLSAKRFPSELTVPDSRQVEVMQVLLQSGVW 209
Db 210 VGTIAADDDVGRPIEKEFREAEERDIDSELI--SQYSDERKIQOVVEVIONSTAKV 267
QY 210 ISLIGSGDVGQVQALQELAEVAPRGICVARKDIVPSARVGDPRQSMQHLQARTTV 269
Db 268 IYVSSGPDLEPLI-KEIVRRNITGRIMLASEMASSSLIAMPYFHVGGTIGFGLAG 326
QY 270 VYVFSN-RHLARVFRSVYLANLGKVVASEDA---IS-T-YITSVG-IQ-GI--G 318
Db 327 QIPGFRFLQVHPRKSVHNGFAKEFWETNCHLQSGAKRPLPYDFFLRGHEGGARLS 386
QY 319 TVLQ---VA-VQOOR-V-P-GL-KEF-EESY---VR-AVTAA-P-S---ACPEG-SW-C 357
Db 387 NSPAPFRICGSEINISSEVENPYMDYTHLRISYNYLAVYIAHLODIYICIRGRLFT 446
QY 358 -S-TN-Q-LECHETFTTRNMPITLGAFSMAVRYEVAVAHQLOLCTIS-- 409
Db 447 NGSCADIKKVEAMOVKLRLHNLFTSNMGEQVTEDECDLAGNYSIIMHLSPEDEGIVE 506
QY 410 --CS-RGPVYPMQLQIYKVNFLH-ENTVAFDDNGDTIGYDIAMONGPE-WT-F 462
Db 507 KEVGIYNYAKGERLFINDEKILMSGFSREVPFSSNCRDLAAGTRKGIIGEPCCPEC 566
QY 463 EIIG-SA-SLSPVHLINKTRKIQHGNNOVPVSVCTTDLAGHRRVYV-GSHHCPEC 518
Db 567 VECPDGEVSDETDASACDPCDDFMSNENHTSAKEIEIFSWTEPFGIALTLFVAVIGIF 626
QY 519 VPCENAGFTLNSELHICOPGTEEMAPKESTICPRIVEFLAMHEPISLIANTLILL 578
Db 627 LTAFLVGLFI-KFRNTPIVKATNRELSTLLFSLCCPSSSLF-FIGEPQDTCRLROPA 684
QY 579 LLVGTAGLFAHFRH-TVPVRSAGRLCFMLGSLVAG-SCSFYSPFGSPYAPACILRPL 636
Db 685 FGISFVLCISILVKTNRVLLVFE-AKIPFSFHKRWGLMLQTLVFLCFPMQIVICAI 742
QY 637 FSLQFAFLSCLTIRSFQVLIIFKSTKVPY-FYRTMQNNGAGLFIYVSTVHLLICLT 695
Db 743 WLNAPSSYNNHELEDEIIFITCEGSLMALGFLIGYC-LIAAICFF-AFKSRKLE 800
QY 696 WLVNMPTRPIREYRFRPLVLTCEEVN--SVGFLATNHNILSISTFVCSYKLEIPE 753
Db 801 NFENAKFTFESMLFFIYVWISFIPAYASTY-GKFSYSAVEVIAIILASGLLACIFENKY 859
QY 754 NYNEKCVTFELLLNLFVSMIAFFTM-ASLYOGSYLPANVYLAGLTLTSGGSGYFLPKCY 812
Db 860 IILFRPSNITE 871

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QY 813 VILCPRLNTE 824

RESULT 2

ID W54844 standard: Protein; 1085 AA.

DT 01-SEP-1998 (first entry)

DE Bovine parathyroid calcium receptor 1 protein 5kb fragment.

KM Calcium ion concentration; parathyroid hormone; homeostasis;

KW kidney; calcium receptor; detection.

OS Bos sp.

PN US5763569-A.

PD 09-JUN-1998.

PF 07-JUN-1995; 484565.

PR 07-JUN-1995; US-484565.

PR 23-AUG-1991; US-749451.

PR 11-FEB-1992; US-834044.

PR 21-AUG-1992; US-934161.

PR 12-FEB-1993; US-017127.

PR 23-FEB-1993; US-009389.

PR 22-OCT-1993; US-141248.

PR 19-AUG-1994; US-292827.

PR 21-OCT-1994; WO-012117.

PR 08-DEC-1994; US-353784.

PA (BGM) BRIGHAM & WOMENS HOSPITAL.

PA (NPS-) NPS PHARM INC.

PI Brown EM, Garrett JE, Hebert SC;

DR WPI: 98-347412/30.

DR N-PSDB; V26962.

PT Calcium receptor poly:peptide(s) - useful for drug screening or

PT antibody production

PS Claim 5; Fig 47; 1749p; English.

CC The bovine parathyroid calcium receptor gene encodes a 1085 amino acid

CC protein. The tissue from which this receptor and receptors from human

CC parathyroid and rat kidney are derived, respond to changes, and control

CC changes, in calcium ion concentration, e.g. parathyroid hormone regulates

CC Ca²⁺ homeostasis in blood and extracellular fluid, and kidney function

CC alters through changes in Ca²⁺ levels in juxtaglomerular and proximal

CC tubule cells in the kidney. The purified receptors (produced

CC recombinantly) can be used to screen for compounds that modulate calcium

CC receptor activity, especially those that can be used to treat diseases

CC associated with the receptors in these tissues. They can also be used

CC to raise antibodies for use in detection assays.

Sequence 1085 AA;

Query Match 20.7%; Score 1311; DB 1; Length 1085;

Best Local Similarity 31.9%; Pred. No. 1.79e-106; Matches 272; Conservative 232; Mismatches 275; Indels 73; Gaps 50;

```

Db 31 GDIIIGLGFPIHFG-VAVKDDDKSRPESVCIRYNGFRWQAMFAIEINSSPALL 89
QY 35 GDFLLAGLFLSHGCLQVRRHPLVTSQDRPDS--FNGHGHLQAMFTVEINSSALL 92
Db 90 PNMTLGRIIDTCNTVSKALEATLSFYAOKNIDSLNIDFNCSEHPISTIYAVGATGSG 149
QY 93 PNITLGEYLIVGSESAVNY-ATLRVLAQGPRIHEIOK--DLRNHSSKVAFIIGPONTD 149
Db 150 ISTVANILGLFYIPQVSYASSSRLSKNOKSFLEITPDEHOATAMADIIEYFRMNM 209
QY 150 HAVTTAALLGFLPLVSYEASSVYLSAKRFPSELTVPDSRQVEVMQVLLQSGVW 209
Db 210 VGTIAADDDVGRPIEKEFREAEERDIDSELI--SQYSDERKIQOVVEVIONSTAKV 267
QY 210 ISLIGSGDVGQVQALQELAEVAPRGICVARKDIVPSARVGDPRQSMQHLQARTTV 269
Db 268 IYVSSGPDLEPLI-KEIVRRNITGRIMLASEMASSSLIAMPYFHVGGTIGFGLAG 326
QY 270 VYVFSN-RHLARVFRSVYLANLGKVVASEDA---IS-T-YITSVG-IQ-GI--G 318
Db 327 QIPGFRFLQVHPRKSVHNGFAKEFWETNCHLQSGAKRPLPYDFFLRGHEGGARLS 386
QY 319 TVLQ---VA-VQOOR-V-P-GL-KEF-EESY---VR-AVTAA-P-S---ACPEG-SW-C 357

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Db	NSPTAFRPLCLGEEISSVEIPYNDYTLRLRSYNYLAVYSIAALADYITCIIGRLFT	446
Db	387	
Oy	358 -S-TL-Q-LCRCACTFTRNMTLGAFGMSAARYEAYEVAAGHLGCGISE--I--	409
Db	447	
Oy	410 ---CG-RGPVYFMWLQOITYVNFLLH-ENTVAEDDNGDILGYDITIAMDNQPE-WT-F	462
Db	507	
Oy	463 ELIG--SA-SLSPVHLDKTKIKQWCKGNQVVPVSVCTDCLDAHHRYVV-GSHCCFEC	518
Db	567	
Oy	519	
Db	627	
Oy	579	
Db	685	
Oy	637	
Db	743	
Oy	696	
Db	801	
Oy	754	
Db	860	
Oy	813	
RESULT	3	
ID	M38272 standard: Protein: 1085 AA.	
AC	M38272:	
DT	08-MAY-1998 (first entry)	
DE	Bovine parathyroid cell calcium receptor 1 (BoPCar 1).	
KW	Bovine parathyroid cell calcium receptor 1; BoPCar 1;	
KW	calcium homeostasis; hyperparathyroidism; osteoporosis.	
OS	Bos sp.	
PN	US5688938-A.	
PD	18-NOV-1997	
PF	07-JUN-1995; 485588.	
PR	23-AUG-1995; US-485588.	
PR	11-FEB-1992; US-749451.	
PR	21-AUG-1992; US-834044.	
PR	12-FEB-1993; US-934161.	
PR	23-FEB-1993; US-009389.	
PR	22-OCT-1993; US-141248.	
PR	19-AUG-1994; US-292827.	
PR	21-OCT-1994; WO-U12117.	
PR	08-DEC-1994; US-353784.	
PA	(BGHM) BRIGHAM & WOMENS HOSPITAL.	
PA	(NPSW-) NPS PHARM INC.	
PI	Brown EM, Fuller FH, Garrett JE, Hebert SC;	
DR	WPI: 98-008040/01.	
DR	N-PSDB: 195857.	
PT	DNA encoding calcium receptor polypeptide(s) - useful for	
PT	therapeutic purposes, e.g. hyperparathyroidism and osteoporosis	
PS	Claim 4; Columns 107-116; 174pp; English.	
CC	The present sequence is bovine parathyroid cell calcium	
CC	receptor 1 (BoPCar 1).	
CC	The specification includes details of molecules that can modulate	
CC	one or more inorganic ion receptor activities, and antibodies and	
CC	antibody fragments targeted to inorganic ion receptor proteins. The	
CC	proteins, nucleic acids and antibodies may be used to treat	
CC	disorders by modulating one or more inorganic ion receptor	

CC	activities, preferably disorders of calcium homeostasis, e.g.
CC	hyperparathyroidism and osteoporosis.
SQ	Sequence 1065 AA;
	Query Match 20.7%; Score 1311; DB 1; Length 1085;
	Best Local Similarity 31.9%; Pred. No. 1.79e+106;
	Matches 272; Conservative 222; Mismatches 275; Indels 73; Gaps 50.

D	b	31	GDILIGLSPFIHPG-VANQDDOLKSRRESVCIYNRGRGRLOAMFEALFEENSSALL	89
Q	y	35	GDFLIAGLFSJHGDGLOHRRRLVTSQDRPS--FNGGTHLPAMFATVEELNSSALL	92
D	b	90	PNMILGYRIPTDCTVSKALEPATLSFYAONKIDSLN,DEFCNGSEH,PTJIAVGAATGSG	149
Q	y	93	PIILGYELDYVCSSEANVY-ATLRVLA,GPRIIE-CK--DLRNHSSKVAFI,GPDNTD	149
D	b	150	ISTAVANLLGFYIPQVSYASSSLLSKNOFKSFLETIPNDEHQATAMADITIEFRMNV	209
Q	y	150	HAVITAAALLGFELMPLVSEYASSVVLSSAKRFPSEFLITVSDRQVQVEVMQLOLQSEGMV	209
D	b	210	VGTIAADQVDRPGIEKREAEERD,ICIDSESL--SQSDEKIQQVVEVIONSRAXV	267
Q	y	210	ISLISYDQYDQLOQALEELAYPRGICVAKDIPVPSARVGDPRMSQMOHLQAATTV	269
D	b	268	IYVFSSGDLEPLI-KEIVRNNIGRIALISEAMASSLSIAMPYFHWVGITIGFGKAG	326
Q	y	270	VYVEN-RLHARVEFRSVYLANL,CKWVWASDEMA----IS-TYISVYG-ID-GI--G	318
D	b	327	QIPGRREFLOVHPRKSVYHNGFAKEEMETFNCHLOGAGKPLDPVDTFLRGHEGGARLS	366
Q	y	319	TVLG--VA-VQORQ-VP-DL-KEF-EESY--VR-AVTAA-P-S--ACEPG-SM-C	357
D	b	387	NSPTAFRLCGEENISSVEELPMYDTHLRSTVYVLYANYSIALADIDITCIGRRLFT	446
Q	y	358	-S-TN-Q-LCECHETTRNNPTLGATSMASAVVYVYVAVALGCHQLIGCTSE--I--	409
D	b	447	NGSCADIRKVMQCVLKHRL,ELNTSNXGEQVTEDECGDLAGNYSIINHMLSPEDGSIVF	506
Q	y	410	--CG-RQPYVPMQLOQIYXVNLH-ENMVARDNGDITLGYDDIAMDNGPE-WT-F	462
D	b	507	KEYGVNYVAKKGERLPIINDEXILMSGFSREVPVPSNCSRDCLAGTRKGIIEGPTCCFEC	566
Q	y	463	ELIG--SA-SLSPVHLIDINKIKIOMHGKNNOPVPSVCTDCLAGHHRVVY-GSHCCFEC	518
D	b	567	VECPGGEUSDENASACQKCDPDMNSNHNHSCIAKEIEFLSWTEPRGIALTLFVAVGIF	626
Q	y	519	VPCEAGTLNSELHICOPCCTEEMAPKESITCGPRVSEFLAMEHPISTVLIAANTLLL	578
D	b	627	LTAFLVGLFYI-KFRNTPVYKATNREL,SYLLFSLLCCFSSSLF-FIGEPDWTCLRLOPA	684
Q	y	579	LLVYTAGLFLAMHFH-TPVYRAGGRCLCFMLGMSLVAG-SCSFYFPEPEPIVPAOLRQPL	636
D	b	665	FGISVCLDISCILTAKTNRVLLVFE-AKIPTSEHRRKMKGLNLOFLVLCOTEMOYICAI	742
Q	y	637	FSLGAIRLSCLITRISFOLVYIEFFSIRKVPF-FRTMAONHAGGLFVIVASTVHLLICLT	699
D	b	743	WLNTAPPSYSNNHLEDDIITTCHEGSMALGVLJYTC-LLAALCFE-ARKSKRLPE	800
Q	y	656	WLVMYTPRTSEYORFPHVLILECTEVN--SVGLAFTHNILLISTFPCSYIGKRLPE	753
D	b	801	NFENAKFTFEMLLFFIYIWISFIPAYASTY-GKVSAAVEVIAI,IAASFGLACIFERKXY	859
Q	y	754	NYNEAKCTVELLNTFVSWIMFFTM-ASIVOGSILPRAVNYLAGITLISGGFSGIFLPCY	812
D	b	860	IILFKPSRNTTE	971
Q	y	813	VICLRPELNTE	824
RESULT 4				
ID W54846 standard; Protein; 1078 AA.				
AC W54846.				
DT 01-SEP-1998 (first entry)				

[illegible]

Db	506	KEVGVYNYAKKGGELFVNEKILMMSGSPREVPFNSNRDCLAGTRKGIIEGPTCCFEC	565
Qy	463	ELIG--SA-SLSPHLDINKTKIOMHGKNNOVPYVCTTDCLAGHHVYV-GSHCCFEC	518
Db	566	VECPDGEYSDETDASACNCKPCDPDWSNENHTSCIAKEIEFLSWTEPGIALTLFVAVGIF	625
Qy	519	VPCEAGTFLNMSLEHICOPCTEEMAPRESPTCEPRTEVFLAMEHPISTVLIAANTULLL	578
Db	626	LTAFLVGFET-KFRNTPYKATNELSYLLFLSLCCPSSSLF-FIEPDQWICRLAQPA	683
Qy	579	LLVGTAGLEFAMHFH-TPVRSAGRLCFLMGSLVAG-SCSFYSFTEPVPALLOPL	636
Db	684	FGISFVLCISCIILVKTNNLVLFV--AKIPSFRRKMGVGNLQPLVFLCTFMOIVICVI	741
Qy	637	FSLGAIPLSLCLTRISQVLVIFEFSTIKVPF-FRTAQNQHAGLFLFVYSTYHLLCLT	695
Db	742	WLTYAPSSSYRNOELEDEIIFITCHESSLMALGFLIGYTC-LLAALICFF-AFKSRKLP	799
Qy	696	WLVMVTPPTREYORFPLVLLETENV--SVGELLFTNHILLISTFVCSYLGKELPE	753
Db	800	NFNEKFTTEMLFEFTYIWISFIYAVASTY-GKRVSAVEYIATILAAFGLLACFFPKIY	858
Qy	754	NYNEKCTYFSLNLNFWSWIAFFTM-ASTYOGSLYPAVNLAGLTLLSGSFGYIPRCY	812
Db	859	IILFKSRNTE 870	
Qy	813	VILCRPELNTE 824	
RESULT	5		
ID	ID	W89565 standard; Protein; 1078 AA.	
AC	AC	W89565;	
DE	DE	19-MAR-1999 (first entry)	
KW	KW	Human parathyroid calcium receptor PHUBCAR 4.0.	
KW	KW	Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;	
KW	KW	calcium homeostasis; hypoparathyroidism; seizure; stroke; epilepsy;	
KW	KW	spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;	
KW	KW	neonatal distress; neurodegenerative disease; Alzheimer's disease;	
KW	KW	Huntington's disease; Parkinson's disease; dementia; muscle tension;	
KW	KW	depression; anxiety.	
OS	OS	Homo sapiens.	
PN	PN	US8538684-A.	
PD	PD	12-JAN-1999.	
PF	PF	07-JUN-1995; 480751.	
PR	PR	07-JUN-1995; US-480751.	
PR	PR	23-AUG-1991; US-749451.	
PR	PR	11-FEB-1992; US-834044.	
PR	PR	12-AUG-1992; US-934161.	
PR	PR	12-FEB-1993; US-011727.	
PR	PR	23-FEB-1993; US-009389.	
PR	PR	22-OCT-1993; US-141248.	
PR	PR	19-AUG-1994; US-292827.	
PR	PR	21-OCT-1994; WO-012117.	
PR	PR	08-DEC-1994; US-353784.	
PA	PA	(BGHM) BRIGHAM & WOMENS HOSPITAL.	
PA	PA	(NNSP-) NPS PHARM INC.	
PI	PI	Balandin MF, Brown EM, Del Mar EG, Garrett JE,	
PI	PI	Hebert SC, Nemeeth EF, Van Wagenen BC;	
PI	PI	WPI: 99-119871/10.	
DR	DR	N-PSDB: W82485.	
PT	PT	Screening for calcium receptor-active compounds - by recombinant	
PT	PT	expression of nucleic acid encoding calcium receptor and determining	
PT	PT	the effect of compounds on calcium receptor activity	
PS	PS	Claim 1; Fig 49; 176pp; English.	
CC	CC	A method has been developed of screening for a compound able to affect	
CC	CC	one or more activities of a calcium receptor (CR) comprises: (A)	
CC	CC	contacting a recombinant cell with a test compound, where the	
CC	CC	recombinant cell comprises a recombinant nucleic acid expressing the CR	
CC	CC	provided that the cell does not have functional CR expression from	
CC	CC	endogenous nucleic acid; (B) determining the ability of the test	
CC	CC	compound to affect one or more activities of the calcium receptor; and	
CC	CC	(C) comparing the ability with the ability of the test compound to	

Query Match	20.48;	Score 1290;	DB 1;	Length 1078;
Best Local Similarity	32.08;	Pred. No. 1.61e-104;		
Matches	273;	Conservative	230;	Mismatches 276;
			Indels	73;
			Gaps	49;

OY	754	NYNNAKCVTFSLLENFWSMIAFTFM-ASIIQSGSYLPVNVV..AGLITLSGPGSCGYLPACY	812
Dd	859	IILFKPSRNITE	870
OY	813	VILICPELANTE	824
RESULT	6		
ID	W11889	standard; Protein: 1078 AA.	
AC	W11889:		
DT	22-APR-1997	(first entry)	
DE	Parathyroid calcium receptor encoded by clone pNUPCarr4.0.		
KW	Calcium receptor; human parathyroid gland adenoma tumour; pPbPCar1;		
KW	primary hyperparathyroidism; Xenopus oocyte; alternative splicing;		
KW	calcium-activated chloride current; agonist; NRS R-467; NPS R-568;		
KW	variant; untranslated region; alternative polyadenylation; probe;		
KW	alternative transcription initiation; pNUPCarr5.2; pNUPCarr4.0;		
KW	human CAR gene; isoform.		
OS	Homo sapiens.		
PN	W09612697-AZ.		
PD	02-MAY-1996.		
PF	23-OCT-1995; U13704.		
PR	21-OCT-1994; W0-U12117.		
PR	08-DEC-1994; US-353784.		
PA	(NPS)- NPS PHARM. INC.		
PI	Balandrin M, Delmar EG, Moe ST, Nemeth EF, Van Wagenen BC;		
DR	Wpi; 96-230520/23.		
NR	N-PDB: T61382.		
PT	New d1:arylalkyl amine cpds. useful for modulating inorganic ion		
PT	receptor activities - esp. for modulating effect of extracellular		
PT	calcium on cell surface calcium receptors, useful for treating e.g.		
PT	hyperparathyroidism, Paget's disease or osteoporosis		
PS	Example 1; Page 93-100; 231pp: English.		
CC	The sequences given in W11888-89 represent functional calcium receptors.		
CC	The cDNAs encoding these sequences were isolated from human parathyroid		
CC	gland adenoma tumor using pBbPCar1 as a hybridisation probe. mRNA was		
CC	isolated from a 39 year old caucasian male diagnosed with primary		
CC	hyperparathyroidism and two clones of approx. 5 and 4 kb were		
CC	identified. These cDNAs were injected into Xenopus oocytes which were		
CC	assayed for the presence of functional calcium receptors. Both clone		
CC	types gave rise to functional calcium receptors as assessed by the		
CC	stimulation of calcium-activated chloride currents upon addition of		
CC	appropriate calcium receptor agonists, e.g. NPS R-467 and NRS R-568.		
CC	Sequence analysis of the two cDNA clones indicated the existence of at		
CC	least two sequence variants differing in the 3' untranslated region and		
CC	which may result from alternative polyadenylation. Sequence variation		
CC	also exists in the 5' end of the inserts. These sequence differences may		
CC	have arisen due to alternative transcription initiation and/or splicing.		
CC	Three additional sites of sequence variation occur within the coding		
CC	regions of cDNA clones pNUPCarr5.2 and pNUPCarr4.0 demonstrating that they		
CC	encode distinct proteins. Sequence analysis of the human CAR gene		
CC	indicates that the additional 30 bp in clone pNUPCarr5.2 as compared to		
CC	pNUPCarr4.0, results from alternative mRNA splicing. This alternative		
CC	splicing is predicted to insert 10 additional amino acids into the CAR		
CC	protein encoded by pNUPCarr5.2 between residues 536 and 537 of the protein		
CC	encoded by pNUPCarr4.0. In addition pNUPCarr4.0 encodes Gln at position		
CC	925 and Gly at position 990. Whereas pNUPCarr5.2 encodes Arg at both		
CC	equivalent positions. The human CAR gene encodes for Gln and Arg		
CC	respectively at these positions. These two receptor isoforms may be		
CC	functionally and/or pharmacologically distinct. Pages 94-99 are		
CC	missing from the specification, sequence information was obtained		
CC	from the EPO.		
SQ	Sequence	1078 AA;	
Query Match	20.4%	Score 1290; DS 1; Length 1078;	
Best Local Similarity	32.0%;	Pred. No. 1,61e-104;	
Matches	273; Conservative	230; Mismatches 276; Indels 73; Gaps 49;	
Dd	30	GDIILGGELPIFHG-AAAKDDDKISRPSEVEICIRNFGRFLQAMIPAEINSPALL	88
OY	35	GDFLLAELFELHDDCLQVHRRLPYLTSCDPPDS-FNGSHYHLFOAMRTVEFINNSALL	92
Dd	89	PNLITGRIIDTGNYSKALEATLTSFAVNCKIDSINTLEDFCNCSHHISTIAVVGATGSG	148


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QY 93 PNILGELDVCSSESNVY-ATLRVALQGPRIEIOK--DLRNHSSKVAFIGPNDT 149
DB 149 VSTRANLGLFTIPQVSYASSRSLSNKNOFKSEFLRTIPNDEHOATAMADIIYFRMNM 208
QY 150 HAYTALLGLFPLMPVLYSEASSVYLSAKKRPFSFLRTVPDRQVEVMQQLQSGWMW 209
DB 209 VGTIAADDDYGRPGIEKFEFEAEERDIDSELI--SQYSDDEEIOHVEVIONSTAKV 266
QY 210 ISLIGSGDYGQGLQVQALAEELAVPRGICVAFKDIYFESARVGDPRMOSMOHLQARTY 269
DB 267 IYVSSSGDLEPLI-KEIVRNITGKIMLASEMASSLLIMPOYFHVGGTIGFALKAG 325
QY 270 VVFSN-RHLARVEFRRSVLANLKGKMWASEDMA---IS-T-YITSVYG-IG-GI--G 318
DB 326 QIPGFEFLKVAHPRKSVHNGFAKEFEETFNCHLOEGAKPLPVDTFLRGHSGDRFS 385
QY 319 TVLG----VA-VQORQ-VP-GL-KEF-EESY---VR-AVTAA-P-S---ACPE-GSM-- 356
DB 386 NSSTAFRPLCTGDNISSEVTPYIDYTHLRISYNYLAVYSIAHALODIYTCPLRGRLFT 445
QY 357 -CSTN-Q-LCRECHTFTRMPTLGAFSMAAAYVEAVVAAGHLQD--L-GC---T 406
DB 446 NGSCADIKKYEANQVLEKHLNFTNNMGEOYTFDECGDLVGNSTIINHLSPEDGSIVF 505
QY 407 SEIS-NGPYPMQQLQOIKRVNFLH-ENTVAEDDNGDTLGYDILIAMDNQGE-WT-F 462
DB 506 KEVGYVNYAKKGERLFINEEKLMSGFSREVPFNSRCDIAGRKGIIGEPTCCPEC 565
QY 463 EIIG-SA-SLSPVHLINKTKIOMHGKNNQVPSVCTTDLACHHRYV-GSHHCCFEC 518
DB 566 VECPDGEYSDETDASACNKPDDFWSNENHSCIAKEIEFLSTWTEPRGIALTLFAVLGIF 625
QY 519 VPCEAGTFLLMSEHLICOPGTEEMAPKESYTCPRVTEFLAMHEPISLVLIANTILL 578
DB 626 LTAFLVGLFI-KERNTPYVATNRELSTLLFSLCCFSSSLF-FIGEPDWTCKRQPA 683
QY 579 LVGTAGLAFAMHFR-TPVRSAGGRCLFGLMSLVAG-SCSFYSFEGEPVPAOLLRQPL 636
DB 684 FGISFVLCISCIIVKTNRLVLFEE-AKIPTSFRKMGWMLQGLVLCFQMOIVICVI 741
QY 637 FSLGALFSLCLTRISQVLYIFKSTIKVPT-FYRTNAQNHGAGLPIYVSTVILLICLT 695
DB 742 WLVTAPSSYRNQDELEIFITCHEGSLMALGFLIGYTC-LLAALCFEF-AFKSRKLP 799
QY 696 WLVMYTRPREYORPFLVILLECTEVN--SVGFLLAFTHNILLISIFVCSYLGKELPE 753
DB 800 NFNNAKFTTSMLEFVWISFIFAYASTY-GKRVSAVEYALIAIASGLLACIFENKIY 858
QY 754 NYNNAKCVTSLNLFVSWIAFFTM-ASIVQSYLPAVNLGLTLTSGGFSGYFLPCY 812
DB 859 ILFKPSRNTIE 870
QY 813 VILCRPELNTE 824

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RESULT 7
ID W38274 standard; Protein; 1078 AA.
AC W38274;

DE 08-MAY-1998 (first entry)
KW Human parathyroid cell calcium receptor 4.0 (Hupcar 4.0).
KW Human parathyroid cell calcium receptor 4.0; Hupcar 4.0;
KW calcium homeostasis; hyperparathyroidism; osteoporosis.
OS Homo sapiens.
PN US5688938-A.
PD 18-NOV-1997.
PF 07-JUN-1995; 485588.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-017127.
PR 23-FEB-1993; US-009389.

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PR 22-OCT-1993; US-141248.  
PR 19-AUG-1994; US-292827.  
PR 21-OCT-1994; WO-012117.  
PR 08-DEC-1994; US-353784.  
PA (BGM) BRIGHAM & WOMEN'S HOSPITAL.  
PA (NPS-) NPS PHARM INC.  
PI Brown EM, Fuller FH, Garrett JE, Hebert SC;  
DR WPI; 98-008040/01.  
PT DNA encoding calcium receptor polypeptide(s) - useful for  
PS therapeutic purposes, e.g. hyperparathyroidism and osteoporosis  
PS Claim 20; Columns 125-134; 174pp; English.  
CC The present sequence is human parathyroid cell calcium  
CC receptor 4.0 (Hupcar 4.0).  
CC The specification includes details of molecules that can modulate  
CC one or more inorganic ion receptor activities, and antibodies and  
CC antibody fragments targeted to inorganic ion receptor proteins. The  
CC proteins, nucleic acids and antibodies may be used to treat  
CC disorders by modulating one or more inorganic ion receptor  
CC activities, preferably disorders of calcium homeostasis, e.g.  
CC hyperparathyroidism and osteoporosis.  
SO Sequence 1078 AA;

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Query Match 20.4%; Score 1290; DB 1; Length 1078;
Best Local Similarity 32.0%; Pred. No. 1.61e-104;
Matches 273; Conservative 230; Mismatches 276; Indels 73; Gaps 49;

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DB 30 GDILGLGFPIHNG-VAAKDQDKSRPSEVCIRYNGRFRMLOAMFAIEINSSPALL 88
QY 35 GDFLAGLESUHGDCGLQVRRRPPLYTSCDRPDS--FNGHGLHQAQNFYEEINSSALL 92
DB 89 PNILGRIPIEDTONTYSKALEATLSFVAONKIDSLNDEFNCSEHPISTIYAVGATGSC 148
QY 93 PNILGELDVCSSESNVY-ATLRVALQGPRIEIOK--DLRNHSSKVAFIGPNDT 149
DB 149 VSTRANLGLFTIPQVSYASSRSLSNKNOFKSEFLRTIPNDEHOATAMADIIYFRMNM 208
QY 150 HAYTALLGLFPLMPVLYSEASSVYLSAKKRPFSFLRTVPDRQVEVMQQLQSGWMW 209
DB 209 VGTIAADDDYGRPGIEKFEFEAEERDIDSELI--SQYSDDEEIOHVEVIONSTAKV 266
QY 210 ISLIGSGDYGQGLQVQALAEELAVPRGICVAFKDIYFESARVGDPRMOSMOHLQARTY 269
DB 267 IYVSSSGDLEPLI-KEIVRNITGKIMLASEMASSLLIMPOYFHVGGTIGFALKAG 325
QY 270 VVFSN-RHLARVEFRRSVLANLKGKMWASEDMA---IS-T-YITSVYG-IG-GI--G 318
DB 326 QIPGFEFLKVAHPRKSVHNGFAKEFEETFNCHLOEGAKGPLPVDTFLRGHSGDRFS 385
QY 319 TVLG----VA-VQORQ-VP-GL-KEF-EESY---VR-AVTAA-P-S---ACPE-GSM-- 356
DB 386 NSSTAFRPLCTGDNISSEVTPYIDYTHLRISYNYLAVYSIAHALODIYTCPLRGRLFT 445
QY 357 -CSTN-Q-LCRECHTFTRMPTLGAFSMAAAYVEAVVAAGHLQD--L-GC---T 406
DB 446 NGSCADIKKYEANQVLEKHLNFTNNMGEOYTFDECGDLVGNSTIINHLSPEDGSIVF 505
QY 407 SEIS-NGPYPMQQLQOIKRVNFLH-ENTVAEDDNGDTLGYDILIAMDNQGE-WT-F 462
DB 506 KEVGYVNYAKKGERLFINEEKLMSGFSREVPFNSRCDIAGRKGIIGEPTCCPEC 565
QY 463 EIIG-SA-SLSPVHLINKTKIOMHGKNNQVPSVCTTDLACHHRYV-GSHHCCFEC 518
DB 566 VECPDGEYSDETDASACNKPDDFWSNENHSCIAKEIEFLSTWTEPRGIALTLFAVLGIF 625
QY 519 VPCEAGTFLLMSEHLICOPGTEEMAPKESYTCPRVTEFLAMHEPISLVLIANTILL 578
DB 626 LTAFLVGLFI-KERNTPYVATNRELSTLLFSLCCFSSSLF-FIGEPDWTCKRQPA 683
QY 579 LVGTAGLAFAMHFR-TPVRSAGGRCLFGLMSLVAG-SCSFYSFEGEPVPAOLLRQPL 636
DB 684 FGISFVLCISCIIVKTNRLVLFEE-AKIPTSFRKMGWMLQGLVLCFQMOIVICVI 741

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CC proximal tubule cells in the kidney. The purified receptors (produced
CC recombinantly) can be used to screen for compounds that modulate calcium
CC receptor activity, especially those that can be used to treat diseases
CC associated with the receptors in these tissues. They can also be used
CC to raise antibodies for use in detection assays.
Sequence 1079 AA;

SQ Sequence 1079 AA;

Query Match	20.38;	Score 1285;	DB 1;	Length 1079;
Best Local Similarity	31.68;	Pred. No. 4.71e-104;		
Matches	272;	Mismatches 285;	Indels 73;	Gaps 50

Dd	30	GDIIIGGEPFHFG-VAAKDDDLSPRSVVCIRYNGRFWMQALFEALIEINSSPIL	88
Qy	35	GDFLIAGLFSHGCDQYRHRPLVTSCDRPS--FNGHGILPDMAFYBEIINSSALL	92
Dd	89	PNMTLGYRIEDTCNTVSKALEBTLISFAVQNKIDSLINDEFCNCEHLPSTIAVVGATGSC	148
Qy	93	PNITGLYELDVDCSESNANY-ATLRLVTLAQDRHIEIOK--DLRNHSSKVAFI.GDPDNT	149
Dd	149	VSTANANLLGLFYIPQVSYASSSRLSKNKYKSFLLIPNDEQOATMADIIEYFFMNM	208
Qy	150	HAVYTAALLGLPMLPVSVEASSVYLAKRRFPSEFLRPVSDRQVEMWOLLOSPGMW	209
Dd	209	VGTIADDDYDRPGIEKEEREAEEDICIDISELI--SQYDEEBEIOQVEVIONSTAKY	266
Qy	210	ISLIGSYDGYOGLQVQALQELAEI.LAVRGICVANKD.IVPSAR.GDRP.RMSMOMHQAQNTVY	269
Dd	267	IYVSSSGPDLEPLI-KEIYVRNITIGRLWLA.SEAMASSLLAMPYFVVGGTIGFGI.KAG	355
Qy	270	YVVEFN-FHLARVEFERSVJVLNLTGKVVAVASEDMA---IS-T-YITSVYG-IO-GI-G	318
Dd	326	QI.PGR.FE.LQY.VHP.RKSV.HNG.FAK.EFM.EET.NCH.LQSGAK.PRL.VP.DFV.FSH.ERG.RTL	385
Qy	319	TYLG-----VA-VQORQ-VP-GL-KEF-EEST---VR-AVTRA-P-S-A-CPE--GSW--	366
Dd	386	NSSTA.FRLCT.GDENINSEVET.PYMDYELR.ISTYNYLAVYSIAHALODIYCLPGRGLT	445
Qy	357	-CSTN-Q-LCRECHETFTTRNPTLGAF.SMAA.YRVEAYVAVAGHLQL--L-GC--T	406
Dd	446	NGSCADIKKVA.MOV.KHL.RH.LNLT.NNMG.EQV.TDECGDLVGNSTIINHLS.PDGS.IVF	505
Qy	407	SEI.CS-KRPVY.PMOLLQIYV.NL.LH-ENTVA.DDMDGDTLGYD.IIAMOMNGPE-WT-F	462
Dd	506	KEVGYNYVYAKGGERLFI.NEEKI.I.MSGFS.REVPF.SNCS.RDQOAGTRKGIIEGEPCCFEC	565
Qy	463	EIIG--SA-SLSPV.HLD.NKTK.IQ.HGKN.NNPV.SVCTT.DC.LAG.HR.VVY-GSHHCCFEC	518
Dd	566	VECPDGEYSETDASACDKCPDDF.MSNNHNTSC.IAKELIEFLA.WTEPRGIALTLFVAVLGI	625
Qy	519	VPCEAGT.LNNSELIHCOPCCTE.EAP.EYESTCTCP.PRV.EFLA.MHEP.ISTVL.IAN.TLL.LL	578
Dd	626	LTAFLVGEFI-KFRNTPYKATNREL.SVLL.FLSLCCFSSSLF-FIEBPDMWCRLMOP	683
Qy	579	LIVGTAGLFANHFH-TPVYRSAGRLCT.LM.GSLVAG-SCSFYSFSEBPVYVPCOLLQPL	636
Dd	684	FGISEVFLCISILVKTNRVLLVFE-ANKIPTSFHRKMWGLNLOFLVFLCTFMOLLICII	741
Qy	637	FSLGPAIFLSCILTRISFQULIIFKFSKVP-FRTMAQN.NGAGLAFVYSVYVALLICLT	695
Dd	742	WLTYAPBSYNNHELEDIITTHBGS.LMALGSLIGTTC-LLAALCTFF-AEFSKRLPE	799
Qy	696	WLVNMTPRPTEYORFPHLVILCTE.VN-SVGLLAFTHN.IILISTFPCSYIGKELPE	753
Dd	800	NFNENKFTFEMLLFEIYIWSIFIPAVASTY-GKRVSAVEVYALIAAFGLACIFENKVV	858
Qy	754	NYNENKCTFSL.LNFVSMIF.FFM-ASITYGSLUPAVNYLAGLTLTSGSGSFTLPCY	812
Dd	859	IILFKPSNTIEEVRSSYTAHA	880
Qy	813	VILCRPELNTEHFOASIODTY	834

1C	AD	W89566 standard; Protein; 1079 AA.
2C	AC	W89566; (first entry)
3C	DT	19-MAR-1999
4C	DE	Rat parathyroid calcium receptor prakCar 3A.
5C	KW	Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;
6C	KW	calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;
7C	KW	spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;
8C	KW	neonatal distress; neurodegenerative disease; Alzheimer's disease;
9C	KW	Huntington's disease; Parkinson's disease; muscle tension;
10C	KW	depression; anxiety.
11C	OS	Rattus sp.
12C	PN	US5858684-A.
13C	PD	12-JAN-1999.
14C	PF	07-JUN-1995; 480751.
15C	PR	07-JUN-1995; US-480751.
16C	PR	23-AUG-1991; US-749451.
17C	PR	11-FEB-1992; US-834044.
18C	PR	21-AUG-1992; US-934161.
19C	PR	12-FEB-1993; US-017127.
20C	PR	23-FEB-1993; US-009389.
21C	PR	22-OCT-1993; US-141249.
22C	PR	19-AUG-1994; US-292827.
23C	PR	21-OCT-1994; WO-012117.
24C	PR	08-DEC-1994; US-353784.
25C	PA	(BGHM) BRIGHAM & WOMENS HOSPITAL.
26C	PA	(NPSP-) NPS PHARM INC.
27C	PI	Belandrin MF, Brown EM, Del Mar EG, Garrett JB,
28C	PI	Hebert SC, Nemeth EF, Van Wagenen BC;
29C	PI	WPI; 99-119871/10.
30C	DR	N-PDSB; Y82486.
31C	PT	Screening for calcium receptor-active compounds - by recombinant
32C	PT	expression of nucleic acid encoding calcium receptor and determining
33C	PT	the effect of compounds on calcium receptor activity
34C	PS	Claim 1, Fig 50; 176pp; English.
35C	CC	A method has been developed of screening for a compound able to affect
36C	CC	one or more activities of a calcium receptor (CR) comprises: (A)
37C	CC	contacting a recombinant cell with a test compound, where the
38C	CC	recombinant cell comprises a recombinant nucleic acid expressing the CR,
39C	CC	provided that the cell does not have functional CR expression from
40C	CC	endogenous nucleic acid; (B) determining the ability of the test
41C	CC	compound to affect one or more activities of the calcium receptor; and
42C	CC	(C) comparing the ability with the ability of the test compound to
43C	CC	affect the one or more CR activities in a cell not comprising the
44C	CC	recombinant nucleic acid. The present sequence represents rat
45C	CC	parathyroid CR, designated a prakCar 3A. The nucleic acid sequence of
46C	CC	prakCar 3A can be used as part of the recombinant nucleic acid in the
47C	CC	method described above. The compounds identified can be used to treat
48C	CC	diseases or disorders characterised by abnormal calcium homeostasis, e.g
49C	CC	hyperparathyroidism, osteoporosis and other bone and mineral-related
50C	CC	disorders. They can also be used for the treatment of diseases and
51C	CC	disorders associated with disrupted Ca2+ responses, e.g. seizures,
52C	CC	stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in
53C	CC	cardiac arrest or neonatal distress, epilepsy, neurodegenerative
54C	CC	diseases such as Alzheimer's disease, Huntington's disease and
55C	CC	Parkinson's disease, dementia, muscle tension, depression, and anxiety.
56C	SQ	Sequence 1079 AA.
57C	Query Match	20.3%; Score 1285; DB 1; Length 1079;
58C	Best Local Similarity	31.6%; Pred. NO. 4.71e-104;
59C	Matches 272;	Conservative 232; Mismatches 285; Indels 73; Gaps 50;
60C	30	GDILGGLFPIHFQ-VAAKDQDLKSRPSEVCIRYNFRGFMLOAMIFAIEINSPSL 88
61C	35	GDPLLAGLFIHSGCQLQVRRRLPVTSDRRDS--FNGHGHLFQAMRFVEEINNSALL 92
62C	Db	89 PNMFLGRIFDTCNTWSKALEATLFSYAONKIDSLNLFDFCNSEHIPTIATVCGATGSG 148
63C	QY	93 PNILIGELLYDVCSSEANVY-ATLRVLTALOGGRHIEIQK-DLRNHSKRYVAFIPDMD 149
64C	Db	149 VSTVAANLIGLFYIPQVSYASSRLLSNKQYSEFLRTIPNEHQATLAADLIEFRNMW 208
65C	QY	150 HAVTTAALGFLMLPVLSTYASSSVLSAKKPFSEFLRTIPSDHDEVVQLLOSGFGMW 209

[illegible][illegible]

D	b	209	VGIAADDDYRPGREKREARENERDIDISELI--SQSDEPEIQOYVEVIONSTAKY	265
Q	y	210	ISLISGYDIDYDGLQVAEELEAVRGLCTVPAKRDVPEFSARVGPBRMOSNQOHLQAATTY	269
D	b	267	IVFSSSGDLEPLI-KEIVRNRITGRILAEWAASSLLIAMPDEYFVVGITIGFGFKAG	325
Q	y	270	VVPSF-RHLRAVFRFSRYVLLNLNLGKVVAVASEDMA-----IS-T-YTISYVG-IQ-GI--G	318
D	b	336	QIPGREFLEQVHPRKSYVHNGFAKEFWEETFNCHLQEGAGKGPLVDITFVSHSEGGNRL	385
Q	y	319	TVLG---VA-VQQRQ--VP-GL-KEF-EESY---V-R-AVIAA-P--S-A-CPE--GSW--	356
D	b	366	NSSTAERPLCTGIDENINSVEFPYNDYELRISIVNYAVYSIAHALDIDITCIPGRGLT	445
Q	y	357	-CSTN-Q-LICECHTFTIRNMPITGAFSMAAKYRVYEAUYAVAHGHLQ-----L-GC--T	406
D	b	446	NGSCADIKYVAMOVLLKRLRLNTNNMGDQVTEDECGDLVGNSTIIMHLSDEDSIVF	505
Q	y	407	SEIGS-RGPVYPMOOLQIYKVNFLH-ENVAFDGDTGLGYDITIAMDMNGPE-WT-F	462
D	b	506	KEVGYYNYAKKGRLEFINEREKILMSGFSREVPFNSCRDQAGTRKGIIEGPTCCFEC	565
Q	y	463	ELIG--SA-SLSPVHLDNKRKTOMHGKNNOVPYSCVTTDCLAGHANYV-GSHRCFEC	518
D	b	566	VECPDGEYSGETDASACDKCPDDEFWSENHTSCIAKEIEFLAMTEPGIALTLFLAVGIF	625
Q	y	519	VPCEGRTFLNMSLEHICOPCTIEBPAPKRESTCPFRVEFLAMHEPISVLIAANLTL	578
D	b	626	LTAFLVGLFI-KFNTPYVAKTNELSYLLFLSLCCFSSLP-FIGEPDWMCRLRQRA	683
Q	y	579	LIVGTAGLEAHHF-HTPVRSAGRGRLCFMLMSI-VAG-SCSFYSFDEGPVPACLLRQPI	636
D	b	684	FGISVLCISCIILKTNRLVLVEF-AKIPSFHRKMWGLNLQGLFELCTEQILICIT	741
Q	y	637	FSLGFAITLSCLTRISQOLVIEFNFSTRKVP-FRTAQNQHGAGLFPYIVSYTHLICTL	695
D	b	742	WLXTAPSSYNNHLEDELIIFITCHEGSLMALGSLIGYTC-LLAALCFP-AFKSRKLE	799
Q	y	696	WLVMVTPRPTREYQRPRLVHLECTEVN--SVGFLAFTNNILSLISTFVCSYLGKLE	753
D	b	800	NFNNAKFTFEMLFFFIWISFIFAVASY-GKVSAAVEVIALIILASFGILACIFNNKY	858
Q	y	754	NYNEAKCTFSLLLNFVSWIIFFTM-ASIQSGSYLPAVNYLAGITLTSGGFSGCYFLPKCY	812
D	b	859	IILFKSRNTIEEVRSFAHA	880
Q	y	813	VILCRPELNTNEHFOASTIDYIT	834
RESULT 11				
ID	W38275 standard: protein: 1079 AA.			
AC	W38275.			
DT	08-MAY-1998 (first entry)			
DE	Rat kidney cell calcium receptor 3A (RakCar 3A).			
KW	Rat kidney cell calcium receptor 3a; RakCar 3A;			
KW	calcium homeostasis; hyperparathyroidism; osteoporosis.			
OS	Rattus sp.			
PN	US5688938-A.			
PD	18-NOV-1997.			
PF	07-JUN-1995: 485588.			
PR	07-JUN-1995: US-485588.			
PR	23-AUG-1991: US-749451.			
PR	11-FEB-1992: US-834044.			
PR	21-AUG-1992: US-934161.			
PR	12-FEB-1993: US-017127.			
PR	23-FEB-1993: US-009389.			
PR	22-OCT-1993: US-141248.			
PR	19-AUG-1994: US-292827.			
PR	21-OCT-1994: WO-012117.			
PR	08-DEC-1994: US-353784.			
RA	(BGMH) BRIGHAM & WOMEN'S HOSPITAL.			
RA	(NSP-) NPS PHARM INC.			
SI	Brown EM, Fuller FH, Garrett JF, Hebert SC			

Query Match	20.3%	Score 1285;	D3 1;	Length 1079;
Best Local Similarity	31.6%	Pred. No. 4.7e-104;		
Matches	277;	Conservative	222;	Mismatches 285;
			Indels	73;
			Gaps	50
D3	30	GDIIIGGLFPFHFG-VAAKDDDKSRPESVCIRYFNGFWMLOAMFAEINSSPLL	88	
QY	35	GDFFLAGFLSLHGDCLOVRRPRTSCDRPDS--FNGHGLFAMARTVEINSSALL	92	
D3	89	PNNLIGRIEPTDCTNVSKEALATISFVNOKRIDSLNDEFCNSEHPISTIAVVGATGSG	148	
QY	93	PNTLIGRIELDYCSSANVY-ATLRVLALOGPRHIELOK--DLRNHSSKYAFLGPNDTD	149	
D3	149	VSTAVANLLGLFYIPDVSASSRLLSKKNQYKSFRTIPNDEHQATMADIIIFYRKNW	208	
QY	150	HAVTAAALLGLFELMPLDYSEASSVYLSAKRKFPEFLRTPVSDRHQVEYMOJLOSFGVMW	209	
D3	209	VGTIADDDYCRPGIEKREAEERDIDKSESL--SQYSEDEEIQVNVYIONSTAKY	266	
QY	210	ISLISYDYOGLQOALELAVRPGICVAKDIPPSARVGRDPMOSKMOHLQARTV	269	
D3	267	IVFSSGGDEPLI-KEIVRRNITGRILVASEAASSLLIMPEYFHVVGSTIFGKLKAG	325	
QY	270	VYFEN-RHLARVFRSRVYLANLIGKVVAVSADMA---IS-T-YIHSYIC-IG-GI-T	318	
D3	326	QIPGRREFLOKVVHPKRSYHNGFAKEFWETFNCHLOEGAKGRLPVDTPVRSHEEGNRLL	385	
QY	319	TVLGG---VA-VQORQ-VP-GL-KEF--EESY--VR-AVTPA-P-S-A-CPE--GSM--	356	
D3	386	NSTAFRRLCTGDEKINSVETPRYDYLHRLTSYVYLAAYSIALADODIYCLPGRGLFT	445	
QY	357	-CSTN-Q-LCEECHTFTTRNPTLTGAFSMAAUYVAYVAAGLHQL--L-GC--T	406	
D3	446	NGSCADIKRYAMQYLKRLHNTNNNGEYTFDECGDLVGNYSINMHLSPDGSIWF	505	
QY	407	SEIGS-RRPVYPMOOLQOITYKVNLLH-ENIVAADNDSDITIGYDITIAMDNQGE-WT-F	462	
D3	506	KEYGYNYVYAKGERELFINEBKILMSGFSRPVPSNCSRDCAQTRKGLIEGEPTCCFEC	565	
QY	463	EIIG--SA-SLSPYHLIDINKTKIQMHGKNNOVPVSVCTDCLAGHRRVY-GSHHCCFEC	518	
D3	566	VECPDGEISGETDASADCKPDDPWSNENHNSCLAKELFELAMTERPCIALTEPLAVLGIF	625	
QY	519	VPCEAGITLNNSEHLIOCPGIEWAPRSESTTCPRVEFLAMEHPSLVLIDANTLLL	578	
D3	626	LTAFLVGLFYI-KERNTPYVAKTARELSYLLFSLCLCFSSSLF-FIEPDQWCTRLOPA	683	
QY	579	LIVGAGLFAHHFH-TPYVRASGRLCFLKMSGLVAG-SCSFYFEBEPYVPAOLLQOPL	636	
D3	684	FGISFVLICSLIVKTNRLVLF--AKIPTSFHRKWMGLNLOELVFLCTFMOLICII	741	
QY	637	FSLGALFSLCITLRSFQVLTIIFFSTKVTPL-FRYTANQNHGALFLVIVSVTHLICLT	695	
D3	742	WLYTAPPSYNNHLEDDIIFITHEGSLMALGSLIGYC-LLAALICFF-AFNSKLPE	799	
QY	696	WLYVMTPTPTREYORFPLHVLLEOTENV--SVGLLAFTHNHLISITFVCSYIGKELPE	753	
D3	800	NENAEKTFITFMLFFFIYWISIFIPAVASTY-GKPVSAVEVYALIAAFGLACIFEFKVV	858	

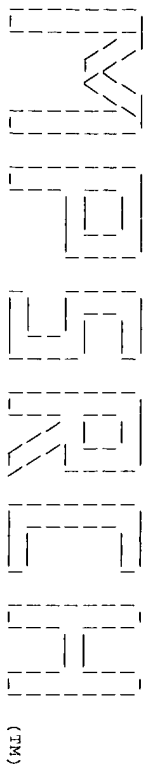
Db 326 QIPGFRRLKVKHPRKSVHNGFAKEFWETFNCHLOEGAKGPLVDFELGHESGDRFS 385
 Qy 319 TVLG---VA-VQGR-V-P-GL-KEF-EESY---VR-AVTAA-P-S---ACPE-GSM-- 356
 Db 386 NSSAFRPLCTGDNISSEVTPYIDYTHLRISYNYAVLSIAHALODITCLPGRGLFT 445
 Qy 357 -CSTN-Q-LCRECHTFTRNMPTLGAFMSMAAYRYEYAVAAHGLHOL---L-GC---T 406
 Db 446 NGSCADIKKVAQVVKHLRLHNTNNGEYVTEDECGDLVGNSTIIMHLSPEDSGIVF 505
 Qy 407 SEICS-RGPVYPMOLLOQIYKYNFLH-ENTVAFDNDGDLGYDIIAMDNNGPE-WT-F 462
 Db 506 KEVGYNYVYAKGGRRLFINEKILMSGFRPLTFVLVLQVPSNCSRDCLAGTRKGI 565
 Qy 463 EIIG--SA-SLSPYHDLNTRKIQMHG--KN-----N-QVPYVCTTDCLAGHHRVYV 509
 Db 566 EGEPTCCFECVCPDGEYSDETASACNCPDPMNSNHTSCIAKEIEFLSWTEPGIA 625
 Qy 510 -GSHHCCFECVPCBAGTFELNMSLHICOPCGTEMAPEKSTCPFRVTEFLAMEPISLV 568
 Db 626 LTLFAVLGIFLTAFLVGLVFI-KFRNTPIVKATNRELSTLLFSLCCFSSSLF-FIGEPQ 683
 Qy 569 LIAANTLLLLVGTAGLEAFNHFR-TPVVRSAAGRLCLMLGSLVAG-SCSFYSPFGEP 626
 Db 684 DMTCLROPAPAGISFVLICISCLVKNRVLVFE-AKIPTSFRKMWGLMLOFLVFLC 741
 Qy 627 VPALLLNQPLFSLGFAIFLSCITRSPLVLIIFKSTKVPF-FRYTAMQNNAGLFIYVS 685
 Db 742 TFMQIVCIVLWLYTAPSSYRNQLEDEIFITCHESSLMALGILGYTC-LLAICEFF 800
 Qy 686 STVHLLCLLTLMVMTPTREYORFPLVILLECTEVN--SVGFLLAFTNHLISSTFV 743
 Db 801 -AFKSRKLPEMKNKAKFTFEMLFEIYVWISFPAVASTY-GKFPVANEVAILAASGL 858
 Qy 744 CSTGKELPEMKNKAKFTFEMLFEIYVWISFPAVASTY-GKFPVANEVAILAASGL 802
 Db 859 LACIFENKIVILFKPSRNTIE 880
 Qy 803 FSGYELPCVYILCRPELNMTE 824
 RESULT 15
 ID W89564 standard; Protein; 1088 AA.
 AC W89564;
 DE 19-MAR-1999 (first entry)
 KW Human parathyroid calcium receptor PHUPCAR 5.2.
 KW Parathyroid calcium receptor; Inorganic ion receptor; osteoporosis;
 KW calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;
 KW spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;
 KW neonatal distress; neurodegenerative disease; Alzheimer's disease;
 KW Huntington's disease; Parkinson's disease; dementia; muscle tension;
 KW depression; anxiety.
 OS Homo sapiens.
 PN US583684-A.
 PD 12-JAN-1999.
 PE 07-JUN-1995; 480751.
 PR 07-JUN-1995; US-480751.
 PR 23-AUG-1991; US-748451.
 PR 11-FEB-1992; US-834044.
 PR 21-AUG-1992; US-934161.
 PR 12-FEB-1993; US-017127.
 PR 23-FEB-1993; US-009389.
 PR 22-OCT-1993; US-141248.
 PR 19-AUG-1994; US-292827.
 PR 21-OCT-1994; WO-012117.
 PR 08-DEC-1994; US-353784.
 PR (BGM) BRIGHAM & WOMENS HOSPITAL.
 PA (NPS-) NPS PHARM INC.
 PI Balandrin MF, Brown EM, Del Mar EG, Garrett JE,
 PI Hebert SC, Nemech EF, Van Wagenen BC.
 DR WPI; 99-119871/10.
 DR N-PSDB; V82484.

PT Screening for calcium receptor-active compounds - by recombinant
 PT expression of nucleic acid encoding calcium receptor and determining
 PT the effect of compounds on calcium receptor activity
 PS Claim 1, Fig 48; 176pp; English.
 CC A method has been developed of screening for a compound able to affect
 CC one or more activities of a calcium receptor (CR) comprises: (A)
 CC contacting a recombinant cell with a test compound, where the
 CC recombinant cell comprises a recombinant nucleic acid expressing the CR,
 CC provided that the cell does not have functional CR expression from
 CC endogenous nucleic acid; (B) determining the ability of the test
 CC compound to affect one or more activities of the calcium receptor; and
 CC (C) comparing the ability with the ability of the test compound to
 CC affect the one or more CR activities in a cell not comprising the
 CC recombinant nucleic acid. The present sequence represents human
 CC parathyroid CR, designated a PHUPCAR 5.2. The nucleic acid sequence of
 CC PHUPCAR 5.2 can be used as part of the recombinant nucleic acid in the
 CC method described above. The compounds identified can be used to treat
 CC diseases or disorders characterized by abnormal calcium homeostasis, e.g.
 CC hyperparathyroidism, osteoporosis and other bone and mineral-related
 CC disorders. They can also be used for the treatment of diseases and
 CC disorders associated with disrupted Ca²⁺ responses, e.g. seizures,
 CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in
 CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative
 CC diseases such as Alzheimer's disease, Huntington's disease and
 CC Parkinson's disease, dementia, muscle tension, depression, and anxiety.
 CC Sequence 1088 AA.
 SQ
 Query Match 18.9%; Score 1198; DB 1; Length 1088;
 Best Local Similarity 31.88; Pred. No. 5,80e 96;
 Matches 274; Conservative 231; Mismatches 274; Indels 83; Gaps 52;
 Db 30 GDILGLGFPIHFG-VAKQDQKSRPESVETIRYNGRGMQAMIFAEINSPALL 88
 Qy 35 GDFLALFELHGCCLQYRRHPLVTSQDRPDS--FNHGCHLQAMFTYEELINSSALL 92
 Db 89 PNLTGIRIDNTQVSKALEATLSEYANQKIDSLNDEFCONSEHPTIYAVGATGSG 148
 Qy 93 PNLTGIRIDNTQVSKALEATLSEYANQKIDSLNDEFCONSEHPTIYAVGATGSG 149
 Db 149 VSTAVANLLGLFYIPQVSYASSRSLSNKNQKFSFRTINDHQATAMDIIEYFPMW 208
 Qy 150 HAVTTAALGPFLMPLVSYASSSVLSAKRKPSEFLTVSDRQYEVMMQLQSEGW 209
 Db 209 VGTIADDYGRPGIEKFEKREAEERDIDFSELI--SQYSDEEIQHVEVIONSTAKY 266
 Qy 210 ISLIGSGDYGQVQALDELAVPKICVAFKDIYPSAVSGPRMGMQHLAQARTV 269
 Db 267 IVFSSGPDLEPL-KETVRNITGKIWLASEMASSSLIAMPQYFHVGGTIGFALKAG 325
 Qy 270 VVVFESN-RHLARVFEFSVLANLTGKVVASEDMA---IS-T-YITSVG-IO-GI--G 318
 Db 326 QIPGFRRLKVKHPRKSVHNGFAKEFWETFNCHLOEGAKGPLVDFELGHESGDRFS 385
 Qy 319 TVLG---VA-VQGR-V-P-GL-KEF-EESY---VR-AVTAA-P-S---ACPE-GSM-- 356
 Db 386 NSSAFRPLCTGDNISSEVTPYIDYTHLRISYNYAVLSIAHALODITCLPGRGLFT 445
 Qy 357 -CSTN-Q-LCRECHTFTRNMPTLGAFMSMAAYRYEYAVAAHGLHOL---L-GC---T 406
 Db 446 NGSCADIKKVAQVVKHLRLHNTNNGEYVTEDECGDLVGNSTIIMHLSPEDSGIVF 505
 Qy 407 SEICS-RGPVYPMOLLOQIYKYNFLH-ENTVAFDNDGDLGYDIIAMDNNGPE-WT-F 462
 Db 506 KEVGYNYVYAKGGRRLFINEKILMSGFRPLTFVLVLQVPSNCSRDCLAGTRKGI 565
 Qy 463 EIIG--SA-SLSPYHDLNTRKIQMHG--KN-----N-QVPYVCTTDCLAGHHRVYV 509
 Db 566 EGEPTCCFECVCPDGEYSDETASACNCPDPMNSNHTSCIAKEIEFLSWTEPGIA 625
 Qy 510 -GSHHCCFECVPCBAGTFELNMSLHICOPCGTEMAPEKSTCPFRVTEFLAMEPISLV 568
 Db 626 LTLFAVLGIFLTAFLVGLVFI-KFRNTPIVKATNRELSTLLFSLCCFSSSLF-FIGEPQ 683

QY 569 LIAANTILLLLLVGTAGLFAMH-FPVRSAGRLCLMLGSLVAG-SCSFVSFFGEPT 626
Db 684 DMTCLROPAFGISFVLCISCIILVKTNRVLVEE--AKIPTSEHRKXWGLNLOFLIVEIC 741
QY 627 VPACLLRQPLFSLGFAIFLSCLTTRSFQLVITFKSTKVPT-FYRTAONHNGAGLEFVIVS 685
Db 742 TFMQIVICVIMLYTAPPSSYRNQLEDEIIFITCHEGSLMALGFLIGYC-LIAAICFF 800
QY 686 STVHLILCLTLMVMMTRPTREYORFPHVLLECTEVN--SVGFLLAFTNHILLISTFV 743
Db 801 -AFKSRKLPENENAKFITFSMLIFFIWMISFIPAYASTY-GKFVSAVEVIAITLASFGL 838
QY 744 CSYLGKELPENYNENAKCVFSLNLFVSWIAFTTM-ASIVOGSYLPAYNVNVLAGLTTLSG 802
Db 859 LACIFENKIVYIILFKPSRNTIE 880
QY 803 FSGYFLPKCYVILCRPELNNTIE 824

Search completed: Fri Mar 17 13:01:48 2000
Job time : 100 secs.





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Mpsrch_p protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:18:18 2000; Maspar time 113.49 Seconds

Tabular output not generated. 514,400 Million cell updates/sec

Title: >US-09-361-652-2

Description: (1-842) from US09361652.pep

Perfect Score: 6366

Sequence: 1 MFWMAHLLLSLQLAIVACW.....NTEHFQASIDYTRCGTT 842

Scoring table: PAM 150

Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

sptrembl12
1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
9:sp.phage 10:sp.plant 11:sp.protein 12:sp.unclassified
13:sp.veterebrate 14:sp.virus

Statistics: Mean 52.594; Variance 100.413; scale 0.524

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	5839	91.7	840 11	Q920R8	PUTATIVE TASTE RECEPTOR	0.00e+00
2	2026	31.8	843 11	Q920R7	PUTATIVE TASTE RECEPTOR	0.00e+00
3	1421	22.3	868 13	Q73636	PHEROMONE RECEPTOR	9.53e-270
4	1388	21.8	848 13	Q93553	PUTATIVE ODORANT RECEPTOR	1.64e-262
5	1358	21.3	864 13	Q73637	PHEROMONE RECEPTOR	6.14e-256
6	1334	21.0	840 13	Q73635	CALCIUM2+ SENSING RECEPTOR	1.10e-250
7	1279	20.1	880 13	Q73552	PHEROMONE RECEPTOR	1.17e-238
8	1258	19.8	844 13	Q73552	PUTATIVE ODORANT RECEPTOR	4.52e-234
9	1251	19.7	855 13	Q73638	PHEROMONE RECEPTOR	1.52e-232
10	1236	19.4	875 13	Q73640	PHEROMONE RECEPTOR	2.86e-229
11	1160	18.2	912 11	Q70410	PUTATIVE PHEROMONE RECEPTOR	1.03e-212
12	1009	15.8	855 11	Q70409	PUTATIVE PHEROMONE RECEPTOR	5.72e-180
13	974	15.3	779 11	Q93269	PUTATIVE PHEROMONE RECEPTOR	2.06e-172
14	881	13.8	458 13	Q93555	PUTATIVE ODORANT RECEPTOR	2.06e-152
15	832	13.1	850 11	Q93189	PUTATIVE PHEROMONE RECEPTOR	6.33e-142
16	815	12.8	408 13	Q93558	PUTATIVE ODORANT RECEPTOR	2.70e-138
17	798	12.5	803 11	Q93191	PUTATIVE PHEROMONE RECEPTOR	1.14e-134
18	787	12.4	983 11	Q92916	METABOTROPIC GLUTAMATE RECEPTOR	2.50e-132
19	785	12.3	866 11	Q93268	PUTATIVE PHEROMONE RECEPTOR	6.67e-132
20	727	11.4	428 11	Q70413	PUTATIVE PHEROMONE RECEPTOR	1.36e-119

21	727	11.4	667 11	Q93267	PUTATIVE PHEROMONE RECEPTOR	1.36e-119
22	721	11.3	350 13	Q93556	PUTATIVE ODORANT RECEPTOR	2.54e-118
23	717	10.9	908 11	Q92945	METABOTROPIC GLUTAMATE RECEPTOR	1.78e-117
24	697	10.3	548 11	Q93265	PUTATIVE PHEROMONE RECEPTOR	2.98e-113
25	682	10.7	852 11	Q93192	PUTATIVE PHEROMONE RECEPTOR	4.33e-110
26	676	10.6	604 11	Q93193	PUTATIVE PHEROMONE RECEPTOR	7.94e-109
27	669	10.5	604 11	Q93194	PUTATIVE PHEROMONE RECEPTOR	2.36e-107
28	663	10.4	723 11	Q93193	PUTATIVE PHEROMONE RECEPTOR	4.31e-106
29	650	10.2	768 11	Q93266	PUTATIVE PHEROMONE RECEPTOR	2.31e-103
30	628	9.9	1267 5	Q93364	F43H11.4 PROTEIN	9.38e-99
31	625	9.8	339 11	Q70411	PUTATIVE PHEROMONE RECEPTOR	3.98e-98
32	617	9.7	695 11	Q93272	PUTATIVE PHEROMONE RECEPTOR	1.87e-96
33	542	8.5	808 11	Q93190	PUTATIVE PHEROMONE RECEPTOR	6.97e-81
34	528	8.3	251 13	Q73652	PHEROMONE RECEPTOR (FRAGMENT)	5.34e-78
35	523	8.2	251 13	Q73647	PHEROMONE RECEPTOR (FRAGMENT)	5.69e-77
36	519	8.2	251 13	Q73654	PHEROMONE RECEPTOR (FRAGMENT)	3.78e-76
37	509	8.0	250 13	Q73649	PHEROMONE RECEPTOR (FRAGMENT)	4.25e-74
38	508	8.0	251 13	Q73653	PHEROMONE RECEPTOR (FRAGMENT)	6.81e-74
39	507	8.0	311 11	Q93363	CALCIUM SENSING RECEPTOR	1.09e-73
40	500	7.9	250 13	Q73646	PHEROMONE RECEPTOR (FRAGMENT)	2.96e-72
41	505	7.9	251 13	Q73655	PHEROMONE RECEPTOR (FRAGMENT)	2.80e-73
42	505	7.9	251 13	Q73656	PHEROMONE RECEPTOR (FRAGMENT)	2.80e-73
43	502	7.9	301 11	Q93364	CALCIUM SENSING RECEPTOR	1.15e-72
44	491	7.7	250 13	Q73651	PHEROMONE RECEPTOR (FRAGMENT)	2.04e-70
45	487	7.7	250 13	Q73650	PHEROMONE RECEPTOR (FRAGMENT)	1.34e-69

ALIGNMENTS

RESULT 1
ID Q920R8 PRELIMINARY: PRT: 840 AA.

DT 01-MAY-1999 (TREMBL) 10, Created
DT 01-MAY-1999 (TREMBL) 10, Last sequence update
DT 01-MAY-1999 (TREMBL) 10, Last annotation update
DE PUTATIVE TASTE RECEPTOR TR1 (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISTAR;
RX MEDLINE: 99159821.
RA HOON M.A., ADLER E., LINDEMEIER J., BATTEY J.F., RYAN N.J.P.,
RA ZUKER C.S.,
RT "putative mammalian taste receptors: a class of taste-specific GPCRs
RT with distinct topographic selectivity."
RL Cell 96:541-551(1999).
DR EXBL: AF127389; AAD18069.1; .
KW Receptor.
FT NON-ITER
SQ
SDQUENCE 840 AA; 93496 MW; B15F564 CRC32;

Query Match 91.7%; Score 5839; DS 11; Length 840;
Best local Similarity 90.0%; Pred. No. 0.00e+00;
Matches 758; Conservative 55; Mismatches 27; Indels 2; Gaps 2;
Db 1 MFWMAHLLLSLQLAIVACWAFSCQRTSSPGSLPDGLIAGLSHGDCLOVRHRLV 58
1 MFWMAHLLLSLQLAIVACWAFSCQRTSSPGSLPDGLIAGLSHGDCLOVRHRLV 60
59 TSCDRSPSENGRHYGLFQAKRFYEEINSSALLPNTTGYELYDVCSSEANNTATRYL 118
61 TSCDRSPSENGRHYGLFQAKRFYEEINSSALLPNTTGYELYDVCSSEANNTATRYL 120
119 ALOGRPIETOKDNRNNSKYVAFIGPDNDHATVTAALGPFIMPLVSEASVLSAK 178
121 AAGCTGHELMORDNRNNSKYVAFIGPDNDHATVTAALGPFIMPLVSEASVLSAK 180
179 KRPFSLRIVPSDRHOEVNVAOLLQSGFWWISLIGSYGDLGYOALEELAVPGICV 238
181 KRPFSLRIVPSDRHOEVNVAOLLQSGFWWISLIGSYGDLGYOALEELAVPGICV 240

Query Match	22.3%	Score 1421	DB 13	Length 868
Best Local Similarity	31.3%	Pred. No 9,536-270		
Matches	257	Conservative 208	Mismatches 320	Indels 35; Gaps 28
Db	58	PAFSKDGDFVIGGVFSIRATVTVAHHNNTTPEEFRCVIDIHDELQSLHAWFAIEEINN	117	
Qy	31	PEFLSGDFLLAGLGLSLHNDLOQYRHR-PLATSCDRSDSFNGHGHYHFLQAMRFVEEINN	89	
Db	118	STELLPGIKGLQIHDSCAAMP-IAVNAFOLNTLDPFVYTGNCOSQSGMVAVGESG	176	
Qy	90	STALLPNTLIGELDYDCSSSNVAYATLRVAOOGTGHLEQDRLRHSKSVVALIIPDN	149	
Db	177	SPFSISIRVSGSPDIPVSHFATCACLSDOKXPSFRITRPSQFOADALYKIKRFGW	236	
Qy	150	TDHATTAALSLPFLMPVSTYEASSVILSGKRKPSFRTIPSDKYQVEYVLRLOSFGW	209	
Db	237	TWIGAVGSDSDYGNNGMAFLHAAQKEGICVEYESF-YRTHP-HSRIKRVDYIRSTA	294	
Qy	210	WVLSVSGYDYGQGVQALFELMTRPRTICAFNDVYFLSNQADPPRQRMRLAART	269	
Db	295	VVVVAFVASTEMMILFELLSHEPSPROWIGSESMTDPDLRFS-PCA-GTI-GFAIQR	351	
Qy	270	TVVVVFSSRHLAGVEFRFSVLANLTGKWIASEDMAISTYITNPGLGISTGLGVAIQQ	329	
Db	332	SVIPDLRDELDSLSSKASSPVLIEFEDSFNCRRLKGEMCGSDEDIMTLOSPYDTS	411	
Qy	330	ROVPLKKEFEESYVOA-WMGAPRTCP--EGSW-C-GTNO-LCRECHAFTWNPDELGA	362	
Db	412	ELRIINMYKAAVYAIHAIHNAV-CODINATTRCSKFTTIPKRVLTOLKTVNSONGYA	470	
Qy	363	SMSAANYVYEAIVNAHRLHOLLCC--TSGT-CAR-GPVYPMOLLOQIYKVNLFHKRT	437	
Db	471	VSFDAAGDPVASTELVNNKKSQSG-SIEVVAVGYDASLPBGEQFTRFD-ITWVDSRQ	528	
Qy	438	VAFDKRGDPLGYDDIADWDKNGPEWTFEVI--G--SASLSPVH-LDINKTKIQWHGKNQ	492	
Db	529	VPVYSCSSCSQGIKRVYLQKRPICQICVOCPEGEISNTDSECTPCLDDEFPNPERN	588	
Qy	493	VPVYSCITDCCLEGGHHR-LVMGSHHCCFCMCCEGTFPNTSELHTCQPCGTEENAPGSS	551	
Db	589	ACFPKPEVFELEFENEYLIILAVFSVAGCACLAVITAAVEFHRT-SPVIRANSELSFL	647	
Qy	552	ACFSFVTEFLQWHEPRLISVLLAANTLL-LLLTGAGLFAFRRLTPPVYRSGGLCLML	610	
Db	648	FSLLCLFLCSL-FTIGABSHLSCLMLRHTAFGITVLCISCVLGT--VVYLMFATLPG	704	
Qy	611	GLVAVGS-CSLVSFPGKRTVPACLLRQLFSLGAFILFSCLTINSFQVLIYFKSTAVPT	669	
Db	705	SNVMKWFPPQOQRMTVVFITSIQVLCICVWLVPNPPFVARNLTYYKERIILECALSSG	764	
Qy	670	FYH-TMAONHGAGFIVIVSSIVHFLCTWTWAMTPTRETREYQRFPHVLIDECTEVNSG	728	
Db	765	FMAYVGYIGLAAVCLAVLARKPDENENAKMITSMLFCAVWTFEIPAVYSSGKF	824	
Qy	729	FLVAFNAHLLISIFVCSYSLGKLEPENYNNAKCVTSLLHLEVSWIAFTMSSITYGST	788	
Db	835	TVAVEIFAIIASSFGLLICFAPKCFIILFPKRNKKHL	864	
Qy	789	LPAVNVLAGLATLSCGSGFYLPKCYVILCRPELNNHEF	828	

[illegible]

Db	688	VKMGPPPOQRRLSVSSFLIIQVILICVLTTPPEPPFNLYFEKILICGNVSGVFW	747
Oy	671	YHTMAQNHGAGFIVYSSVTHFLCLTLYLMTAMTRPRREYGRFHLVILBCTEVANSGL	7303
Db	748	AVLGTIGLLALICEFLAFLLARKLPDNEAKFTTFSMIFCAVIAITPAVYSSPGKFTV	807
Oy	721	VAFANILLISTEFVCSYSGIKELPENYEAACVFSLLHFWSIATFEFTMSIYQSGYLP	7907
Db	808	AVEVEFALLASTYGMFCJFIPRCVYITLLKPPKNSKKH	845
Oy	791	AVNVLAGLATISGCGFSGYFLPRCYVILCRPELNTNEHF	828
RESULT	5		
ID	073637	PRELIMINARY;	PRT; 864 AA.
AC	073637		
DT	01-AUG-1998 (TREMBLrel. 07, Created)		
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)		
DT	01-NOV-1999 (TREMBLrel. 12, last annotation update)		
DE	PHEROMONE RECEPTOR.		
GN	CA09.		
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;		
OC	Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorphia;		
OC	Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE; 98226768.		
RA	NATO T., SATO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,		
RA	NAKANISHI S., BRENNER S.;		
RT	"Putative pheromone receptors related to the Ca2+-sensing receptor in		
RT	Fugu."		
RL	Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).		
DR	EMBL; AB008859; BAA26124.1; -.		
DR	PFAM; PF00003; 7cm.3; 1.		
DR	PFAM; PF01094; ANF_receptor; 1.		
DR	PRINTS; PR00248; GPCRMR.		
KM	Pheromone.		
SO	SEQUENCE 864 AA; 96216 MW; E26A0114 CRC32;		
Query Match	21.3%; Score 1358; DB 13; Length 864;		
Best Local Similarity	30.7%; Pred. NO. 6,14e-266;		
Matches	252; Conservative 226; Mismatches 298; Indels 45; Gaps		
Db	44	PGDVLGGLFOVHYSSV-FRENTFISPEHQVYCTRFDLGRHAKMTAFVAQVETNKRPDL	1020
Oy	36	PGDFLHLLFSLHADCLQVRHRPRLVTSQDRSD-S-FNCHGHLFQARFVTEETNNSTAL	93
Db	103	LPNLILGRLVDCNGALVYVSGALATLASQGEA-FALQGS-CAGSPVLGIVGDSLSTF	160
Oy	94	LPNLILGEIVDYCESSESNVYA-TLRVPAQCGTGHLEMRDLNRHNSKVVALLIPDWTDH	150
Db	161	TIASASVYGLKIPMYVSFFATCSCLTNRQRPSPFRITPSDDFOVRAMQILKHFQWTW	220
Oy	153	AVTTAAALISPLIMPLVSYEASVILSGKRKPPSPFLRTIPSKYQVEVIVRLQSFQWVI	212
Db	221	GLTVSDDDDYGLHVAFSPQSDVLOSQGGGLATLEVLRPMONTYLSNR--RIY-HYKKESTAR	277
Oy	213	SLVSGYGGYQGLQVQALE-ELATPFGITVAKKDVVPLSAQAGDRPMQRMILKARATT-	270
Db	278	VLMVFAHOSHMI-HLMEEVQRKYGTGLQMLASEMTGTFTPL-QTPDEMPYLNGLTGAIR	335
Oy	271	VYVVEGSNR-HLAGVFERSVLANLTKGVKIVASEDMALSTITVNPGLQGS-IGTVLGAVALQ	328
Db	336	KREITGLADEFLIRIPGSSNNSTSIDMVOQVWEVSFOCKFPASSAABACTGDEIVIOQVA	395
Oy	329	QNOVGLKEFESESY--VOAYVNGAP-RTCPD--G-SW-C--GTNOLCEBCNAF-TTMMN-P	377
Db	396	ERLDVSNLRPEKNYIKAYVALATAYALDDMLQCEPGRGPGSSGGSDIKHLPEMQVAVLQH	455
Oy	378	E-LGAFMSMAATVYEAATVYAAHGHQHLQGC-----T-SG-TCARGP-VYPMQLQDQIYK	428
Db	456	VNFITTFQDQVSEFDENGDVLPIYDILNMQMLPDGRTOVQNVANGVKRSPSRGEEQLQHEK	515

QY	VFNLH - KKTAFADKDGPGIYIILAMDMWPEMT - FEVIGASLSYPH - --LDINKR	483
Db	IFWNEESKPPHVSSESCEPPTMSRRKGOPVCCFDCLLCSBSKISNTTDSNECTSCPE	575
QY	IOWHKNNOVSVSCTRCJCEGHRLVWGSHH - CCFECMCCEATFINTSLHTCQPCGT	542
Db	DWMSQPQDHCVPKTEPLSYHEHBLGICLTAAISLGTIVISVVLGFIHHRSPPVANN	635
QY	EWMAEGSSACFSRVEPLGWEHPEISLVLAANTLILLILIGTAGLEAMRLHPVVASAG	602
Db	SESLFLLVSLKLCFLCSLL - FIGRPRLMTCOLRHAAFGISFVLCVSCILVKTWVLAVF	694
QY	GRLCFLMIGSL - VAGSCSLVSFFPKPTVACILRQPLFSICFALFSLCITRSFOLVIF	661
Db	RASKPGGATLAKWGAVOQRT - VLGSLTIOALCFWMLSSSKPKHKNQYHDKVFE	753
QY	KFSIKVPTFTYTW - AONNAGIPIVSVTHLFCILTWLMMWPPRPREQRPHEVILE	720
Db	CVVSGTVGFAYLLSVIGLALISFLAFLANLPDENENAKLITFSMLICAWVAEVA	813
QY	CTEVNSVGFVAFANHLLISTSTVCSYGLKEPENNENAKVTFISLLHFWSIATFTM	780
Db	YINSGKATADAVEVFAITTSFGILLVAFGPKYIILFRPE	854
QY	SSIVGGSTYLPANVNLATLISGSGFYLPKCYVILCRPE	821
RESULT	6 PRELIMINARY; PRT; 940 AA.	
AC	073635.	
DT	01-AUG-1998 (TREMBLrel. 07, Created)	
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)	
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)	
DE	CALCIW2+ SENSING RECEPTOR.	
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;	
OC	Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;	
OC	Tetradontiformes; Tetradontidae; Tetradontidae; Fugu.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE; 98226788.	
RA	NATO T., SATO Y., YAMAMOTO J., NOZAKI Y., TOMODA K., HAZAMA M.,	
RA	NAKANISHI S., BENNER S.	
RT	*Putative pheromone receptors related to the Ca2+-sensing receptor in	
RT	Fugu.	
RL	Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).	
DR	EMBL; AB008857; BAA26122.1; .	
DR	PFAM; PF00003; 7tm.3; 1.	
DR	PFAM; PF01094; ANF_receptor; 1.	
DR	PRINTS; PR00248; GPCRMR.	
DR	PRINTS; PR00592; CASENSINGR.	
QY	SEQUENCE 940 AA; 105814 MW; 034CB09E CRC32;	
Query Match	21.0%; Score 1334; D9 13; Length 940;	
Best Local Similarity	30.7%; Pred. No. 1,10e-250;	
Matches	255; Conservative 238; Mismatches 283; Indels 55; Gaps 35.	
Db	29 MTGDLILGLGFPIHFG - ISSKDEVLARPESTKCVRFNFGFRMLQAMVAIEFINNSS	87
QY	LPGLFIALGLSEHADCIQVHRRLVTSQRSDS - FNGHGYHLGFQAMRFVEEINNSTA	92
Db	LLPNTLTGRIFFDNCNTYSKALTEATISPVQNKIDSLNIDLEFCQCDHIFATIAVVAAG	147
QY	LLPNTLTGRIFFDNCNTYSKALTEATISPVQNKIDSLNIDLEFCQCDHIFATIAVVAAG	147
Db	148 SAVSTAVANLSTFPIPIQDISYASSSRLSNKQYKSMRTIPTDEHOATAMADVIEYFOW	207
QY	TDHATTAALISPLMLPLVSYEASSVILSGKRRKPSFLRTIPSKQYVEIVTRLQSGFW	209
Db	NWVIAVASDDYIGRPIGKFEKMEERDICHILNELISQYFEDCEIK - A - LVDIRIENSTA	265
QY	WISIVSGYGYGGLGVQALBELATPGICAFVDFVPLSNQADDPROMRMRLATART	269

Db 266 KVIIVEASGDIEPLIKEMVRNITDRIMLASEMASSSLIAKREYLDVEGTIGFVLKA 325
 270 TVVVSNSRLACVFFFSVLANLTGKWLASEDMAISTITN---VPGIOG-IGTVL-- 323
 Db 326 GNIFGRREFLQOVQPKRGSINEFREFMEETFNCLYLEDSPLOESGSDSPRLCTSEE 385
 324 G-VA-10Q--RQV-P--G-----LKEF-EESYQAVMGABRTG-PESGMCCTGTLQCRECH 369
 Db 386 DINSVEPRYLDHTHLRSTYVAVVAVSIAHALODILSCCTGHHGFANNSCADIKKMAWQ 445
 370 AFTTMNPGLGAFSMAAYVVEAVVAHGLLOLGCIG-----TGA-RGVPYVWQ 421
 Db 446 VLKRLHLNTNSMGEVHFEDENADMEANYTIIMWRSADGSVAFREYVYHMHARGA 505
 422 LLOQYKYNLHLK-RKVARDDKGDPLGYDIIAMDKNGE-W-TFVTSASLI-SP--V 475
 Db 506 KLIDNTKMMWNAYSSEVPVPSNCSDECEPTRGKIIDSMPTCCPECTECSDGEYSDHKA 565
 476 HLDINKTKIQMHGKNQVPVSVCTRDCEGHHLRMGS-HHCEFCMPCEAGTFLNTSEL 534
 Db 566 SICTKCGNNSMSSGNHFCCLKELEFLANSEPGIALAICAVLCVLTATVMGVFRN 625
 535 HTQPCGTEEMWABEGSSACFSRTVEFLGMHBPISLVLLAANTLLLLIGTAGIFANRLH 594
 Db 626 TPVKAASNRELSTVLLSLICCFSSSLI-FIGEPDWTCLRQPAFISVPLCISCTLVK 684
 595 TPVRSAGSLCFLMLCSLVAG-SCSLYSEFGKPTVACLLRQPLBSLGAIFLSCITIR 653
 Db 685 TNRVLVFE-AKIPFSIRKMGMLQFLVFLCTFVOVMICVWMLYNAPSSYRNHD- 741
 654 SFQVLIIFFKSTKVP-FYHTMAONHGAGIFIVYSTVHLFLCLTAMWTPRPTREYQR 712
 Db 742 IDLIIFITCESSVMLGFLIGTC-LLAICFF-AFKSRKLPENTTEAKFTFCULIF 799
 713 FPHLVLECE--VNSGVFLVAFAHNLLISITFCVSYLCKELPENNEKCVTFSLHL 770
 Db 800 FIWVSIFAPYFSTY-GKEVSAVEALAILASSYGMACIFENKYYITLFRP 849
 771 FVSMIAFFIMS-SIYQSYLPAVNVLGLATLSGFGSYLPCVCYLCP 820
 QY

RESULT 7
 ID 073639 PRELIMINARY: PRT: 880 AA.
 AC 073639:
 DT 01-AUG-1998 (TREMblrel. 07, Created)
 DT 01-NOV-1998 (TREMblrel. 07, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE PHEROMONE RECEPTOR.
 GN CAL3.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorphia;
 OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98226788.
 RA NAITO T., SAITO Y., YAMAMOTO J., NOZAKI Y., TOKURA K., HAZAMA M.,
 RA NAKAMISHI S., BRENNER S.,
 RT Putative pheromone receptors related to the Ca2+-sensing receptor in
 RT Fugu.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).
 RL EMBL: AB008861; BAA26126.1; .
 DR PRAM: PF010003; 7tm_3.1.
 DR PRAM: PF01094; ANF_receptor; 1.
 DR PRINTS: PF00248; GPCRMRG.
 KW Pheromone.
 SQ SEQUENCE 880 AA: 97464 MW: 91072807 CRC32:
 Query Match 20.1%; Score 1279; DB 13; Length 880;
 Best Local Similarity 29.1%; Pted. No. 1,17e-238;
 Matches 243; Conservative 230; Mismatches 318; Indels 45; Gaps 35;

Db 53 GDIIIGLESFLDMVVE-PNLPTSTPPTIOCTRESFRTFWQVTFVAVEEIRNRAEIL 111
 37 GDFLLAGLFLSLHADCLQVRRRLPLVTSDDSD-S-FNGHGHLLQANRFTVEELINNSTALL 94
 Db 112 PNITLKKIYDSCSTPHOSIKAAIDMGSEKDSQFEGKIQRECGDNVPAVIGDGSSTOS 171
 95 PNITLGEIYDVCSSESNVY-ATLRVPAOOGTGHLEMOBDRLNHSSKVAALLIPDNTDHA 153
 Db 172 LAVARFLGVHNPQVYFSSCACLSDKTOFPAFLRTPBGLPEQVGLYLQYKFGTYWG 231
 154 VTTAALSLPLMLPVLSEVASSVILSGRKFPSFLRTIPSDKQOVENVIRLOSFGVWVLS 213
 QY 232 VIAGDDYGRGAIPANEVRLGACIALYEMIP-RTOS-QAAISSIINIRSSGARVYL 289
 214 LVESYDYGQGLGQVQALBELATPRGICVAFKDVPLSLAQAGDPRMQMMLRIARARTVV 273
 Db 290 VFVEDQVAREDEAVRQKITG:QWLASEMSTAALITSPKRYHILQSGMGAIRADI 349
 274 VFSNRHLAGVFFRSVVLANTLGKWLASEDMAISTITVPGIOG-GLVGLVAAIQOROV 332
 Db 350 PGLQDFLRLHPSASADDDPFLPFWEVYFQCSLDPRHSHSEKRCSCGTEELRSKNY 409
 333 PGLKEF--E-ESTYQAVMGAPRTCP--EGSW-CGTA-Q-LC--RECHAFTT-WNPEL- 379
 QY 410 SDVSOLRISYNYKAYALATAIKARSCSEKSGSPSOACPDLDNIHPQLHHYTKOYN 469
 380 GAFS-HSAANVYEAHYVAHGHQLGC-T-SG-----TCAR-GVYVWQLOQYKYN 430
 QY 470 YINRFGDEIKFDENGPAAWYDILNNQLIPGDMDFVYQKFDIAGTRKNHIEEKI 529
 431 FLHL-KKTVAFDOKDPLGYDIIAMDWN-GPEMTFVIGS-ASLSPV--HLDINKTKI 484
 Db 530 VNMGNMNPVLSVSSICPPRTKKAIRPNYPTICHCQVCTAELINQDATICACGLE 569
 485 QWEGKNQVVPVSVCTDCEGHRLWGSNH-CCEFCXCEAGTFLNTSELHTQPCGTE 543
 QY 590 FMSNADRTACVPKQVEFLSFGDTIGIALVY-SLISGSLCAVALVFFHRTSPIRAN 648
 544 EMAPDESSACFSRTVEFLGMHBPISLVLLAANTLLLLIGTAGL-FANRLHPPVRSAG 602
 QY 603 GRCLFIMLGSLVAGS-CSLYSEFGKPTVACLLRQPLBSLGAIFLSCITIRSFOLVIF 661
 Db 649 SDLSFLLSFLCLFCLSL-TFISPSQWSCMLRHTAGITFVLCISCLIGKTIIVLMAF 707
 603 GRCLFIMLGSLVAGS-CSLYSEFGKPTVACLLRQPLBSLGAIFLSCITIRSFOLVIF 661
 Db 708 R-ATLGSQDMKMFQGGKQKAITF-SILVOVYICVWLNV-APPYROYMRESAIIIL 764
 662 KSTKVPFVYHTV-AONHGAGIFIVYSTVHLFLCLTAMWTPRPTREY-QRPHLVIL 719
 QY 765 LCDEGTIAFSVLGYIGVLACQCFLLAFARLDPNEVBARLIARSMILFCVWVAFP 824
 720 ECEVSVGLVAFANILLISITFCVSYLGLKELPENNYEAKCVTSLHLHPSWIAFT 779
 Db 825 AYISSPGKSTLIEIFAILASSYGLGICFAPKCYIILKSEKTRKHLMSKSERF 880
 780 MSSYQGSYLPVAVNLVAGLATLSGFGSYLPCVCYLCPLELNTENHROASIODY 835
 QY

RESULT 8
 ID 093552 PRELIMINARY: PRT: 844 AA.
 AC 093552:
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE PUTATIVE ODORANT RECEPTOR.
 GN GFB1.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinidae; Cyprinidae; Carassius.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE-OLFACTORY EPITHELIUM;
 MEDLINE: 98426265.

RA CAO Y., OH B.C., STRYER L.;
RT "Cloning and localization of two multigene receptor families in
RT goldfish olfactory epithelium";
RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
DR EMBL: AF083080; AAC64075.1; -.
DR PFAM: PF00003; 7tm_3; 1.
DR PFAM: PF01094; ANF_receptor; 1.
DR PRINTS: PR00248; GPCRMR.
SQ SEQUENCE 844 AA: 94599 MW: 7A84F7AC CRC32:

Query Match 19.8% Score 1258; DB 13; Length 844;
Best Local Similarity 28.9% Pred. No. 4,52e-234;
Matches 235; Conservative 216; Mismatches 334; Indels 27; Gaps 24;

DB 32 PLESKDVGIVGIGFAIRKETLPSEFFTOKPOPLSCSVNLRDLRLAQTMTALQEIINK 91
QY 31 PGSLEPDLFLAGFLSLHA-DCLQVRHRLPLVTSODRSDRNGHYHLFQAMRFTVEEINN 89
DB 92 NEILLPNISIGYIIYTDCGRSLTMTATMGLMNSQDFGPGNT-CN--GHSP-IHAITGES 147
QY 90 STALLPNTLTGELYDYCES-SNVYATLRVPAOQGTGHLEMDRLNHSKVALALIGPD 148
DB 148 ETSAIVLSTGTGPKIPVISHSSCECLSNRKNYPSFEFTISDYHQSAIASIVKHG 207
QY 149 NTHAVTTALLSPFLPLVSEASSVILSGKRFPSEFLTIPSDKYQVEVYIRLQISFG 208
DB 208 MSWVGAIVSNDYGNNGMAIFLKTVOEGICVEY-SYKRYETET-E-KLKVVDITIKGT 264
QY 209 WWSIVLGVSYGQGLQVQALELATPRGICVAFKDVYPLSAQGDPRMRMLRLARAR 268
DB 265 AKYIVAFISVEKGLLEQSIONITGOMIGVEPWITANTYTP-KSLHAMEGSLGFAM 323
QY 269 TTYVAVFNSHLAGVFRSVLANLTGKWIASEDM-AISTYITNYPGIGIGIVLGVAI 327
DB 324 KKNIBGEFAAKKPFMDTAPSCS--EGNY-SKVALSCREBELALNKNYEDVTEHR 380
QY 328 QORQVGLKFE-ESTYQAVMGAPRICEBSWCTNOL-CRECHAFYTMNPELGAFSMS 385
DB 381 YSNVYKAVYAVASHLSLKICQEGCEKGLPIQPOVVELTKKINFATKTDGRWFDS 440
QY 386 AAVNVYAVYAVAHGLHQLLGCTG-GTCARG-PYPMQQLQIKVFLHMK-KTAVFDD 442
DB 441 TGGVVALYEVNNQOOSDGYORKSVGYASLEPTYNLHNVENITWAGHLEKPSAC 500
QY 443 KGPPLGYDDIAMDNGPE-WTEFEVIG--SASISPVH-LDINKTKIQMHGKNQOVPSVC 498
DB 501 SESCPGTRAAQGRPCYDIPCAGEISNETRINCKPCQWEXMAEKKNVCYLA 560
QY 499 TRQCLBCHRLV-MGSHHCCFECAPCEAGTFLNTSELHTCOPGTEEMAEBSGACFSRT 557
DB 561 VEFLESTELMGVVLVFEFSLGVGLTLLVALLEFYNNKDTPVKANKSELSTLFLSLCF 620
QY 558 VERLGMHEPISVLAMANTLLLLLTIGTAGLFAMRLHTPYVRSAGRLCLMLGSLVAGS 617
DB 621 LGLL-FTIGPTEMSCLMTAFGITVLCISVGLKTYVLAFAK-AITPGNNIMKMG 678
QY 618 -CLYSFEGKPTVACILRPLPSLGFALPISCLTIRSFVLIFKSTVPTPTFYHTAQ 676
DB 679 PAQORSLVLAFTLQVILQVLMLTISPFPYKMKYKKEIILCESGSIIPFNAVLYTI 728
QY 677 NHAGAFIVYISVTHFLCTLWLMAMTPTPTREOPRPHLVILCTEYVNSVGLVVAHNN 726
DB 739 SLALFLCFLIAPLARTLPDKFNKAITFPMILFCVAMITIPAYVSPKFTVAEIFA 798
QY 737 ILLSIFVCSYIGKELPENYNEAKVTFSLLHFSVMAFFMSSLYQSSYLPVAVVLA 796
DB 799 ILSSEGLLEGIAPKCYITLLKPBONTKQHL 830
QY 797 GLATLSGGSFGYELPKCYITLLCRPELNTEHF 828

RESULT 9 PRELIMINARY; PRT; 856 AA.

AC 073638;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE PHEROMONE RECEPTOR.
GN CAL2.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98226788.
RA NAITO T., SAITO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,
RA NAKANISHI S., BRENNER S.;
RT "Putative pheromone receptors related to the Ca2+-sensing receptor in
RT Fugu";
RL Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).
DR EMBL: AB008860; BAA26125.1; -.
DR PFAM: PF00003; 7tm_3; 1.
DR PFAM: PF01094; ANF_receptor; 1.
DR PRINTS: PR00248; GPCRMR.
KW Pheromone.
SQ SEQUENCE 856 AA: 94590 MW: 7B8395C7 CRC32:

Query Match 19.7% Score 1251; DB 13; Length 856;
Best Local Similarity 29.7% Pred. No. 1.52e-232;
Matches 246; Conservative 234; Mismatches 302; Indels 17; Gaps 38;

DB 35 PLISQEDITIGGAFILHQ-MKPSLSEFTEPEDITCRINLRERFQTMIFALEIN 93
QY 31 PGSLEPDLFLAGFLSLHADCLQVRHRLPLV-TSCRS-DSFGHGHFLQAMRFTVEEINN 88
DB 94 NSSSLPNISIGYKVPDGTGTLPTSTRAV-MALMNGKTRTP-EGGSSRST-VHAIGAS 150
QY 89 NSTALLPNTLTGELYDYCESSESNVYATLRVPAOQGTGHLEMDRLNHSKVALALIGPD 148
DB 151 ESSSTIMLQISGIFQIPYISHFATCACLNSRKEPSPFRITIPDFYQSRALAKYKHG 210
QY 149 NTHAVTTALLSPFLPLVSEASSVILSGKRFPSEFLTIPSDKYQVEVYIRLQISFG 208
DB 211 WTVVGAIVSNDYGNNGMLFTFMAEGVCEYISGFS-WTDPSF-QIARVYTYKSS 268
QY 209 WWSIVLGVSYGQGLQVQALELATPRGICVAFKDVYPLSAQGDPRMRMLRLARAR 268
DB 269 ARVLAFLQSEKSALEAVKONLTGLQWGESVITGHLA-LKYSAILTGLSIFPI 327
QY 269 TTYVAVFNSHLAGVFRSVLANLTGKWIASEDMAITTYITNYPGIGIGT-VLGVAI 327
DB 328 RKTITGLOEFLQVNPSONPNLLKEFETFGCSFQSDVHGATQCSGVERKLDIQNP 387
QY 328 QORQVGLKFE-ESTYQAVMGAP-RICEPSW-CG--TN-OLCRECHAFYTM-NMPE- 378
DB 388 FTDSLELRISNNYKAVYAVAHAMHMLKCGSGEAVNOSCITTKKDFELQYVEHQSIN 447
QY 379 LGAFS-MSAAYEVYAVAHGLHQLLCT-SG-----TCARGPYPW-QLLQOYLYKN 430
DB 448 FTLOSGERVYFDYGPAPAYELVNQORSPREGTVVVGNDASOPNOCFTMMNINT 507
QY 431 FLHMK-KTAVFDDKGPRLGYITDIAMDNGPEPT-FEVIGSLSL-PV-HDINKTKIQ 485
DB 508 MAARLQRPVLSVCSOSICGFQAVYIKGRPICCTCVCACAGEISNNSASACLOPLEF 567
QY 486 WHQKNQOVVSVCTRCBLG-HHRLVMSHCCFECMPEAGTFLNTSLHRCOCGTGE 544
DB 568 WSNEDSQVYPKVIFFLSEETMG-ALLAVALFGAALSLVFCVF-PFRITPLVYKASN 625
QY 545 WAEQSSAFCSRTVERLGMHEPISVLAMANTLLLLLTIGTAG-LFAMWL-HTPVRSAG 602
DB 626 SELSFLLSITLCLFCSL-TFIGRSPMSCVLRHTAFGITFALCSCVLAAT--VAVLF 682
QY 603 GRCLTMLGSLVAGS-CSLYSFEKPTVPACILRPLPSLGFALPISCLTIRSFQLYITF 661

Df	683	AETARPCNTENYGS-VPLORTSVFACI--TLOYVICMLTLAPRPHKMTAKXRII	739
Oy	662	KFTSTVP--T-FYHTMAONHGAGIFIVYSVTHLFLCTITLMATWTPRTBYOAFPHLI	718
Df	740	LECNLSGFWFMVVVLGYIGTLAVICFILAFARKLDPNFNEAKPTFSMILFCAWWTFI	799
Oy	719	LECTEVNSVGFLVAFAHILLISITFYOSYICKLEPENYNNAKVTSLLHFWSIAFF	778
Df	800	PAYVSSPEKFTVAVEIFAIIASSFGCLFCIFAPKCYYILLIKPEKNTRKH	848
Oy	779	TMSIYOQSYPLPAVNLGLATLSGGFGSGYFLPCKVCYILCPRELNTEH	827
RESULT	10	PRELIMINARY;	PRT; 875 AA.
ID	073640		
AC	073640:		
DT	01-AUG-1998 (TREMBLrel. 07, Created)		
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)		
DT	01-Nov-1998 (TREMBLrel. 12, Last annotation update)		
DE	PEROMONE RECEPTOR.		
GN	Ca15.1.		
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).		
OC	Euryarchaea; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;		
CC	Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorphae;		
CC	Tetraodontiformes; Tetraodonotoidei; Tetraodontidae; Fugu.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE; 98226788.		
RA	NAITO T., SAITO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,		
RA	NAKANISHI S., BRENNER S.;		
RT	*Putative pheromone receptors related to the Ca2+-sensing receptor in		
RL	Fugu.*		
RL	Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).		
DR	EMBL; AB008862; BAA26127.1; .		
DR	PFAM; PF00003; Tm_3; 1.		
DR	PFAM; PF01094; ANF_receptor; 1.		
DR	PRINTS; PR00248; GPCRMR.		
SW	Phenome.		
QY	SEQUENCE 875 AA; 94934 MW; 8FC188F2 CRC32;		
Query Match	19.4%; Score 1236; DB 13; Length 875;		
Best Local Similarity	30.6%; Pred. No. 2.86e+29;		
Matches	261; Conservative 222; Mismatches 315; Indels 55; Gaps 41.		
Df	30	ALTCQSWMSTEEOGLFDGDGVHWGLEFNLTHTPDRTANNFTQOSHXYACTGLENTPLQVI	89
Oy	21	AFSC-QR-TESSPGFSLPDGLLAGLESLNDJCQVHR-RPLYISCRDSRFSNGHYHLF	77
Df	90	YAMPFVBEIHSAALBPVKLGTHIRDSCLAHPTQTQAIALVALVAGSASCELATPADYS	149
Oy	78	QAMRTVEEINNSTALLPNITLGEYELDYCS-ESSNYATDLR-VPAAQGCHILEMDRLR	135
Df	150	AETSEKKAASVPLIIGGASSNAKKILGLTSLPSISYTASCPSTSRHRYPRFFRMAS	209
Oy	136	NHSKSVVALIG-PDNTDAVTAA-LSPFLMPL-VSTEMSSVYLSSKRKPSSLRTIPS	192
Df	210	DIYQAOLAOQLREBNFTWIGAVVANNDGHVAANKVFQEQTOGKGVALAEVLETRETIIV	269
Oy	193	DKYQVEIVLRLOGFGMWISLVSGYGQGLGOALBELATPRGLCVAFKRDVPLSAQA	252
Df	270	ADAVRAARTI-QASTAR--VLIVS-WTYDGHLFRLOLQINTVDROFLASEANSTSEVL	335
Oy	253	GDP-RMQHMRLRLRARTRTVVVSNSHLA-GVFFRSVLANLTKGWIASDEMAISTYI	310
Df	326	LKDDPTSVAGGVAVMASOHIEGDFRFLGMLPSLRPSDKPLEOFWEDEFQSPSPS	385
Oy	311	TNPGLIOGIG-VLGAVALQQRQVPG---LKEF-----ESTYQAVMGAPRTC-PEGSM	358
Df	386	SETSGDINASLPPCSGAESELGCVNHPTDSLHLYTNVYLVAANAALSHLSCEITHN	445
Oy	359	CCTN-QL-C-RECHAFTTW-MPE-LGAPS-MEAAVNVEAVYAHAHGLHQLLGC----	407
Df	446	SPSGTSHCTSKGIKTTELLOHLSKVNFTTPQGNHLYFGCADIP-AMYDLINMO-SGITDG	503

[illegible]

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-CS7B16/TJ.

RX MEDLINE: 97433087.

RA MATSUMI H., BUCK L.B.,

RT "A multigene family encoding a diverse array of putative pheromone

receptors in mammals."

RL Cell 90:775-784(1997).

DR EMBL: AF014111: AAC53401.1.

DR MGD; MGI:131668; VZT1.

DR PFAM: PF00003; 7tm_3; 1.

DR PFAM: PF01094; ANF_receptor; 1.

SQ SEQUENCE 850 AA; 97415 MW; 3CA08744 CRC32;

Query Match 13.1%; Score 832; DB 11; Length 850;

Best Local Similarity 26.8%; Pred. No. 6.3e-142;

Matches 210; Conservative 195; Mismatches 323; Indels 55; Gaps 49;

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Db      75 YEFLVAFALDEINRNPYLPTLMFS-F-IGNCODLRVMDQAVTQINGHNFVNY 132
QY      74 YHLEQAMRFTYEELINNTALLPNTTIGELYDVCSESNVATLRVAQOCTGHEMQRD 133
Db      133 PCYLDSCAIGLGPSTKT-SKLA-MHS--MPLVFFGPPNPLRDRLPHVQVAPK 188
QY      134 LRN-HSSKVVALLPDMTHAVTTAALLSPFLMPLVSEASSVILSGKRKPSFLRTIPS 192
Db      189 DTHSHGMVSLMFPRMTWIGLVISDDOGIQLSDLRSSQRHGICLAFNMIPENMOI 248
QY      193 DKYVEYIVRLLOSFGWVWISLVGSYGQGVQVLELTPRGICAFKDVVPLSAQA 252
Db      249 YMTREAIYDKHIMTSKAVVIYGENNSTEASFRMEELGA-R-RIVITTSQMDVITNK 306
QY      253 GDRPMQRMMLRLARARTVYVVFNSRH--LAGVFFRSVLANLGKVAIASEDAISTYI 310
Db      307 KDFT-LNLFHGIITFE-HHREIPKLKEMQTMNTAKYPVDISHTILEWNTFNCISKNS 364
QY      311 TNVPGIOGIGVLGVAIQOR-QVPLKEFESESYQA--VMGAPRTCPG-GSM-CGTNOLC 365
Db      365 IRMHITFNNLTLEWTSLNHYOV-AMSDEGYLNAYAVAHATHEHYEQVESOKKAPK 423
QY      366 RECH-AFT-T--W-NMPELCAFMSA-AYNVYEAVAHAGLHQ-LLG-CTSGTCARGP 416
Db      424 RYFTACQOVSSIMKTRVFTNVEGLVNMKHNRENOCTEYDIFI-IMNFPQIGLKYKIGSY 482
QY      417 VY-FW-QLLQIYKVN-FLHK-KTVAFDKGDPLGYDILAMDNGPE-WTFEV-IGS- 469
Db      483 LPCFPOROKLHISDD-LEMAKGTSPQVPSVSVACTAGFRKIYQKETADCCFCVQCP 541
QY      470 -ASISPVH-LDINKTKIQW-HG-KNQVPVSVCTRDCLGHHRLV-MGSHHCFCPCMC 524
Db      542 ENELSNETDMQCVRCDDKANTIEQTHCSRAVSFLAYEDSLGALGMAISATITL 601
QY      525 AGFTLNTSELTCOPCGTEEMAPGSSACFSRTVEFLGWHPEISLVL-LAANTLLDLL 582
Db      602 ILVT-FVKYK-DPTVAKNRILSYILLISLVEFLCSIL-FIGPPQVTCIFQOTTEGV 658
QY      583 IGTAGLFAMRHTHTPVASAGRLCFIMGLSVAGS-CSLYSFFGRPTVPACLLRQPLPSL 641
Db      659 LFTVSVSTVLAKITVVAEFLTPGRRM-RG-MMMTGAPRLVIPICLLIQVLGIMLV 716
QY      642 GFAIFLSCLTFRSQVLIIFKSTKVPFTFYHTMAQNHGAGIFVL-VSSTVHLFLCLTFLA 700
Db      717 TSPFIDRDIOSEHGKIVIL-CNKGSVIAFHVVLGSLAGSFTLAFLARNLPDTFNE 775
QY      701 MTRPRPTREYOR-FPHVYLIECTEVSNGFLVAHAHNLISISTFVCSYLKEKLPEYNE 759
Db      776 AKFLFSLV-FCSWITFLPVYHSTRGVVWVEVSIASSAGLLMCIFVPRCYVILI 834
QY      760 AKCYTFSLHLFVS-WIAFTMSIYQGSYLPANVNLAGLATLSGFGSGLFLPKCYILC 818
Db      835 RPD 837
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QY 819 RPE 821

Search completed: Fri Mar 17 13:22:28 2000
 Job time : 250 secs.


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FT CHAIN 20 1085 EXTRACELLULAR CALCIUM-SENSING RECEPTOR.
FT DOMAIN 20 613 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 614 636 I (POTENTIAL).
FT DOMAIN 637 650 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 651 671 II (POTENTIAL).
FT DOMAIN 672 682 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 683 701 III (POTENTIAL).
FT DOMAIN 702 725 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 726 746 IV (POTENTIAL).
FT DOMAIN 747 770 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 771 793 V (POTENTIAL).
FT DOMAIN 794 806 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 807 829 VI (POTENTIAL).
FT DOMAIN 830 837 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 838 863 VII (POTENTIAL).
FT DOMAIN 864 1085 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 91 91 POTENTIAL.
FT CARBOHYD 131 131 POTENTIAL.
FT CARBOHYD 262 262 POTENTIAL.
FT CARBOHYD 288 288 POTENTIAL.
FT CARBOHYD 401 401 POTENTIAL.
FT CARBOHYD 447 447 POTENTIAL.
FT CARBOHYD 469 469 POTENTIAL.
FT CARBOHYD 489 489 POTENTIAL.
FT CARBOHYD 542 542 POTENTIAL.
FT CARBOHYD 595 595 POTENTIAL.
SQ SEQUENCE 1085 AA; 121170 MM; 501F66CD CRC32;

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Query Match 20.7%; Score 1316; DB 1; Length 1085;
 Best Local Similarity 31.9%; Pred. No. 9.34e-272;
 Matches 272; Conservative 234; Mismatches 273; Indels 73; Gaps 51;

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Db 31 GDIILGLGPEPIHG-VAAKQDILKSPREVECTRYNFRGRWLOAMIFAEINSSPALL 89
QY 37 GDFLAGLGFSLHADCLQVHRPLVTSQRSDS--FNGHGHLQFQAMFTEELINNSTALL 94
Db 90 PNNLTGRIPTDONTYNSKALEATLSVAONKIDSLNDEFCNSENIPSTIYAVGATGSG 149
QY 95 PNITLGYEYLDVCESSSNV-ATLRVPAOGTGHLEMQR--DLRNHSSKVALIGDPNTD 151
Db 150 ISPAVNNLGLFIPOVSVAASSRLSNKQNFSLRTIPNDEHOATAMADIIEFRMWN 209
QY 152 HATTTALLSPFLMPLVSYSAVVIIISGKRKFSFLRTIPSDXYQVEYVIRLQSGWVW 211
Db 210 VGTIADDDYGRGRIEIKFREAEERDICIPELSISOYDE-B-KIQOVVEYIQTSTAKV 267
QY 212 ISLVGYGYDYGQVQALELATPRGICVAFKQVPLSAQAGPRQRMRLRLARATTY 271
Db 268 IYVFSSGPDLEPI-KEIYARNITGRWLAASEMASSSLIAMEYRHYVGGTIGFGLKAG 326
QY 272 VYVFSN-RHLAGVFRRSVLANLTGKWLIASEDMA---IS-T-YITNPG-IO-GI--G 320
Db 327 QIGFREFLOKVPKRSVNHGFAKEFEWERTFNCHLOEGAKGPRVPYDFLGHGEGARLS 386
QY 321 TYLGV-A-IO--O-RO-VP-GL-KEF-EESY---VO-AVNGA-P-----RTCEEG-SW-C 359
Db 387 NSPTARPLCTGENISVETPYMDYTHLRISYNYLAVYSIAHALODIYTCIPGRGLFT 446
QY 360 -G-TN-Q-LCRCHAFITMMPELGAFMSGAAYNYEAVYAHAHGLQLLGC-----T 408
Db 447 NSGADIKYKVAOVYKHLRLNFTSMGEQVTFDECGDLAGNYSTIIMHLSPEDSIYF 506
QY 409 SGTC-A-RGPYPMQLLOQIYKVFLLHK-KTVAFDDKGDPLGYDIIAMDMNGPE-WT-F 464
Db 507 KEYGYNYVAKKGRLEINDEKILMSGFSEVPEFNSQRCIAGTRKGIIEGEPCCFEC 566
QY 465 EYVG--SA-SLSVHLDDINKTKIOMHGKNQVSVCTRCLDGHNR-LWGSHHCCFEC 520
Db 567 VECPEDEYSDTDASADCKPDDFWSNENHTSCIAKEIEFLSTWEPGLALTFEAVLGIF 626
QY 521 MPEBAGFLNTSLHQCQPCGTEGMARPESSACFSRTVELGWHFPISTVLLAANTLLLL 580
Db 627 LTFVVLGVFIKFR-NTPYIKATNRELSYLLFSLCCCFSSSLF-FTGEPODMTCRLRQPA 684

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QY 581 LLIGTAGLPA-WRLHPVYRSAGGRCLFIMLSIVAG--SCSIYSEFGKPTVPACILRQPL 638
Db 685 FGISFELGSCILYKNNRLVLEE-AKIPSPHKKWMLNQFLVYFCTMOVICAL 742
QY 639 FSLGFIPLSCILTRSFQVILFKSTKVPF-FYHTMAONHAGIFVIVSSVHLFCIT 697
Db 743 WLNTAPSSYRNHELEDEIFITCHEGSLMALGFLGYTC-LLAACPEFF-AFKSRKLE 800
QY 698 WLAMPFPTREYQRPHLVILECTEVN--SVGLVAFANHLILSLSTVCSYLKRELE 755
Db 801 NNEAFTIFSMLIFITWISFIPAYASTY-KREYSAVEVIALIASFGLACIFPNKY 859
QY 756 NNEACVVFSLHNFVSWIAFEFTM-SSIYQSGYLPVAVNVLGATLSGSGFYFLPKCY 814
Db 860 IILFKPSRNTIE 871
QY 815 VILCRPELNNTIE 826

```

RESULT 2

ID CASR_HUMAN STANDARD; PRT: 1078 AA.
 AC P41180: Q13912; Q16379; Q16108; Q16109; Q16110;

DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID
 DE CELL CALCIUM-SENSING RECEPTOR).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.

NP SEQUENCE FROM N.A.
 RA PEARCE S.H.S., THAKKER R.V.;
 RL submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.

RN [2]
 RC SEQUENCE FROM N.A.
 RP TISSUE-PARATHYROID;
 RX MEDLINE: 95279439.

RA GARETT J.E., CAUVANO I.V., HAMMERLAND L.G., HUNG B.C., BROWN E.M.,
 RA HERBERT S.C., NEMETH E.F., FULLER F.;
 RT "Molecular cloning and functional expression of human parathyroid
 RT calcium receptor cDNAs."
 RL J. Biol. Chem. 270:12919-12925(1995).

RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RX MEDLINE: 95408281.
 RA AIDA K., KOISHI S., TAMATA M., ONAYA T.;
 RT "Molecular cloning of a putative Ca(2+)-sensing receptor cDNA from
 RT human kidney."
 RL Biochem. Biophys. Res. Commun. 214:524-529(1995).

RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96343808.
 RA FREICHEL M., ZINK-LORENZ A., HOLLOSCHI A., HAFNER M., FLOCKERZI V.,
 RA RAUE F.;
 RT "Expression of a calcium-sensing receptor in a human medullary
 RT thyroid carcinoma cell line and its contribution to calcitonin
 RT secretion."
 RL Endocrinology 137:3842-3848(1996).

RN [5]
 RP VARIANTS FHH GLU-185, LYS-297 AND TRP-795.

RX MEDLINE: 94094324.
 RA POLIAK M.R., BROWN E.M., CHOU Y.H., HERBERT S.C., MARK S.J.,
 RA STEINMANN B., LEVI T., SEIDMAN C.E., SEIDMAN J.G.;
 RT "Mutations in the human Ca(2+)-sensing receptor gene cause familial
 RT hypocalcemic hypercalcemia and neonatal severe
 RT hyperparathyroidism."
 RL Cell 75:1297-1303(1993).

RN [6]
 RP VARIANT ADH ALA-127.

RX MEDLINE: 95179179.
 RA POLIAK M.R., BROWN E.M., ESTEP H.T., MC LAINE P.N., KIFOR O., PARK J.,
 RA HEBERT S.C., SEIDMAN C.E., SEIDMAN J.G.;
 RT "Autosomal dominant hypocalcaemia caused by a Ca(2+)-sensing receptor
 gene mutation.";
 RL Nat. Genet. 8:303-307(1994).
 RN [17]
 RP VARIANTS FHH MET-62; CYS-56; MET-138; GLU-143 AND GLN-227.
 RX MEDLINE: 95243227.
 RA CHOU Y.-H.W., POLIAK M.R., BRANDI M.L., TOSS G., ANNOVIST H.,
 RA ATKINSON A.B., PAPAPOULOS S.E., MARK S., BROWN E.M., SEIDMAN J.G.,
 RA SEIDMAN C.E.;
 RT "Mutations in the human Ca(2+)-sensing receptor gene that cause
 familial hypocalcemic hypercalcaemia.";
 RL Am. J. Hum. Genet. 56:1075-1079(1995).
 RN [8]
 RP SEQUENCE OF 1-61 FROM N.A., AND VARIANT FHH ALA-39.
 RX MEDLINE: 95403641.
 RA AIDA K., KOISHI S., INOUE M., NAKAZATO M., TAMATA M., ONAYA T.;
 RT "Familial hypocalcemic hypercalcaemia associated with mutation in the
 human Ca(2+)-sensing receptor gene.";
 RL J. Clin. Endocrinol. Metab. 80:2594-2598(1995).
 RN [9]
 RP VARIANTS NSHPT LEU-227 AND TYR-598.
 RX MEDLINE: 96292293.
 RA PEARCE S.H.S., TRUMP D., WOODING C., BESSER G.M., CHEW S.L.,
 RA GRANT D.B., HEATH D.A., HUGHES I.A., PATERSON C.R., WHITE M.P.,
 RA THAKKER R.V.;
 RT "Calcium-sensing receptor mutations in familial benign hypercalcaemia
 and neonatal hyperparathyroidism.";
 RL J. Clin. Invest. 96:2683-2692(1995).
 RN [10]
 RP VARIANTS ADHP THR-116; HIS-681 AND SER-806, AND VARIANT SFR-851.
 RX MEDLINE: 96311554.
 RA BARON J., WINER R.K., YANOVSKI J.A., CUNNINGHAM A.W., LAUE L.,
 RA ZIMMERMAN D., CUTLER G.B. JR.;
 RT "Mutations in the Ca(2+)-sensing receptor gene cause autosomal
 dominant and sporadic hypoparathyroidism.";
 RL Hum. Mol. Genet. 5:601-606(1996).
 RN [11]
 RP VARIANT FHH ARG-174.
 RX MEDLINE: 97442275.
 RA WARD B.K., STOCKEY B.G.A., GUTTERIDGE D.H., LAING N.G., PULLAN P.T.,
 RA RATACZAK T.;
 RT "A novel mutation (L174R) in the Ca2+-sensing receptor gene
 associated with familial hypocalcemic hypercalcaemia.";
 RL Hum. Mutat. 10:233-235(1997).
 CC -I- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF
 CC CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A
 CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM.
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -I- ALTERNATIVE PRODUCTS: TWO ISOFORMS SEEM TO BE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -I- TISSUE SPECIFICITY: FOUND IN KIDNEY, BUT NOT IN BRAIN, LUNG,
 CC LIVER, HEART, SKELETAL MUSCLE, OR PLECENTA.
 CC -I- DISEASE: DEFECTS IN CASR ARE A CAUSE OF FAMILIAL HYPOCALCAEMIC
 CC HYPERCALCAEMIA (FHH) AND NEONATAL SEVERE HYPERPARATHYROIDISM
 CC (NSHPT), TWO INHERITED CONDITIONS CHARACTERIZED BY ALTERED CALCIUM
 CC HOMEOSTASIS. THE MUTATIONS REDUCE THE ACTIVITY OF THE RECEPTOR.
 CC FHH AFFECTED INDIVIDUALS EXHIBIT MILD OR MODEST HYPERCALCAEMIA,
 CC RELATIVE HYPOCALCAEMIA, AND INAPPROPRIATELY NORMAL PTH LEVELS. IN
 CC CONTRAST, NSHPT IS A RARE AUTOSOMAL RECESSIVE LIFE-THREATENING
 CC DISORDER CHARACTERIZED BY VERY HIGH SERUM CALCIUM CONCENTRATIONS,
 CC SKELETAL DEMINERALIZATION, AND PARATHYROID HYPERPLASIA. IN SOME
 CC INSTANCES NSHPT HAS BEEN DEMONSTRATED TO BE THE HOMOZYGOUS FORM OF
 CC FHH.
 CC -I- DISEASE: DEFECTS IN CASR ARE ALSO THE CAUSE OF AUTOSOMAL DOMINANT
 CC HYPOCALCAEMIA (ADH) IN WHICH THE RECEPTOR IS ACTIVATED AT SUBNORMAL
 CC CA(2+) LEVELS.
 CC -I- DISEASE: DEFECTS IN PCAR1 ARE ALSO THE CAUSE OF AUTOSOMAL DOMINANT
 CC HYPOPARATHYROIDISM (ADHP). ADHP IS CHARACTERIZED BY HYPOCALCAEMIA
 CC AND HYPERPHOSPHATEMIA DUE TO INADEQUATE SECRETION OF PARATHYROID

CC HORMONE. SYMPTOMS ARE SEIZURES, TETANY AND CRAMPS.
 CC -I- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC DR EMBL: U20759; AAA86503.1; -
 CC DR EMBL: U20760; AAA86504.1; -
 CC DR EMBL: D50855; BAA09453.1; -
 CC DR EMBL: S83176; AAB36873.1; -
 CC DR EMBL: S79217; AAB35262.1; -
 CC DR EMBL: S68032; AAB29413.1; -
 CC DR EMBL: S68033; AAB29414.1; -
 CC DR EMBL: S68036; AAB29415.1; -
 CC DR GCRDB: GCR_1337; -
 CC DR GCRDB: GCR_1874; -
 CC DR GCRDB: GCR_2012; -
 CC DR GCRDB: GCR_2013; -
 CC DR GCRDB: GCR_2596; -
 CC DR GCRDB: GCR_2597; -
 CC DR MIM: 601198; -
 CC DR MIM: 145980; -
 CC DR MIM: 601198; -
 CC DR PROSITE: PS00979; G-PROTEIN_RECEP_F3_1; 1.
 CC DR PROSITE: PS00980; G-PROTEIN_RECEP_F3_2; 1.
 CC DR PROSITE: PS00981; G-PROTEIN_RECEP_F3_3; 1.
 CC DR PFAM: PF00003; 7tm_3; 1.
 CC DR PFAM: PF01094; ANF_receptor; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 CC KW Disease mutation; Alternative splicing; Polymorphism.
 CC FT SIGNAL 1 19
 CC FT CHAIN 20 1078
 CC FT DOMAIN 20 612
 CC FT TRANSMEM 613 635
 CC FT DOMAIN 638 649
 CC FT TRANSMEM 650 670
 CC FT DOMAIN 671 681
 CC FT TRANSMEM 682 700
 CC FT DOMAIN 701 724
 CC FT TRANSMEM 725 745
 CC FT DOMAIN 746 769
 CC FT TRANSMEM 770 792
 CC FT DOMAIN 793 805
 CC FT TRANSMEM 806 828
 CC FT DOMAIN 829 836
 CC FT TRANSMEM 837 862
 CC FT DOMAIN 863 1078
 CC FT CARBOHYD 90 90
 CC FT CARBOHYD 130 130
 CC FT CARBOHYD 261 261
 CC FT CARBOHYD 287 287
 CC FT CARBOHYD 386 386
 CC FT CARBOHYD 400 400
 CC FT CARBOHYD 446 446
 CC FT CARBOHYD 468 468
 CC FT CARBOHYD 488 488
 CC FT CARBOHYD 541 541
 CC FT CARBOHYD 594 594
 CC FT CARBOHYD 536 536
 CC FT VARSPPLIC 39 39
 CC FT VARIANT 62 62
 CC FT VARIANT 66 66
 CC FT VARIANT 116 116
 CC FT VARIANT 116 116
 CC /FTID=VAR_003585.
 CC R -> M (IN MILD FHH AND NSHPT).
 CC /FTID=VAR_003586.
 CC R -> C (IN FHH).
 CC /FTID=VAR_003587.
 CC A -> T (IN ADHP).
 CC /FTID=VAR_003588.


```

FT DOMAIN 715 737 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 738 759 V (POTENTIAL).
FT DOMAIN 760 772 CYTOSOL (POTENTIAL).
FT TRANSSEM 773 795 VI (POTENTIAL).
FT DOMAIN 796 801 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 802 827 VII (POTENTIAL).
FT DOMAIN 828 1212 CYTOSOL (POTENTIAL).
FT CARBOHYD 88 88 POTENTIAL.
FT CARBOHYD 210 210 POTENTIAL.
FT CARBOHYD 378 378 POTENTIAL.
FT CARBOHYD 382 382 POTENTIAL.
FT CARBOHYD 445 445 POTENTIAL.
FT CARBOHYD 734 734 POTENTIAL.
FT VARSPLIC 877 908 MISSING (IN ISOFORM 5A).
SO SEQUENCE 1212 AA; 132468 MW; 1681574 CIRC32;

Query Match 12.9%; Score 819; DB 1; Length 1212;
Best Local Similarity 27.0%; Pred. No. 3,02e-133;
Matches 233; Conservative 229; Mismatches 334; Indels 68; Gaps 58;

Db 5 LILSVLLKEEDVRG-SAQSSEERYVAHMGDIIGALFVSHOP-TV-DKVERKCG-AV 60
QY 8 LILSVLLKEEDVRG-SAQSSEERYVAHMGDIIGALFVSHOP-TV-DKVERKCG-AV 67
Db 61 R-EQYIGQVEMLTHERINSDDLPLNITLGEIRDSCHMSAVALEBOSIEFIRDSLIS 119
QY 68 SFNGHYHLFOAMRTVEINNSTALPLNITLGEYLDVCSBS-NVY-AT-LR---VP 120
Db 120 SEEEGLVRCVDCSSSRSKKPIYGVYIGPSSSAIVQVOMLQNFIPQALYSTSMDL 179
QY 121 AQQGTGHE-MORDIRN-HSKK-VALLGPNTDHAVTALLSEFLMPLVSEASSVYL 177
Db 180 SDRLEFKFMVPSDAQAARAMDIVRYMYTVAHTGNGSEMEAFKMSAKES 239
QY 178 SGKRKPFELKTIKQVYVRLLOSFGVWVSLVSGIDQGLQVQALELATPRG 237
Db 240 ICLASHYKI-YSN-AGEOSFDKLKLTSHLPKARVACFCEGVTNGLMAMRLG-LA 296
QY 238 ICVAFKDVYPLSAQAGDPRQRMMLRLA-R-ARTVVVFSN-RLLAGVFRSVLANLT 294
Db 297 GEFLLGSDGA-DRYDT-DGYQ-REAVGGLTLQ-OSPDYKFFDYLLKRPETNRN 352
QY 295 GK-VWIAIEDMAISTYITNVPGIDQIGVLAIQORVPLKEEESYQAVMGAPRTC 353
Db 353 PMFQEFMQRHO-CRLGEPQENSKYKTKNSLTHTHODSGMGVINAISMAVGL 411
QY 354 P-BGSMGCTQOLCR-E-CHAFTWMPBELGAFSMAAY--N-V-Y-EAVYAVAHGL 401
Db 412 HNMOMSLCPGYAGLADAKPIDGRKLLSLMKYFTGVSGDITLEDENGSPGRYEIMNF 471
QY 402 HQI-LG-CT--SGTC-ANGPYVPMQLLIQYKVNFL-LHKRTVAFDDKGDPLGYDITAM 455
Db 472 KEMGRDY-FDIYNGSMWNGELKMDDEV-WSKSNIR-SYCSPECKGQIKYIRKEV 528
QY 456 DWNPBEMTFEYIGSASLSVPHLDIKTKIOWHGKNQVPSVCTREDCLEGHRVY-MGSH 514
Db 529 SCCMTCPCCKENRYE-DE-YTCRACQSGSWPTDITGCDLIPQYLKMGDPPIAAVVE 586
QY 515 HCEECPCPCENGTFLNSELHTCQPCGTEEMAPBESSKCFSTYVEFLW-H-EPISLVLL 572
Db 587 ACGLGLATLFV-TVFFIYR-DTPVAKSSRELCTYIIGLGLYCH-FCLLAKPROIY 643
QY 573 AANLGLLGLTGLAGLFWMLRHTPVRSAGRLCFMLGSLVAGS-CLSYFFGFPYPA 631
Db 644 CYLORIGIGLSPAMSYSLVTKTNIAIILGSKKIKTKKPRFMSACQALVIAFILICI 703
QY 632 CLNQPLFSLGFAFLFSLTIRSFQLYIIFKSTR-VPTFHTVAQNAGAGIFVYSTV 690
Db 704 QLGIIIVAFIEPDDIMDYDSIRE-VYLICNTN-LGVNPIGVNGLIISCFE-YAFK 760
QY 651 HFLCLTLMAMTRPREIREYRFPPLVLECTEVNSVGLVAFAFANILLIS-IFVCSYL 749
Db 761 TRNPANENKAKYIAFTWYTCIIMLAF--VP-IFYGSNYKIITWCFVS-LSATVALGC 816

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QY 750 GKELPENYNEAKVCTFSLHFWSWIAFTMSIYQGSYIPAVVLAGLATLSGGSF-GY 808
Db 817 MEVPKVIILLAKPRNRYSAFTS 840
QY 809 -FLPKCYVILLCPRLNTEHFOAS 831

RESULT 5
ID MGR5-RAT STANDARD; PRT; 1203 AA.
AC P31424;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.
GN GRM5 OR MGLR5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RX MEDLINE; 92317054.
RA ABE T., SUGIHARA H., NAWA H., SHIGEMOTO R., MIZUNO N., NAKANISHI S.;
RT "Molecular characterization of a novel metabotropic glutamate
RT receptor mglur5 coupled to inositol phosphate/Ca2+ signal
RT transduction."
RL J. Biol. Chem. 267:13361-13368(1992).
RN [2]
RP SEQUENCE OF 859-923 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE-BRAIN.
RX MEDLINE; 93343913.
RA NAKAMAKI R., KATSUKI F., SUGIYAMA H.;
RT "A variant of metabotropic glutamate receptor subtype 5: an
RT evolutionally conserved insertion with no termination codon."
RL Biochem. Biophys. Res. Commun. 194:622-627(1993).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
CC CHLORIDE CURRENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS; 5A (SHOWN HERE) AND 5B; ARE
CC PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF
CC 32 RESIDUES.
CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN NEURONAL CELLS OF THE
CC CENTRAL NERVOUS SYSTEM.
CC -1- MISCELLANEOUS: ACTIVATED BY GLUTAMATE > GLUTAMATE > IBOTENATE >
CC TRANS-1- AMINOCYCLOPENTYL-1,3-DICARBOXYLATE.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR1.
CC *****
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CC *****
DR EMBL; D10891; -; NOT_ANNOTATED_CDS.
DR EMBL; S64315; AAB27666.1; -.
DR PIR; A42916; A42916.
DR GCRDB; GCR 0444; -.
DR GCRDB; GCR 0760; -.
DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
DR PFAM; PF00003; 7tm_3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Alternative splicing.
FT SIGNAL 1
FT CHAIN 21 1203 METABOTROPIC GLUTAMATE RECEPTOR 5.

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578 22 578 12.8% Score 814; DB 1; Length 1203;
FT DOMAIN 579 601 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 579 601 I (POTENTIAL).
FT DOMAIN 602 615 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 616 636 II (POTENTIAL).
FT DOMAIN 637 647 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 648 666 III (POTENTIAL).
FT DOMAIN 667 692 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 693 713 IV (POTENTIAL).
FT DOMAIN 714 736 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 737 758 V (POTENTIAL).
FT DOMAIN 759 771 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 772 794 VI (POTENTIAL).
FT DOMAIN 795 800 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 801 826 VII (POTENTIAL).
FT DOMAIN 827 1203 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 88 88 POTENTIAL.
FT CARBOHYD 209 209 POTENTIAL.
FT CARBOHYD 377 377 POTENTIAL.
FT CARBOHYD 381 381 POTENTIAL.
FT CARBOHYD 444 444 POTENTIAL.
FT CARBOHYD 733 733 POTENTIAL.
FT VARSELC 876 907 MISSING (IN ISOCFORM 5A).
SQ SEQUENCE 1203 AA; 131885 MW; 2955EA33 CRC32;
```

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Query Match 12.8% Score 814; DB 1; Length 1203;
Best local similarity 27.1% Pred. No. 4,52e-152;
Matches 234; Conservative 222; Mismatches 340; Indels 67; Gaps 60;
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5 LITSLVLLKEDVNG-SAQSERRVVAHMPGDIIGALFSVNHQ-TV-DKHERKCG-AV 60
8 LLTSLQLAVAVCWAFSCORTSSPGSLPDGFLAGFLSHADCLQVRRHPLVTSQRSD 67
61 R-DGYQIQVREAMHLHLERINSDPILPTTIGCELRDSQWHSNAVALEQIEIRSLIS 119
68 SFGHGHTLHFOARRFTVEELNNSTALPNTLLDLYELDYCESSESNVA-TLR-VPAQ-Q 124
120 SEEEGLVRCVDSSEFSRKKPIVGIYGPSSVAIOVNTLQLFNPQIAYSATSDLS 179
125 TGHLE-MQR--D-LRN-HSK--VVALIGPNTDHAVTALLSPFLMPLVSYASSVILS 178
180 DKLFYFPMRVPSDAQARAWDIYKRYWTVYSAVHEGNGESGMEAFKMSAKEGI 239
179 GKRFPSFIRLTIPSDKYQVEVIVRLQSEFGWVIVSLVSGYDQGLQVLALELAPRGI 238
240 CIAHSKXI-YSN-AGEOSRDKLLKLRSHPRKRVVACPEEGTIVGLMAMRLG-LAG 296
239 CVAFKQVPLSAQAGPRMQRMLRL-AR-ARTVVVFSN-RHLGVEFRSVLANLTG 295
297 EFLLGSDGMA-DRYDVT-DGYQ-REAVGIIITKL-QSPDKKFPDDYKLRPETNLNP 352
296 K-VWASEDMALSTYITNTPGLOGITGLVALQOQOVPELKEFEESYQAVNGAP-RTG 353
353 WFOEFMOHRFQ-CLEGEFAOENSKYKTCNSLTFLTHVYODSKMGFVINAISYAGLH 411
354 -DEGSMCGTNOQLR-E--CHAFTTMNPDELGAFSMSAAV--N-Y-Y-EAVVAVHGLH 402
412 NMQMSLCPEYAGICDAMKPRIDGKLLDSLKTFTGVSGMILFPDENGSPGKYEINERK 471
403 QL-LG-CT--SGTC-ARGPYPMQLLOQITKYVFL-LHKRTVAFDQDGLGYDRIIAMD 456
472 EMGKDY-PDYINNGSWDNGELKMDDEV-MSKKNIIIR-SVCESEPEKGOIKYIRGEVS 528
457 WNPPEMTFEVIGASLSPYHLINKTKIQMHGKNNOVPVSVCTRDCLGHRILY-MGSHH 515
529 CCWCTCPCKENEYVF-DE-YTCAACOLGSWPTDGLGCDLIPVOYLRMGSDPIAAVFA 586
516 CCEPCAPCEAGTFLNTSELTCOPCGTEEWAPEGSSACEFRIVEFLGW-H-EPISLVLLA 573
587 CGLGLATLEV-YIIFIIR-DTPVWSSSRELCTYIILAGICGLYLT-PELLAKPKQIYC 643
574 ANTLGLLGLTGLFLAWRLHTPVRSAGRGFLWLGSLVAGS-OSLVSFEKRPVPAC 632
644 YIORIGISLSPMSYSALVTKTNRIRIILAGSKKIKCTKPRMSACQAVIAFIICIQ 703
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633 LIRQPLFSIGFALFSLCLIRSRQGLVIRKFSRK-VPTRYHTWAQNHAGIPIVASTH 691
704 LGITVALFMEPPDINHDPISIRE-VYLCNTN-IGVTPPLGYNLLISCTF-YAFRT 760
692 LFLCITLWAMPRPRYQRPFLVILLECTEYNSVGFLVAFNHLISLS-TFVCSYIG 750
761 RNVPANFNKAYIAFMYTTCIIMLAF--VP--IYGSNNKIITMCRFSV-TSATVLSGM 816
751 KSLPENYENKCVTFSLLEHVSIMAFFTWSSITQSYIPAVNVLAGLATLSGGS-GY- 808
817 EVPKYVYIILAKPERNRSATFTS 839
809 FLKPCVYILCRPLNTEHFQAS 831

RESULT 6
ID MGR1_RAT STANDARD; PRT: 1199 AA.
AC P23385;
DT 01-NOV-1991 (rel. 20, last sequence update)
DT 01-NOV-1991 (rel. 20, last sequence update)
DE 15-DEC-1999 (rel. 39, last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 1 PRECURSOR.
GN GRM1 OR MGLUR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE: 91156047.
RA MASU M., TANABE Y., TSUCHIDA K., SHIGEMOTO R., NAKANISHI S.;
RT "Sequence and expression of a metabotropic glutamate receptor.";
RL Nature 349:760-765(1991).
RN [2]
RP SEQUENCE FROM N.A.
RP TISSUE=BRAIN;
RX MEDLINE: 92022526.
RA HOUAMED K.M., KUIJPER J.L., GILBERT T.L., HALDEMAN B.A., O'HARA P.J.,
RA MULLVHILL E.R., ALMERS W., HAGEN F.S.;
RT "Cloning, expression, and gene structure of a G protein-coupled
RT glutamate receptor from rat brain.";
RL Science 252:1318-1321(1991).
RN [3]
RP ALTERNATIVE SPLICING (1B).
RC TISSUE=BRAIN;
RX MEDLINE: 92110002.
RA TANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;
RT "A family of metabotropic glutamate receptors.";
RL Neuron 8:169-179(1992).
RN [4]
RP ALTERNATIVE SPLICING (1C).
RC TISSUE=BRAIN;
RX MEDLINE: 93066232.
RA PIN J.-P., MABER C., PREZEAU L., BOCKAERT J., HEINEMANN S.F.;
RT "Alternative splicing generates metabotropic glutamate receptors
RT inducing different patterns of calcium release in Xenopus oocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10331-10335(1992).
CC - FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CC CATIONIC SECOND MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL
CC ACTION OF GLUTAMATE IN THE CNS, SUCH AS LONG-TERM POTENTIATION IN
CC THE HIPPOCAMPUS AND LONG-TERM DEPRESSION IN THE CEREBELLUM.
CC SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC - ALTERNATIVE PRODUCTS: THREE ISOFORMS, 1A (SHOWN HERE), 1B AND 1C;
CC ARE PRODUCED BY ALTERNATIVE SPLICING. 1B AND 1C ARE C-TERMINALLY
CC TRUNCATED FORMS OF 1A.
CC - TISSUE SPECIFICITY: IS PREDOMINANTLY EXPRESSED IN CEREBELLAR
CC PURKINJE CELLS, CA2-CA3 PYRAMIDAL CELLS OF THE HIPPOCAMPUS, AND
CC MITRAL AND TUFTED CELLS OF THE OLFACTORY BULB.
CC TRANS-1- AMINOCYCLOPENTYL-L-3-DICARBOXYLATE; INHIBITED BY
CC 2-AMINO- 3-PHOSPHONOPROPIONATE.
```


CC - FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.
 CC MAY MEDIATES SUPPRESSION OF NEUROTRANSMISSION OR MAY BE INVOLVED IN
 CC SYNAPTOGENESIS OR SYNAPTIC STABILIZATION.
 CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC - TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS AND PROMINENT
 CC PARTICULAR NEURONAL CELLS IN OTHER BRAIN REGIONS.
 CC - SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST, TO MGUR3.
 CC -----
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 CC or send an email to license@sdb.ch).
 CC -----
 CC EMBL: M92075; NOT_ANNOTATED_CDS.
 CC PIR: JH0561; JH0561.
 CC GCRDB: GCR_0361; --
 CC HSP: P06612; IECL.
 CC GCRDB: GCR_0361; --
 CC PROSITE: PS00879; G_PROTEIN_RECP_F3_1; 1.
 CC PROSITE: PS00880; G_PROTEIN_RECP_F3_2; 1.
 CC PROSITE: PS00981; G_PROTEIN_RECP_F3_3; 1.
 CC PFAM: PF00003; 7tm_3; 1.
 CC PFAM: PF01094; ANF_receptor; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 CC Multigene family.
 CC SIGNAL 1 18
 CC CHAIN 1 872
 CC FT DOMAIN 19 872 METABOTROPIC GLUTAMATE RECEPTOR 2.
 CC FT TRANSMEM 567 567 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 568 590 I (POTENTIAL).
 CC FT TRANSMEM 591 604 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 605 625 II (POTENTIAL).
 CC FT TRANSMEM 636 636 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 637 655 III (POTENTIAL).
 CC FT TRANSMEM 656 679 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 701 725 IV (POTENTIAL).
 CC FT TRANSMEM 726 747 V (POTENTIAL).
 CC FT TRANSMEM 748 760 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 761 783 VI (POTENTIAL).
 CC FT TRANSMEM 784 793 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 820 872 VII (POTENTIAL).
 CC FT TRANSMEM 820 872 CYTOPLASMIC (POTENTIAL).
 CC FT CARBOHYD 203 203 POTENTIAL.
 CC FT CARBOHYD 286 286 POTENTIAL.
 CC FT CARBOHYD 338 338 POTENTIAL.
 CC FT CARBOHYD 402 402 POTENTIAL.
 CC FT CARBOHYD 547 547 POTENTIAL.
 CC SEQUENCE 872 AA; 95773 MW; C3C3467E CRC32;
 CC -----
 CC Query Match 12.18; Score 769; DB 1; Length 872;
 CC Best Local Similarity 25.48; Pred. No. 1,60e-141;
 CC Matches 210; Conservative 218; Mismatches 343; Indels 56; Gaps 43;
 CC -----
 CC Db 26 LTLGGVGVGGFPPV---O-KGGP-AEECGVNE-H-RGIRLRLAMFALDIRNDRH 77
 CC 33 FSLPGDFLGLGFLSLADCLQVNRPLVTSCHSDSDFNGHYLFLPAMRFTVEINNSTA 92
 CC 78 LPLGVRLGAHILDCSKDTHALEQALDFVRASLSRGADGSRHICPDGSYATSDAPTAVT 137
 CC 93 LPLNITLGLVELDYCESSESNVYA-TL--RVPAQGT-G-HL-EMQMDLRHSSKVYA 143
 CC 138 GYIGGSYSVSQVAVNLALFQIPQISYSTAKLSDKSRIDYFAFTVPPDFQAAAMAE 197
 CC 144 -LIGPDNTHAATLALSLPFLMPLVSYEASVYLSGKRFPSFELTITPSDKQVAVIR 202
 CC 198 ILRFNFWTVSTVASGDGGETIGAEFLAARARNCVATSEKVGSRAMAAEGVVRAL 257
 CC 203 LLSFGVWVWISLVGSGIDGGLGVQLLEELAPRGICVAFKDVVPVLS-AQAGDPFRMRM 261

Db 258 LOKPSAR--VAALFTRSEDARELLAATORLN-ASEFTWASDGMALGESVASERAAEGA 314
 Qy 262 LKLARARTVVVVFENRNLHAGVFERSVYLANLGTWVLAISEDMAISTITNPQIGIGT 321
 Db 315 I-TITLASFIDSPDSIOSLDPMNNSRNPFRERWERFHCFSQO--RQCAHSLRAVP 371
 Qy 322 VLGVAIQOQVQVGLKEFESESYQ-AVMGAP--RTCPESGS-CGTQQLRECAFTTMMNP 377
 Db 372 FQESKIMFVNAVYAMAHAL-HNMHRAL-CGNTHLGDAMPVGRRLYKDFVNLNVED 429
 Qy 378 -ELGAFNSAAVNYEAYAVAHGLHOLIGTSGT--C-ARQPVTPWOLLOO-ITKAVF- 431
 Db 430 APEFPADTDEVERFRFGDIGNYNIFFYLRAAGSR-YR-YOKVYMAEGTLIDTSFIPW 487
 Qy 432 L-LHK-KT---VAFDQKGPGLGYDILAMDWGPMTVEIGSASLSVHDIINKTKIOW 486
 Db 488 ASPSAQPLPASCSEPCLONEYKSVQPEVCCWLCIPQPPRY-RLDER-TCADCGLGIV 545
 Qy 487 HG-KNNQVPVSVCTRDCLGHHRLVWGSNHCCECPCEAGFELNTSELHCQPCGTREW 545
 Db 546 PNASLTGCELPQEXIRMGDAMAVGPVITACIGALATLFFVGFVRNATPVYKASREL 605
 Qy 546 APEGSAGCSRTVEFLGMHEPISVLALANTLLLLIGTGLFAMRLHTPVARSAGRL 605
 Db 606 CYLLGVEFLCYCMTFVFIAPKSTAVCTLRGLGTAESVCYALLTKTNRIARIFG-GA 664
 Qy 606 CFLMGSLVAGSCSLYFSGKPTVPACLLRPLFSLGAIFLSCLTINSFQVILFKFST 665
 Db 665 REGA-QRPFFISPAQVAICLALISGOLLIVAAVLVEAPGKGTAEAREVVTLRCH 723
 Qy 666 KVPTEHYTHMAQNHGAGIVYVS-STVHLFLCLTWLMTPREPREYORPPH-LVTLCTE 723
 Db 724 RDA-SMLGSLAVNVLIALCTL-YAFKTRKCPENENKKEFGFTWYTCIILAPLPIFY 781
 Qy 724 VNSVGFVLAFAFNILL-STSTVCSYLKELPENNEAKCVTFSLILFVSAITAFIWS 782
 Db 782 VNSDVRQVTTMCVSVLSIGSVLGCLEFAPRLHILFQPOKNNVSH 828
 Qy 783 IYQGSYLPVAVNVLACLATLSSGFS-GY-FLPRCYVILRPELINTNEH 827
 CC -----
 CC RESULT 11
 CC ID MGR3_HUMAN STANDARD: PRT; 877 AA.
 CC AC Q14832;
 CC DT 01-NOV-1997 (Rel. 35, Created)
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
 CC DT 01-NOV-1997 (Rel. 35, Last annotation update)
 CC DE METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR.
 CC GN GRM3 OR MGUR3.
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE-BRAIN;
 CC RX MEDLINE; 96437205.
 CC RA MAROFF A., VOLPE F., LETCHUK R., HARRINGTON K., EXSON P.;
 CC FT "Molecular characterization and localization of human metabotropic
 CC glutamate receptor type 3.";
 CC RL Brain Res. Mol. Brain Res. 40:55-63(1996).
 CC CC - FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
 CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
 CC ACTIVITY.
 CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC - SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST, TO MGUR3.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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CC -----

DR EMBL: X77748: CA54796.1: -

DR GCRDB: GCR_2070: -

DR MIM: 60115: -

DR PROSITE: PS00979: G-PROTEIN_RECEP_F3_1: 1.

DR PROSITE: PS00980: G-PROTEIN_RECEP_F3_2: 1.

DR PROSITE: PS00981: G-PROTEIN_RECEP_F3_3: 1.

DR PRAM: PF00003: 7tm_3: 1.

DR PRAM: PF01094: ANF_receptor: 1.

DR G-protein coupled receptor: Transmembrane; Glycoprotein; signal;

KW Multigene family.

FT SIGNAL 1 20

FT CHAIN 1 877

FT DOMAIN 21 574

FT TRANSSEM 575 597

FT TRANSSEM 598 611

FT TRANSSEM 612 632

FT TRANSSEM 633 643

FT TRANSSEM 644 662

FT TRANSSEM 663 686

FT TRANSSEM 687 707

FT TRANSSEM 708 732

FT TRANSSEM 733 754

FT TRANSSEM 755 767

FT TRANSSEM 768 790

FT TRANSSEM 791 800

FT TRANSSEM 801 825

FT TRANSSEM 827 877

FT CARBOHYD 207 207

FT CARBOHYD 290 290

FT CARBOHYD 412 412

FT CARBOHYD 437 437

FT SEQUENCE 877 AA: 98619 MW: 8504655 CRC32:

Query Match 12.0%; Score 764; DB 1; Length 877;

Best Local Similarity 25.9%; Pred. No. 2,36e-140;

Matches 207; Conservative 203; Mismatches 338; Indels 50; Gaps 44;

Db 55 CGRINE-D-RGICRLEMLFAIDKDYLLPGVKLGVLHLDTCSDRTALEDSLEFVR 112

QY 63 CDRSDSFGNGHYHLQAMRFVEEINNSTALLPNTILGEYELDYCS-ESSNVATLR-VP 120

Db 113 ASLTKVDAEVMCPDGYAIOENIPLLIAGYIGSSVSIOVANNLLRPIQDISVAST 172

QY 121 AQOQT-GHLE-M-Q-R-DLRNHSKVVA-LIGPDNTDHAHTAALLSPFLMPLVSEAS 173

Db 173 SAKLSKSRDYFARTVPPEFYQAKAAEILRFNMTYVSTVASEGDYGETGEAEFEQEA 232

QY 174 SVLSGKRKPPSEFLRTIPSDKYVEIVRLQSGWVWISLVSGYDQGLQGALEELA 233

Db 233 RLNRICATAEKVGSRNRSYSYVIRELLOKPNAR--VVLEKRSDDSRLLAASRAN 290

QY 234 TPRICAFADYVPLSA-QADDPROMRMLARARITVVVVFENRHLAGVFERSVVLAN 292

Db 291 -ASFTWASGWMGQESLIGSEHVAIGAILLELASQVRFQDFDYFQSLNNHNRNPF 349

QY 293 LTGKVMIASEDMASTIITNPGIIGITV-LGYALDQ-RQVPGKFEESYVOAVNGAP 350

Db 350 RDEWQKFOCSLQNR-RNHRVCDKHLAIDSSNYEOKSIFVNVAYAMAHALHKMQRT 408

QY 351 RTEGEGSW-CGTNOLCRCHAFITWNNP-ELGAFSMAAAY-VYEAVYAAVHGHQLL-G 406

Db 409 LCPPTTLCKAMKLLDCKKLYDLKINFTAPNPKNKADSIYKEDTFGDGKRYNEN 468

QY 407 -CTSGT--C-A-R---CP-YYPMLLOQIYKVNFLHKKT--VA-FDQKGPDLGYDIIA 454

Db 469 FQNVGKYSYLVKVGHMA-ETLSLDVN-S-IHM-SRNS-VPIRSDSCDCAPEKMNMGPD 523

QY 455 WDMNGPMTVEIVISASLSPYHLDINKTKIOWHKKNOVPVSVCTRDLSGHRLVNGSH 514

Db 524 VCCMICIPCEPEYVL-ADEF-TCMDGSGGOWPTADLTGCYDLPEDYIRWEDMAIGPTI 581

QY 515 HCCECHPCCEAGFTLNTSELTCQPCGTIEWAPGSSACFSRTVEFLGWHEPILVELAA 574

Db 582 ACLEFNCCTAMVYVFTHANNTPYKASGRELCYLLGVGLSYMTFFFAKPSPVICAL 641

QY 575 NTLILLIGTAGFAMRLHPVRSAGRGFLCMLSLVAGSCSLYSFFGKPTVPACL 634

Db 642 RRLGSSFAICYAALLTKNCIARIFD-GVKNAGACGCKET-SPSSOVFICLGLILVOIV 699

QY 635 RQPLPSGLFALFLSCLTRISQVLIHFKSEKVPTEHYEWAQNGAGIEIVVST-VHLP 693

Db 700 MYSVWILLEAP-GTRRYTLAEKRETVILKC-NVADSSYLSTIYDVLIVILCYAAKTR 757

QY 694 LCLVWLMWMPRTREXQRP-H-LVILECEVNSCEELVAFANILLISTIFVCSYLGK 751

Db 758 KCPENEAEAFISTMTTCIWLAFPIRYVSSDRVCTTMCISVLSGFEVLCCLP 817

QY 752 ELPENYEAKCVTSLLHFEVSWIAFTMSIYOGSVLPVAVNLAGIATLSGGFS-GY-F 809

Db 818 APKVHILFOPKRVYTH 835

QY 810 LPKCYILCPRELNTEH 827

RESULT 12

ID MGR2.HUMAN STANDARD; PRT; 872 AA.

AC 014415:

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-DEC-1999 (Rel. 39, Last annotation update)

DE METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR.

GN GRM2 OR GLUR2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homnidae; Homo.

RP [1]

RN SEQUENCE FROM N.A.

RX MEDLINE: 95346007.

RA FLOR P.J., LINDAUER K., PUTNER I., RUEGG D., LUKIC S., KNOPEL T., KOHN R.;

RT "Molecular cloning, functional expression and pharmacological characterization of the human metabotropic glutamate receptor type 2.";

RL Eur. J. Neurosci. 7:622-629(1995).

CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLYLATE CYCLASE ACTIVITY.

CC MAY MEDIATE SUPPRESSION OF NEUROTRANSMISSION OR MAY BE INVOLVED IN SYNAPTONEGENESIS OR SYNAPTIC STABILIZATION.

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT REGIONS OF THE ADULT BRAIN AS WELL AS IN FETAL BRAIN.

CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS. STRONGEST, TO GLUR3.

CC -----

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CC -----

DR EMBL: L35318: AAA76855.1: -

DR GCRDB: GCR_1846: -

DR MIM: 604099: -

DR PROSITE: PS00979: G-PROTEIN_RECEP_F3_1: 1.

DR PROSITE: PS00980: G-PROTEIN_RECEP_F3_2: 1.

DR PROSITE: PS00981: G-PROTEIN_RECEP_F3_3: 1.

DR PRAM: PF00003: 7tm_3: 1.

DR PRAM: PF01094: ANF_receptor: 1.

DR G-protein coupled receptor: Transmembrane; Glycoprotein; signal;

KW Multigene family.

FT SIGNAL 1 18

FT POTENTIAL.


```

FT DOMAIN 757 769 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 770 792 VI (POTENTIAL).
FT DOMAIN 793 802 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 803 828 VII (POTENTIAL).
FT DOMAIN 829 879 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 209 209 POTENTIAL.
FT CARBOHYD 292 292 POTENTIAL.
FT CARBOHYD 414 414 POTENTIAL.
FT CARBOHYD 439 439 POTENTIAL.
SQ SEQUENCE 879 AA: 98959 MW: 0283AE8B CRC32:

Query Match 11.9%: Score 759; DB 1; Length 879;
Best Local Similarity 25.8%; Pred. No. 3,48e-139;
Matches 206; Conservative 202; Mismatches 340; Indels 50; Gaps 44;

Db 57 CGRNE-D-RGIORLEMLAIDINKNDNLLPGVKIGVHLDPGCSDDTYALEQSLFEVR 114
63 CDRDSFGNGHYLFLFOAMRFTVEINNSTALLPNTITLGYELYDVS-ESSNVAATLR-VP 120
115 ASLTKYDEAYMCPDGSYAIQENIPLLIAGVIGSSYSIOVANLRLFOIPQISYAST 174
121 AOGST-GHLE-M-Q-R-DLRNHSKYVA-LIGPDNDHATVTTALLSPFLPLVSTEAS 173
175 SAKLSKRYDYFARIVPDPFYQAKAAEILRFENMTYVSTVASEGDYGETGIEAFPOEA 234
174 SVLLSGKRKFPSEFLRTIPSDKYQEVIVRLQSGWVWISLVGSDYGDYGOGLQALELA 233
235 RLNRICLATEKYGKRSNIRKSYDSVITELLQKPNAR--VVYLFMRSDSKRELLIAANRVN 292
234 TPRICIAKEDVYPLSA-QAGDPRMOXMLRLAKARTVVVYVFSNRHLAGYFFRSVYLAN 292
293 -ASFTWASDGMGMOESIVGSEHVAYGATLLELASHPRVDFRFOSLPNYNNHRPW 351
293 LTGKVMIASDWMALSTIITVPQIGIGIV-LGVAIQ-QVPGCLKFEESYVOAVNGAP 350
352 RDFEQRFOGSLONK-RNHRVOCDKLALIDSNEYDESKIMFVNAVAYAMAHAKKQRT 410
351 RCPREGSM-CGTNOLCRECHAFITMNP-ELGAFMSAAVN-VYEAVYVAHGHQLL-G 406
411 LCRNTTLCQAMKILDSKIKYELKINFTAPNPKKGDSYKFTPDGDKGRVAVFN 470
407 -CISGT-C-A-R--GP-YPMOLLQOIYKNVFLHR-KTYA-FDDKGDPLGYDIIA 454
471 LQOTGKYSYLYKVGWMA-ETLSLDVD-S-IHM-SRNS-VPTSOCSDCAENKKNMOPGD 525
455 WDMNGPMTREVIGSASLSVHLDINKTIQMHKKNQOVVSVCTRCLDGHRLVWGS 514
526 VCCMICIPCEPEYEL-VDEF-TCMDCGPGQPTADLSGCYNLEPDYIKMDAMAGPVI 583
515 HCFECMPCEAGTFLNTSELHTCOPGTEEMAPEGSACSRTVEFLGWHPEPISLVLLAA 574
584 ACGLFCLTCIVITVFINHNTPLVKASGRELCTYLLFGVSLSCMTFFFAKSPVICAL 643
575 NTLLELLITAGFAWRLLTPVVRSGRGLCELMGLSIVAGSGLSLEPCKPTVPACL 634
644 RRLGLGTFPAICYSALTTKNCIARIPD-GVKNQAQRKPI-SPSSOVFCLGLIIVQIV 701
635 KQPLFSIGFAIFLSCLTIRSFOLVITFKSTKPTPIHTAQNQGAIFIVYST-VHLE 693
702 MVSVAWILEP-STRATLEKRETVILKC-NKDSMSLSLYDVVLLCTVYAKTR 759
694 ICLTILAMTPRPTREVO-RFPH-LVILECTEVNSVGFVAFAANILLISTFVCSYLGK 751
760 KCEENFEAKFIPTWTTTIIILAPLPIFYVSSDQVRVOTTCMIGVSLSGFVGLCLF 819
752 ELDPENNEACVFLSLHLFVSWIAFTMSIYQGSYLPVAVNVLAGLALGSGFS-GY-F 809
820 APKVHILFQPKNVYTH 837
810 LPRCYVILCRPELNTNTH 827

```

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ID MGR6_HUMAN STANDARD: PRT; 877 AA.
AC 015303;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.
GN GRM6 OR MGLUR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97358610.
RA HASHIMOTO T., INAWA Y., OKAMOTO N., TAGAWA Y., BESSHO Y., HONDA Y.,
RA NAKAHISHI S.;
RT "The whole nucleotide sequence and chromosomal localisation of the
RT gene for human metabotropic glutamate receptor subtype 6."
RL Eur. J. Neurosci. 9:1226-1235(1997).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR4.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EXBL: 082083; AAB82058.1; -.
CC
DR GCRDB: GCR_2607; -.
DR MIM: 604096; -.
DR PROSITE: PS00979; G_PROTEIN_RECP_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_RECP_F3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_RECP_F3_3; 1.
DR PFAM: PF00003; 7tm_3; 1.
DR PFAM: PF01094; ANF_receptor; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; signal;
KW Multigene family; Vision.
KW
FT CHAIN 1 24 POTENTIAL.
FT DOMAIN 25 877 METABOTROPIC GLUTAMATE RECEPTOR 6.
FT TRANSMEM 25 585 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 585 608 I (POTENTIAL).
FT DOMAIN 609 622 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 623 643 II (POTENTIAL).
FT TRANSMEM 644 654 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 655 673 III (POTENTIAL).
FT TRANSMEM 674 697 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 698 718 IV (POTENTIAL).
FT TRANSMEM 719 748 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 749 770 V (POTENTIAL).
FT TRANSMEM 771 783 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 784 806 VI (POTENTIAL).
FT TRANSMEM 807 819 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 820 845 VII (POTENTIAL).
FT TRANSMEM 846 877 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 296 296 POTENTIAL.
FT CARBOHYD 451 451 POTENTIAL.
FT CARBOHYD 479 479 POTENTIAL.
FT CARBOHYD 567 567 POTENTIAL.
SQ SEQUENCE 877 AA: 95436 MW: D5A6C038 CRC32:

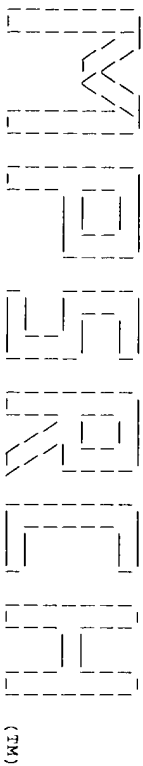
Query Match 11.6%: Score 741; DB 1; Length 877;
Best Local Similarity 25.3%; Pred. No. 5,56e-135;
Matches 204; Conservative 233; Mismatches 297; Indels 71; Gaps 57;

Db 64 QGVHLEAMLYALDRVNADELLPGVRLGARLIDTCSDDTYALEQALSFVQALIRGSDG 123
72 HGHYLFQAKRFTVEINNSTALLPNTITLGYELYDVS-ESSNVAATLR-VPAG-QGTGHL 128

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QY 242 FPDVVPLSAQAD-PRMORMLRLARATVVVVFESNRH-LAGVFFRSVYLANLTGK-VW 298
Db 306 IGSDSMG-SK-IAPVYQOEIAGAVTILPKRASIDGFEDEFRSRTLANNRRANVWFAEFS 363
QY 299 IASEDMAISTYITNPGIOGIGTVLGAIOQRO-VPGL-KEFEESTYQAVMGAPR-T-CP 354
Db 364 EGNFGCKSGSHGKRNSHIKKCTGLERIARDSYEOBGKVOFVIDAVYSMAVALHNHMKEL 423
QY 355 EGSW-C-GTNOCRECHAFT-T-WN-MPELGATSMGAAYN-VYEAIVAAVHGLHOLL-G- 406
Db 424 CPGYIGLCPRMWTIGKELIGYIRAVNENGAGTPTYENENGDPGRYDIFQYQINNKT 483
QY 407 CTS--GTGAR-GPVYPMQLOQIYKVNFLHKKT-VAFDCKGDPGLGYDIIAMDWNGPEW 462
Db 484 EYKIIIGHWT-NQHLKVED--MOMANREHTHPASVCSLPCKPGEKKTYKGVPCCKWCGR 540
QY 463 TFEVIGSASLSPVHLDINKTKIQMHGKNNQVPVSVCTROCLEGHRLVMGSHHCFCFCMP 522
Db 541 CEGYNY-QVDEL-SCELCPLDQRPINRTGCCORIPILKLEWSPMAVVPVLLAIIAT 598
QY 523 CEAGTFLNLTSELHTCOPCGTEEMAPEGSSACFSRTVEFLGMHEPISLVLLAANTLLLL 582
Db 599 TEVIYTFVRYNDTPIVRASGRELSYVLTGIFLCYSITFLMAAPDTIICSEFRIFLG 658
QY 583 IGTAGLFAMRLHPVYRSAGRLCFMLGLSVAGSCSLYSPFGKPTVPACLLRQPLFSLG 642
Db 659 MCFESYALLTKTRIRHIFEQCKSVTAKEFISPASOLVITFELIS--VOLGVEFWFV 716
QY 643 FALFELCLTIRSFOLVILIKFSIK-VPTFYHTWAQNHGAGIFVIVSSYVHLEFLCLTWLAM 701
Db 717 DPPHTIIDYGEORTLDPENARGYLK-DISDLSLISLGSYILAMVCTVYAIKTRGVP 775
QY 702 WMPRPRTREV--QR-F-P-HL-VILECTEVNSGVFLVAFANHILSLISTFVCSYLGEKLEP 755
Db 776 TENEAAPIGFTMYTTCIILWAFIPFIFGTAQSAEKMYIOTTTIVSMS--LSASVSLGMLY 834
QY 756 NYNEACVTFSLHLHFWSWIAFTMS-SIYQGS--YLPVAVNLAGLATLSGGFS-G-YF 809
Db 835 MPKVYIIFHPPEON 848
QY 810 LPRCYVILCRPELN 823

Search completed: Fri Mar 17 13:17:59 2000
Job time : 101 secs.



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MSearch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Mar 17 13:15:12 2000; Maspar time 35.30 Seconds
955.673 Million cell updates/sec
Tabular output not generated.

Title: >US-09-361-652-2
Description: (1-842) from US09361652.pep
Perfect score: 6366
Sequence: 1 MLFWAHLHLSTQLAVAYCW.....NTEHFOASIDYTRRCGTT 842

Scoring table: PAM 150
Gap 11
Searched: 122810 seqs, 40068593 residues
Post-processing: Minimum Match 08
Listing first 45 summaries

Database: p1r62
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 52.559; Variance 107.285; scale 0.490

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1316	20.7	1085	2	S40476	Ca(2+)-sensing recept	6.36e-231
2	1296	20.4	1078	2	S49341	calcium-sensing recep	7.84e-227
3	1293	20.3	1078	2	A56715	calcium receptor (clo	3.22e-225
4	1282	20.1	1079	2	I59362	calcium/polyvalent ca	5.70e-224
5	1201	18.9	1088	2	B56715	calcium receptor (clo	1.95e-207
6	819	12.9	1213	2	JC2132	metabotropic glutamat	2.87e-130
7	819	12.9	1212	2	JC2131	metabotropic glutamat	2.86e-129
8	814	12.8	1171	2	A42916	metabotropic glutamat	2.86e-129
9	810	12.7	1199	2	A41939	G protein-coupled glu	1.80e-128
10	799	12.5	912	2	JH0563	metabotropic glutamat	2.81e-126
11	798	12.5	912	2	I58149	metabotropic glutamat	4.45e-116
12	797	12.5	1218	2	S71376	glutamate receptor ho	7.04e-136
13	769	12.1	872	2	JH0561	metabotropic glutamat	2.64e-120
14	759	11.9	879	2	JH0562	metabotropic glutamat	2.56e-118
15	740	11.6	908	2	I49142	metabotropic glutamat	1.51e-114
16	730	11.5	915	2	A49874	metabotropic glutamat	1.45e-112
17	727	11.4	871	2	A46742	metabotropic glutamat	5.69e-112
18	241	3.8	958	2	T02741	probable ligand-gated	2.29e-20
19	186	2.9	938	2	T01809	hypothetical protein	2.05e-11
20	175	2.7	934	2	T02742	probable ligand-gated	1.02e-09
21	172	2.7	940	2	T02740	probable ligand-gated	2.90e-09
22	172	2.7	960	2	JE0356	gamma-aminobutyric ac	2.90e-09
23	171	2.7	1005	2	S33525	guanylate cyclase (EC	4.10e-09

24	151	2.4	962	2	C43274	N-methyl-D-aspartate	3.59e-06
25	154	2.4	1203	2	I53456	N-methyl-D-aspartate	1.33e-06
26	155	2.4	1239	2	I49705	glutamate receptor ch	9.54e-07
27	150	2.4	1230	2	945219	N-methyl-D-aspartate	4.98e-06
28	143	2.2	965	2	I51244	N-methyl-D-aspartate	4.82e-05
29	132	2.1	370	2	E70341	conserved hypothetical	1.52e-03
30	127	2.0	885	2	JN0339	N-methyl-D-aspartate	6.94e-03
31	127	2.0	901	2	JN0337	N-methyl-D-aspartate	6.94e-03
32	127	2.0	922	2	JN0338	N-methyl-D-aspartate	6.94e-03
33	127	2.0	938	2	S19710	N-methyl-D-aspartate	6.94e-03
34	125	2.0	938	2	S21104	N-methyl-D-aspartate	1.26e-02
35	125	2.0	1333	2	S27224	N-methyl-D-aspartate	1.26e-02
36	125	2.0	1333	2	I78557	N-methyl-D-aspartate	1.26e-02
37	125	2.0	1356	2	C45219	N-methyl-D-aspartate	1.26e-02
38	125	2.0	1464	2	S47555	N-methyl-D-aspartate	1.26e-02
39	124	1.9	885	2	A47551	N-methyl-D-aspartate	1.69e-02
40	124	1.9	938	2	A46612	N-methyl-D-aspartate	1.69e-02
41	121	1.9	986	1	OYURGA	speract receptor prec	4.08e-02
42	121	1.9	1125	1	OYURCP	speract receptor prec	4.08e-02
43	121	1.9	1464	2	S29159	glutamate receptor, N	4.08e-02
44	121	1.9	1464	2	A43274	N-methyl-D-aspartate	4.08e-02
45	124	1.9	2731	1	VFIRH	genome polypeptide 1b	1.69e-02

ALIGNMENTS

RESULT 1
ENTRY S40476 #type complete
TITLE Ca(2+)-sensing receptor - bovine
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999

ACCESSIONS S40476
REFERENCE S40476
#authors Brown, E.M.; Gamba, G.; Ricciardi, D.; Lombardi, M.; Butters, R.; Kitor, O.; Sun, A.; Hediger, M.A.; Lytton, J.; Hebert, S.C.
#journal Nature (1993) 366:575-580
#title Cloning and characterization of an extracellular Ca (2+)-sensing receptor from bovine parathyroid.
#cross-references M01D:94077182
#accession S40476
#status preliminary
#molecule_type mRNA
##residues 1-1085 ##label BRO

SUMMARY
Query Match Score 1316; DB 2; Length 1085;
Best local Similarity 31.9%; Pred. No. 6.36e-231;
Matches 272; Conservative 234; Mismatches 273; Indels 73; Gaps 51;

DB	31	GDIILGGLPPIHFG-VAYKQDJKSPESVCEIRYRFGFRMLQAKIFAIEINSSPAUL	89
QY	37	GFLLAGLFLSHADCLQVHRPLVTSQDSDS--FNGSHYHDFQAFRFEVEINNSTALL	94
DB	90	PNNITGGRIFEDCNVYSKRLLENTLSFAQNKIDSLNDFQNCSEHIEPTIYVAGTSG	149
QY	95	PNITLLELYDVCSSESSNY-ATLRVPAQGGTGLEMKR--DURNSSKVVVALIGDND	151
DB	150	ISTAVANLGLYPIPOVSVASSRSLSNKQCFSPFRTIPNDEHQATAADIIIEFRMWN	209
QY	152	HAVTTAALSLPLMLPVSVLEASSVLSGKRFPFLRTIPSKYQVEIVRLQSGWWM	211
DB	210	VGTIADDDYGRPGIKFEFEAEKSDICIDFSELLSQSYDE-E-KIQVVEVYKONSTAKV	267
QY	212	ISLVGSGYGDGLQVALBELATPRGICVAFKDVPLSLQAQADPPQVQKMLARARITV	271
DB	268	IYFSSGPEPLELI-KEIYRNRITGRWVASEAMWSSSIANPEVFNHVGCTGEGKMG	326
QY	272	VVVFESN-RHLAGVFRSVLVANLTGKWTASBDWA---IS-T-YITNPG-IG-GI-G	320
DB	327	QIPGFEFLQKYPRKSVYNGFAKEFWETTFNCHQOEGAKGFLPYDTLFGHEEGARLS	386

QY 321 TVLGV-A-1Q--O-RO-VP-GL-KEF-EESY---VO-AVNGA-P-----RTCEBG-SW-C 359

Db 387 NSPTAFPLCTGENTSVETPYMDYTHLRISYNYLAVYSIAHALODITYCIPGRGLFT 446

QY 360 -G-TN-Q-LCRECHAFITTMMPLEGAFMSAAYNYEAYVAHGHQLG-----T 408

Db 447 NSGCADIKKVEAMOVKHLRHNFETSMGBOYTFDECDLAGNYSIINHLSPEDSIVF 506

QY 409 SGCA-RGPYPMOLLQOIKVNFLLHK-KTVAFDKDGPLYDYDIAMDNGPE-WT-F 464

Db 507 KEYGYNYVAKKGERLFINDKILMSGFSRDEVPFNSRCCLAGTRKGIIEGPTCCFEC 566

QY 465 EYIG--SA-SLSFVHLIDINTKIQMHGKNQVPVSVCTRDCEGHR-LVMSGHCCFEC 520

Db 567 VECPEGEYSETDASACNCPDFMSENHTSCIAKEIEFLSWTEPFGIALTFAYLGIF 626

QY 521 MPEBAGTFLNTSELHTCQPCGTBEMAPESGACFSRTVEFLGHEPISVLLAANTLLIL 580

Db 627 LTAFLVGVIFKFR-NPIVKAIRNELSYLLFLSLCCFSSSLF-FIGEPDWTCLRLQPA 684

QY 581 LLITAGLFA-WRLHFPVRSAGGRCLFMLGSLVAG-SCSLVSFEGRKPTVACLLRQPL 638

Db 685 FGISFLVLCISCIIVKTRVLVFE--AKIPTSHRKMWGLNQLFLVLCFMQIVICAI 742

QY 639 FSLGFAIFLSCLTIRSFQVLIIFKSTKVPT-FYHTWAQNHGAGIFVIVSTVHLFCLT 697

Db 743 WLNTAPSSRYRNEHLEDEIFITCHEGSLMAGFLIGTC-LTAALCFE-APKSRKLP 800

QY 698 WLMTMPRPREFRQRPFLVILECTEYN--SVGLFVAFANILLISTFPCSTLGRKLP 755

Db 801 NENAEFTFESMLIFLWISFIPAVASTY-GKFSVAEVIATILASFGLLACIFENKVV 839

QY 756 NYNEACVTFESLLHFVSMTAFFTM-SIYOGSYLPAVNIAGLATSFGSGVFLPKCY 814

Db 860 IILFKPSRNTIE 871

QY 815 VILCRELNTIE 826

RESULT 2

ENTRY 2

TITLE S49341 #type complete

ORGANISM calcium-sensing receptor - human

DATE 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 03-Aug-1995

ACCESSIONS S49341: A49419; B49419; C49419

REFERENCE S49341

#authors Pearce, S.H.S.; Thakker, R.V.

#submision submitted to the EMBL Data Library, August 1994

#accession S49341

#status preliminary

#molecule_type DNA

#residues 1-1078 #label PEA

#cross-references EMBL:X81086

REFERENCE A49419

#authors Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi, T.; Seidman, C.E.; Seidman, J.G.

#journal Cell (1993) 75:1297-1303

#title Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalcemic hyperparathyroidism.

#cross-references M01D:94094324

#accession A49419

#status preliminary

#molecule_type DNA

#residues 178-180, 'K', 182-192 #label POL

#experimental_source family N

#note sequence inconsistent with nucleotide translation

#note sequence modified after extraction from NCBI backbone

#note 186-Arg mutation is associated with familial hypocalcemic hyperparathyroidism

#note hypocalcemic hyperparathyroidism

#note sequence extracted from NCBI backbone (NCBIN:142453)

#accession B49419

#status preliminary

#molecule_type DNA

#residues 289-303 #label PO2

#experimental_source family E

#note sequence modified after extraction from NCBI backbone

#note 298-Lys mutation is associated with familial hypocalcemic hyperparathyroidism

#note sequence extracted from NCBI backbone (NCBIN:142455)

#accession C49419

#status preliminary

#molecule_type DNA

#residues 788-802 #label PO3

#experimental_source family J

#note sequence modified after extraction from NCBI backbone

#note 796-Tyr mutation is associated with familial hypocalcemic hyperparathyroidism

#note sequence extracted from NCBI backbone (NCBIN:142457)

SUMMARY

#note

length 1078 #molecular_weight 120672 #checksum 8159

Query Match 20.4%; Score 1296; DB 2; Length 1078;

Best Local Similarity 31.8%; Pred. No. 7, 84e-227;

Matches 271; Conservative 234; Mismatches 274; Indels 73; Gaps 48;

Db 30 GDIIIGLFPPIHNG-VAADODLKSRESVECIKRYFGRFMLOAMIFAEINSSPALL 88

QY 37 GDFLLGLFSLHADCLQVNRPLVTSRDS--FNGHGYHLEFQARFTVEELNSTALL 94

Db 89 PNLTLGRIEDICNTYSKALETLSEFAQNKIDSLNDEFNCSEHPISTIYAVATGSG 148

QY 95 PNTTLGYELDYCESSESNY-ATLRVPAQGGTGLEMQ--DLRNSKVALIGDNTD 151

Db 149 VSTAVANLLGLPIPOVSTASSRLLSNKNOFSRTLPNDHQATADADIIYFRMW 208

QY 152 HAVTATALLSPFLMPLVSEASSVILSGKRKPSFLRTIPSKYQVEYIVRLQSGMW 211

Db 209 VGTIADDDYGRPGIKFEEAEERDIDFSELISQYDDEE--TOHVEVYIONSTAV 266

QY 212 ISLVSGYDGLGVADLELATPRGICVAFNDVPLSQAGDPKQRMRLARAKTIV 271

Db 267 IYVSGSPDLEPI-KEIVRRITGKIWLASBAMSSLIAMPQYFVVGGTIGFALAKG 325

QY 272 VYVESN-RHLAGYFRSVLANLTGKWIASBDMA---IS-T-YTNVP-G-GI--G 320

Db 326 QIPGREFLKKYHPRKSVNGFAKEFWETFNCHQEGKGPLVDFTLRGHESSDRS 385

QY 321 TVLGV---VA-100RO-VP-GL-KEF-EESY---VO-AVNGA-P-----RTCEP-GSW-- 358

Db 386 NSSTAFPLCTGENTSVETPYMDYTHLRISYNYLAVYSIAHALODITYCIPGRGLFT 445

QY 359 -GCTN-Q-LCRECHAFITTMMPLEGAFMSAAYNYEAYVAHGHQL---L-GC---T 408

Db 446 NSGCADIKKVEAMOVKHLRHNFETSMGBOYTFDECDLAGNYSIINHLSPEDSIVF 505

QY 409 SGCA-RGPYPMOLLQOIKVNFLLHK-KTVAFDKDGPLYDYDIAMDNGPE-WT-F 464

Db 506 KEYGYNYVAKKGERLFINDKILMSGFSRDEVPFNSRCCLAGTRKGIIEGPTCCFEC 565

QY 465 EYIG--SA-SLSFVHLIDINTKIQMHGKNQVPVSVCTRDCEGHR-LVMSGHCCFEC 520

Db 566 VECPEGEYSETDASACNCPDFMSENHTSCIAKEIEFLSWTEPFGIALTFAYLGIF 625

QY 521 MPEBAGTFLNTSELHTCQPCGTBEMAPESGACFSRTVEFLGHEPISVLLAANTLLIL 580

Db 626 LTAFLVGVIFKFR-NPIVKAIRNELSYLLFLSLCCFSSSLF-FIGEPDWTCLRLQPA 683

QY 581 LLITAGLFA-WRLHFPVRSAGGRCLFMLGSLVAG-SCSLVSFEGRKPTVACLLRQPL 638

Db 684 FGISFLVLCISCIIVKTRVLVFE--AKIPTSHRKMWGLNQLFLVLCFMQIVICAI 741

QY 639 FSLGFAIFLSCLTIRSFQVLIIFKSTKVPT-FYHTWAQNHGAGIFVIVSTVHLFCLT 697


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Db 742 WLYTAPSSYRNOELDELFITCHEGSLMALGLGYTC-LTAAICFFP-AFKSKRPE 799
  || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 698 WLAMTPRPREYORPPHVLIECTEVN--SVGFVAFANILLISTFVCSYLKELPE 755
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 800 NENEAKFTFSMLFIETWISFIPAYASTY-GKFSVAVEVIAIIAASFGLACIFENKIX 858
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 756 NYNEAKCVTFSLHLFVSWIAFFTM--SSIYQSGYDPAVNVLAGLATLSGGFSGYFLPKCY 814
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 859 IILFKPSRNTIE 870
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 815 VILCRPELNNTIE 826

RESULT 3
ENTRY A56715 #type complete
TITLE calcium receptor (clone pNPCR-4.0) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change
17-Mar-1999

ACCESSIONS A56715
REFERENCE A56715
#authors Garrett, J.E.; Capuano, I.V.; Hamerlund, L.G.; Hung, B.C.P.;
#journal Brown, E.M.; Hebert, S.C.; Nemeth, E.F.; Fuller, F.
#title J. Biol. Chem. (1995) 270:12919-12925
Molecular cloning and functional expression of human
parathyroid calcium receptor cDNAs.
#cross-references MUID:95279439
#accession A56715
#status preliminary
#molecule_type mRNA
#residues 1-1078 #label GAR
#cross-references GB:U20759; NID:9683744; PID:9683745
glycoprotein; receptor; transmembrane protein
KEYWORDS #length 1078 #molecular_weight 120573 #checksum 7668
SUMMARY

Query Match 20.3%; Score 1293; DB 2; Length 1078;
Best local similarity 31.8%; Pred. No. 3,22e-226;
Matches 271; Conservative 234; Mismatches 274; Indels 73; Gaps 48;

Db 30 GDIITGLGPIHFG-VAARDQDKSPESVEECIRYFRGRWLOAMIFALEINSSPALL 88
  ||:|||||: : : : : : : : : : : : : : : : : : : : : :
Qy 37 GDFLLAGLSLHADCLOVHRRLPTSCDRSDS--FNGHGHLQFQAMFTVEEINNSTALL 94
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 89 PNLTIGYRFDICNTVSKALEATLSVAQNKIDSLNDEFCONSEHPIPIAVVATGSS 148
  ||:|||||: : : : : : : : : : : : : : : : : : : : : :
Qy 95 PNLTIGYRFDICNTVSKALEATLSVAQNKIDSLNDEFCONSEHPIPIAVVATGSS 151
  ||:|||||: : : : : : : : : : : : : : : : : : : : : :
Db 149 VSTAVANLGLFYIPQVYASSSRLLSNKQKFSPLTIPNDEHOATAMADIEFRWV 208
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 152 HAVTTAALLSPLMLPLVSEASSVILSGKRKFPFLRTIPSDKYQVEVIRLQSGTW 211
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 209 VGTIADDDYGRPGIEKFEAEERDIDCFSLISQYSDDEE--IQHVEVVIQNSTAKY 266
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 212 ISLVGSGYGGOLGVALLELATPRGICVAFKQVPLSAQGDPRMQRMMLRLARATTV 271
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 267 IYVESGSGPLEPLI-KEIYRNRITKIMLASEMASSSLIAMQYRHHVVGITGFALKAG 325
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 272 VVVFSL-RLHAGFFRSVVLANTGKMWIASERMA---IS-T-YTTNPG-IO-GI-G 320
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 326 QJPGFEFEKVKVPRKSVNGFAKFEWETFNCHLOEGAKGPLVDTFLGHEESGDRFS 385
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 321 TVLG----VA-IQGRQ-VF-GI-KEF-ESSY---VO-AVMGA-P-----RTCP-ESW-- 358
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 386 NSSTAFRLPCTDENSIVETPYIDTHIRISYNYLAVYSIAHALQDIYTCPLGSGFLT 445
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 359 -CGTN-Q-LCREHAFTTNMPELGAFSMAAYNYEAVVAHGLHQL--L-GC---T 408
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 446 NSGCAIIRKVEAMQVAKHLRLNFTNNMGEQVTFDECGDLYGVYSIINHLSEDSGIYF 505
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 409 SGCA-GRGVYPMQLQIYKVNFLHK-KTVAFEDKGPLGDIYIADWNPPE-WT-F 464
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 506 KEYGYNYVAKKGERLFINEEKILMGFSREVPFNSCRDCLAGTRKGIIEGPTCCFEC 565

```

```

Qy 465 EYVG--SA-SLSPVHDINKTKIQWGHKKNQVPSVCTEDCC-EGHNR-LYMGSHHCCFEC 520
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 566 VECPODEYSDVDASACNKPDDPFMSNENHTSCIAKEIFPLSTPEFGALTIIFANLGI 625
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 521 MPEACTFLNTSLHCTQCGTEEMWPEGSSACFSRTVEFLWHEPIISVLLAANLILL 580
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 626 LPAFLVGLIKRP-NPIYKATNRBELSYLLFSLCCFSSSLF-FLGPDQDMTCRLRPA 683
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 581 LLITGAGLFA-WRLHTPVRSAGGRICFLMLGSLVAG--SCSLYSPFGKTPVPCILRQPL 638
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 684 FGISFVLCISCLIKTNRLVLFVE--AKIPSFHRKMGINLOFLVFCTEMQIVCY 741
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 639 FSLGFAIFLSCULIRSPQVLIIFFKSTKVP-T-FYHWAQNHGAGIVYSSVHFLCLT 697
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 742 WLYTAPSSYRNOELDELFITCHEGSLMALGLGYTC-LTAAICFFP-AFKSKRPE 799
  || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 698 WLAMTPRPREYORPPHVLIECTEVN--SVGFVAFANILLISTFVCSYLKELPE 755
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 800 NENEAKFTFSMLFIETWISFIPAYASTY-GKFSVAVEVIAIIAASFGLACIFENKIX 858
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 756 NYNEAKCVTFSLHLFVSWIAFFTM--SSIYQSGYDPAVNVLAGLATLSGGFSGYFLPKCY 814
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 859 IILFKPSRNTIE 870
  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 815 VILCRPELNNTIE 826

RESULT 4
ENTRY 159362 #type complete
TITLE calcium/polyvalent cation-sensing receptor precursor - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
01-May-1998

ACCESSIONS 159362; A55594
REFERENCE 159362
#authors Ruat, M.; Molliver, M.E.; Snowman, A.M.; Snyder, S.H.
#journal Proc. Natl. Acad. Sci. U.S.A. (1995) 92:3161-3165
#title Calcium sensing receptor: molecular cloning in rat and
localization to nerve terminals.
#cross-references MUID:95241465
#accession 159362
#status translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-1079 #label RES
#cross-references EMBL:U20285; NID:9790578; PID:9790579
#experimental_source striatal
REFERENCE A55594
#authors Ricciardi, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.;
Hebert, S.C.
#journal Proc. Natl. Acad. Sci. U.S.A. (1995) 92:131-135
#title Cloning and functional expression of a rat kidney
extracellular calcium/polyvalent cation-sensing receptor.
#cross-references MUID:95116508
#accession A55594
#molecule_type mRNA
#residues 1-133, 'X', 135-1079 #label RIC
#cross-references GB:U10354
#experimental_source kidney
KEYWORDS calcium; glycoprotein; phosphoprotein; transmembrane protein
FEATURE
1-20 #domain signal sequence #status predicted #label SIG\
187-212 #region hydrophobic\
613-635 #domain transmembrane #status predicted #label TM1\
630-670 #domain transmembrane #status predicted #label TM2\
683-700 #domain transmembrane #status predicted #label TM3\
728-744 #domain transmembrane #status predicted #label TM4\
770-790 #domain transmembrane #status predicted #label TM5\
800-828 #domain transmembrane #status predicted #label TM6\
841-850 #domain transmembrane #status predicted #label TM7\
901-261,287,386,468, #domain transmembrane #status predicted #label TM\
488,594,893,1005 #binding_site carbohydrate (Asn) (covalent) #status
predicted\

```


Qy	354	P-2EGSMGCTQQLCR-E--CAFTFTNMNPELGASMSAAV--N--V-Y--EAVYVAHGL	401
Db	412	HNMQSLCPAGYALCDADKAPIDGSKLLLESKMTFTGVSGDTIFIDENGSGPYGEITMNF	471
Qy	402	HQL-LG-CT--SGTC-ARGPYVPMLOOLQIYKVFLL-LHKTKVAFDDKGDPLGYDDIIM	455
Db	472	KEMGKDY-FDYINNGSMWNGSLMKDDDEV--MSKSNIIIR--SYGSECEPKGQIKYIRGGEV	528
Qy	456	DMNGPEWTFEVIYGASLSVPHLDLNTKRTIQWNGKNNVPPVSVCTRCDEEGHRLV-NGSH	514
Db	529	SCCWCTPCKENVEYF-DE-YTCAQACQIGSPWIDTLGCDLIPYQIRMGDPPIAAVF	586
Qy	515	HCCFCMPCMEAGTFLNTESELTQCPCGTEENAPGSSACSPRIYEFILGW-H-EPISLVLL	572
Db	587	ACLGILATLV-YVFTIYR-DTPVWSSSSNELCYIIAGICLGICT-PLCIAPKQIY	643
Qy	573	AANTLLLLLLLGTGLFPMRLHTPVVRAGRGRLCLFMIGSLVMAOS-CLSYSEFKRPVPA	631
Db	644	CYLQRIIGISLPASYSALVTKTRIRIILAGSKKCICTKPRFMSACQAVIAFICI	703
Qy	632	CLIRPLESLGFAIFLSCLTIRSQVLITFEFSIK-VPTFHTMAQNHGAGIPIYIVSTV	690
Db	704	QGIIVAFIPEPPDIIMHDPYSIRE-VYLICNTN-LGVVTPILGNGLLISCTF-YAFK	760
Qy	691	HLFLCLITLAWTFPRTPREYORFPHVLILECTEYNSGYELVAFANHLLISIS-ITVCSYL	749
Db	761	TRNVAENENKIAIAFTYTICIIIMAF--VP-IYFCSNYKIIIMCFSVS-TSMTVALGC	816
Qy	750	GKLEPENENKCYVIFSLLFHFVSMIAFTVSSITQSGYLDPAVNVLAGLISGFS-GY	808
Db	817	MEVPKVIILAKPERNVSATFTS	840
Qy	809	FLPCGYIILRPELNTEHFQAS	831
RESULT	7		
ENTRY	JC2131	#type complete	
TITLE		metabotropic glutamate receptor 5 B - human	
ORGANISM		#formal_name Homo sapiens #common_name man	
DATE		28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996	
ACCESSIONS	JC2131		
REFERENCE	JC2131		
#authors	Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.		
#journal	Biochem. Biophys. Res. Commun. (1994) 199:1136-1143		
#title	Molecular cloning and the functional expression of two isoforms of human metabotropic glutamate receptor subtype 5.		
	5.		
	#cross-references Xref:94197596		
	#accession JC2131		
	#molecule_type mRNA		
COMMENT	1-1212 #label MIN		
KEYWORDS	##residues This protein is coupled to guanine nucleotide binding proteins. glycoprotein; neurotransmitter; receptor; transmembrane protein		
FEATURE			
	580-604	#domain transmembrane #status predicted #label TM1\	
	617-637	#domain transmembrane #status predicted #label TM2\	
	644-664	#domain transmembrane #status predicted #label TM3\	
	694-714	#domain transmembrane #status predicted #label TM4\	
	738-759	#domain transmembrane #status predicted #label TM5\	
	773-794	#domain transmembrane #status predicted #label TM6\	
	803-827	#domain transmembrane #status predicted #label TM7\	
SUMMARY	#length 1212 #molecular-weight 132579 #checksum 3155		
Query Match	12.9%: Score 819; DB 2; length 1212;		
Best Local Similarity	27.0%: Pred. No. 2,876-130;		
Matches	233; Conservative 229; Mismatches 334; Indels 68; Gaps 58		
Db	5	LILSVLLKEDVRG-SAQSERRVAHPGDIIIGALFSVHHDP-TV-DKVERKCG-AV	60
Qy	8	LILSVLLKEDVRG-SAQSERRVAHPGDIIIGALFSVHHDP-TV-DKVERKCG-AV	67

Dd	61	R-EOXGJORVEMHTEHTLRINSDPLNLTNLGCEIRDSCHWSVALEQSEJFRDLSIS	119
Qy	68	SFNGCHYHFOAMRTVEIEINNSTRALLEPNITLGEIYDVCESSE-NY-AI--LR---VP	120
Dd	120	SEEEBGLRVCDVSSSSFSRKKPIYVIGTGPSSVAIQONMLOLEFNIPQIASATSMDL	179
Qy	121	AQOGTGHE-MORDLRN-HSSK-VYALIGPNDTHAVTALLSPFLMPLVSYEASSVIL	177
Dd	180	SDKTLFKEMRVPSDAQOARAMDIVAKRYMWTYSANHTGSGNGESGMEAFKMSAREG	233
Qy	178	SGKRFPSEFLRTPSDKTOVEYVNLQSFQMWVSTLGSIGDGQGLQVQLEELAPRG	237
Dd	240	ICIAHSYKI-YSN-AGEOSFDFLTKLTKLSHPKARVAVACPEGATVGHILAMARLG-LA	299
Qy	238	ICVAKRDVYPLSAQGDPRMORMRLA-R-ARTTVYVEEN-RHLAGVFERSVYLANLT	296
Dd	297	GEFLLIGSDGMA-DRYDVT-DOYO-REAVGSGITKL-OSPDVKMFDDYUCLKREPTNHRN	355
Qy	295	GK-VWIAJEDMAISTYIINNVGIGIGTVLVAIQOROPVLPKFEFESYVQAVGABRTC	353
Dd	353	PMFOFMQHRRO-CLBEGFPOENSKYNTCKSSJLTKHNVODSKMGVINAISMAVGL	411
Qy	354	P-BESSWCGTNOLCR-E-CHAFTHWAPDELGAFSMSAAY--N-V-Y-EAVYVAHGL	401
Dd	412	HNMMOISLCPGVAGLDAMKPIDGRKLTLSMKTFEYTGSDTILFEDENGSPGRYEIMNF	471
Qy	402	HQL-LG-CT--SGTC-ANGPVYPMQILQIQIKVNF-LHKTKVAFDQGDPLGYDILIAW	455
Dd	412	KEMGKDY-FDIYINGSWONGELKMDDEY-WSKSNITR-SYCEPCEKQIKVIRGGEV	528
Qy	456	DWNGEWMTEFEVIGSASTLSPVHLIDIKTKTIQWNGKNQVAPVSCYRCDLCEGHHRLV-MGSH	514
Dd	529	SCCMWTCPCKEENEYAF-DE-YTKRACQJGSMPTDLCGCDLPIQYLRMBGPDEIAVWF	586
Qy	515	HCCFECMCCEAGTFLNYSBELHTCQPCGIEEWAPESSACSFRYBFLGW-H-EPLISVYL	572
Dd	587	ACGLGLLATLV-TVVEIIR-DTPVAKSSSHELCTIILAGICLGLCT-FCLIAKPROY	643
Qy	573	AANTLLLLLLISTAGLFAMRLHTPVRSAGRGFLMLGSLVAGS-CSLYSFEOKPIYPA	631
Dd	644	CYLQKIGIGLSPAMYSALVYKTKINLAIIILAGSKKIKTKKPRMSACQIVIAFILCI	703
Qy	632	CLLRPPLSLGALPFLSCLTIKRSFQVLIIFFSK-VPEFYHTWAQNHGAGIFIVYSTV	690
Dd	704	OLGIVALEFIMEPPDIMHDYPSIRE-VYLICNTN-LEVVYPLGNGILLISCF-YAFK	766
Qy	691	HLFLCLTLMAMTTPRPTREYQRFPHLYLBCTEVNSVGFVAFANILILIS-TPVCSYL	749
Dd	761	TRNVPANFNEAKYIAFTWITTCIILWAF--VP-IYGSNKKIITMWCFSV-TSAPVALG	818
Qy	750	GKEIPEENNEAKCYFSLILHFVSIATFETMSIYOGSYLPAVVYAGLIALSGFS-GY	808
Dd	817	MEVPKYVITIIIAKPERNVRSAFTIS	840
Qy	809	-FLPKYIILCRPELNTNTEHROS	831

RESULT	ENTRY	8
TITLE	A42916	#type complete
ORGANISM	metabotropic glutamate receptor mglur5 - rat	
DATE	#formal_name Rattus norvegicus #common_name Norway rat	
ACCESSIONS	04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change	
REFERENCE	29-Jan-1999	
#authors	A42916	
#journal	A42916	
#title	Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.	
	J. Biol. Chem. (1992) 267:13361-13368	
	Molecular characterization of a novel metabotropic glutamate	
	receptor mglur5 coupled to inositol phosphate/Ca ²⁺ signal	
	transduction.	
#cross-references	MUID:9231/054	

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#accession A42916
##status preliminary
##molecule_type mRNA
##residues 1-1171 ##label ABE
##cross-references GB:DI0891; NID:9220813; PID:01002186; PID:9220814
##experimental_source brain
##note
sequence extracted from NCBI backbone (NCBIN:107749,
NCBIP:107750)
KEYWORDS G protein-coupled receptor; transmembrane protein
SUMMARY #length 1171 #molecular-weight 18289 #checksum 8594
```

Query Match	12.8%;	Score 814;	DB 2;	Length 1171;
Best Local Similarity	27.1%;	Pred. No. 2.86e-129;		
Matches 234;	Conservative 222;	Mismatches 340;	Indels 67;	Gaps 60.

```

Db 5 LILSVLLLKEDVRG-SNASSRRRYVAHHPGIIITIGALFSVHNOR-TV-DKYNHEKCG-AV 60
OY 8 LLLSLQTLAVAYCMAFSCORTSSPGFSLPGDFLLAGLESFSLADLOVHRHRLVYTSICRSD 67
Db 61 R-EQYGIORVEMAMHTHERINSDPTLLPNITLGEIRDSCSHSAVALAESJEFIRDSLS 119
OY 68 SPNGCHYLLPQAMRFTVEINNSRALLPNITLGLVELVDYCESSNYYA-ILR-VPAQ-G 124
Db 120 SEEEGLVRCVDSGSSSEFSKRPVIGVIGPGSSVAIOVONLQLEFNIPOLAYSATSMDS 179
OY 125 TGHLE-MOR-D-LRN-HSSK-VVALIGPDNTDAVTTAALLSPFLIMPLIYSFASVYLS 178
Db 180 DKLTFKMYRVRVPSDAQARAMVDIVRYNMTYVSAVHTBEVNEGEOMEAFKMSAEGI 239
OY 179 GKRPSPSLRTRIPDSKTOVEYVILKLSFGVWVSLVSGVSIGDYQOLQDALEELIATRGI 238
Db 240 CIAHSYKI-YEN-AGEOSFDKLKLLKLSHLKARVAVACEGMYRGLLMLMRRLG-LAG 296
OY 239 CVAFMDVPLBAQAGDPROMQMLRL-AR-ARTVVVYFS-RRLAGVFPFSVVLNLTG 295
Db 297 EFLILGSGMA-DRYDT-DGY-Q-REAVGITTLL-OSPDVKMFDDYLLKIRPETNLNRP 352
OY 296 K-VMIASHEDMAISTYITNVPGIGIGTVLGAALIOQROVPGLKEFEESYVOAVMGAP-RTC 353
Db 353 WFOEWMORPQ-CRLEGRAGNENSKYNTKTCNSLLRLRHHNODSKMGVINYATYMAAGL 411
OY 354 -PEGWCGTNDLGR-E-CHAFITWNNPELGAFFMSAAY-N-V-Y-EVVAVALAGHL 402
Db 412 NMQSLSCGAVGLCDAMKPIDGRKLLDSIMKNTFTGVSQGMILFEDMGDSFGRYENFK 471
OY 403 QL-LG-CI- -SGTC-ARBPVYPMQLQIYVNL-LHKRTVARDKDGPIGYDIIAMD 456
Db 472 EMKQDY-FDIYNVGSWMDNGELKMDDEY-WSKNNIIR-SYCSPECEKQIATYRKEVS 528
OY 457 WNGSPMTEVEVGSASLSFVHLIDIKTKIOWMKGNNOVPASVCTDCEGHRILV-MGSHH 515
Db 529 CCMOTPOCKENBYAF-DE-YTCKACQOLGSMWTDLDGDLIPVQYLKMGDEPEIAAVFA 586
OY 516 CCFECMPDEACTFLMTSLHTCQPCGEBEMPEBSSACFSATVEFLGW-H-EPLISVLLA 573
Db 587 CLGLLATEFV-TVIFIIIR-DTPVAKSSSRBLCYIILAGLIGLYCT-FCLIANPKOYIC 643
OY 574 ANTLILLILLIGAGLFAHRLHTPVYRSAGSLCFLMLGSLVAGS-CSLISPFGRPTYBAC 632
Db 644 YLORIGLSPAMYSALVYKTNRIARILLAGSKKICTKPREMSACQOLYAFIILICIO 703
OY 633 LLROPLFELIGAIPLSCLTIRSFOLVIFKFSFK-VPTFYHTMAQNAGACIFIVSVTH 691
Db 704 LGLIYALIMBPDIIMHCHYSIRE-VYLICNTN-LGVVPLVNGILLISCTF-VAPKT 760
OY 692 LFLCTLWLAAMTPRPTREYORFPHVLVIECTEVNSVGLVAFAINILLIS-ITVCSITLG 750
Db 761 RNVAPNENEAARYAFATWTTCTIIMLAF-VY-IFYGSNYKIITKCFVS-LSATVALGCM 816
OY 751 KELPENYNEACVYFSLHLHVSMAIAFTMSITOGSVLPAVNVNLAGLATISGGFS-GY- 808
Db 817 FVPKYVILIAEPERNVRSATTS 839

```


QY 809 FLPRCYVILCRPELNTEHFOAS 831

RESULT 9

ENTRY A41939 #type complete

TITLE G protein-coupled glutamate receptor - rat

ORANISM #formal_name Rattus norvegicus #common_name Norway rat

DATE 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998

ACCESSIONS A41939: S15362

REFERENCE A41939

#authors Houamed, K.M.; Kuiper, J.L.; Gilbert, T.L.; Halteman, B.A.; O'Hara, P.J.; Mulvihill, E.R.; Almers, W.; Hagen, F.S.

#journal Science (1991) 252:1318-1321

#title Cloning, expression, and gene structure of a G protein-coupled glutamate receptor from rat brain.

#cross-references M01D:9202526

#accession A41939

#status preliminary: not compared with conceptual translation

#molecule_type nucleic acid

##residues 1-1199 ##label HOU

##cross-references GB:M61099; NID:g9397806; PID:g204460

##experimental_source cerebellum

#note sequence extracted from NCBI backbone (NCBI:60785)

REFERENCE S15362

#authors Masu, M.; Tanabe, Y.; Tsuchida, K.; Shigemoto, R.; Nakanishi, S.

#journal Nature (1991) 349:760-765

#title Sequence and expression of a metabotropic glutamate receptor.

#cross-references M01D:91156047

#accession S15362

##status preliminary

##molecule_type mRNA

##residues 1-1199 ##label MAS

##cross-references EMBL:X57569; NID:g56646; PID:g56647

KEYWORDS G protein-coupled receptor; transmembrane protein

SUMMARY #length 1199 #molecular_weight 133335 #checksum 5211

Query Match 12.7%; Score 810; DB 2; Length 1199;

Best Local Similarity 27.68; Pred. No. 1,80e+128;

Matches 231; Conservative 216; Mismatches 325; Indels 66; Gaps 52;

Db 41 MDDVITIGALFSVHOPPAEVK-P-ERKC--GEIREQYGIORVEMFHTDKINADPVL 96

QY 35 LPBDFLLAGFLSHADCLQYRHRPLVTSRDSFNGHGLQAMFTVEELNSTALL 94

Db 97 PNITGSEIRDSQWSSVALEQSIIEFIRDSLSIRDEKDLNRCPLDGOQLPPGRIKPT 156

QY 95 PNITGSEIRDSQWSSVALEQSIIEFIRDSLSIRDEKDLNRCPLDGOQLPPGRIKPT 142

Db 157 AGVIGGSSVAIQVONLQDLPIDPAISATISIDSKLILYFLRVSOTLQARAML 216

QY 143 A-DIGDNDTHAATTAALLSPFLMPLVSYEASSVILSGKRKPFSLTIPSDYQVEIV 201

Db 217 DIYKRYNMVSAVHTEGNGSGMDAFKELAOEGICIAHSPKI-YSN-AGEKSEIRLL 274

QY 202 RLQSGGWVWISLVGSGIDGQLGVQALBELATPRGICVAFKDVVPSAAGDPRMORRM 261

Db 275 RKLRELRPKARVVVCEGNTVRGLSAMRRLGVGSEFSLIGSDQWADRDEV--IEGEY- 331

QY 262 LRL-AR-ARTVVVFSN--RHLAGVFFRSVVLNLTGKVMIASDMDAISTYITNVPIQG 318

Db 332 VEANGGITTL-OSPEVRSDDYFLKRLDTNTRNPFPE-FMQHRQ-CRLGGLLENP 388

QY 319 IGVLVGAIQOROVPGIKKEEESYQAVMGA-PRTC--PGSGMGTNQLDR-ECHAFITW 374

Db 389 NFKVCTGNSLEENYQDSKMGFVIAIYAMAAGLQNMHALCPGVGICDAMKPIDGR 448

QY 375 NMEEL--GASMSAAY--N--V-Y--EAYVAVHGLHOLL-G-CTS--GTC-ARGPYTPW 420

Db 449 KLIDFLIKSSFVSGEEVWDEKGDAPGRYDINMLOYTEANR-YDYVHVHGVHGEVLNI 507

QY 421 QLLQGIYKAVFL-LHKKTVAFDXGDFLGYDDIAMDWNPENMTFVIGSASLSPLHDI 479

Db 508 DDYKIO-MNKGWVR-SYCESEPCIKGQIKVIRKGEVSCCICACKENEFVO-DEF-TGR 563

QY 480 NKTITQMGKKNNOVPYSVCTRCCLBGRHLY-MGSHCCFCFECMPCAGTFLWTSHTCQ 538

Db 564 ACDIGMWPNAELTGCEPIPVRYLEMSDIEISIAIAFSC-GILVTLFVLIFVLYR-DIPV 622

QY 539 PCGTENMAPGSSACSRIYVEFLGWHEPISVYLAANTLILLLLIGTALFA-WRLHTVP 597

Db 623 VSSSRELCYIILAGIFLGYCP-FTLLAKPTTSCYDORLLVGLSSAMCYSAIYTKNR 681

QY 598 VRSAGRLCFMLIGSLVAG-SCSLYSFFCKPTVPACLLRQPLFSIGFAIFLSCILIRSPQ 656

Db 682 IATILAGSKKICTRPRMSAMQYIATISILISQTLIVTLILMEPMLTSPSIRE 741

QY 657 LVITFEFSTR-VPTFYHTMAQNHGACIFYVSSIVHFLCLTLMWMTPTPTREIQRPH 715

Db 742 -VYLIC-NTSNLGVAVPVNGLLIMCTY-YAFKRNVPANFENKAYIAFTYTCTIIM 798

QY 716 LVILBCTEVNSGFLVAFANILSTS-IFVCSYLKELPEMYNEAKCVTFILHLFVSM 774

Db 799 LAF--VP-IYFGSNYKIITTCFAVSLSVYALGCFKPKXYIILAKPEKNVSAFTTS 853

QY 775 IAFFTMSIYQGS-YLPVAVNLAGLATLSGFGSGLFPCQYVILCRPELNTEHFOAS 831

RESULT 10

ENTRY JH0563 #type complete

TITLE metabotropic glutamate receptor 4 precursor - rat

ORANISM #formal_name Rattus norvegicus #common_name Norway rat

DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998

ACCESSIONS JH0563

REFERENCE JH0561

#authors Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.

#journal Neuron (1992) 8:169-179

#title A family of metabotropic glutamate receptors.

#cross-references M01D:92110002

#accession JH0563

##molecule_type mRNA

##residues 1-912 ##label TAN

#experimental_source brain

COMMENT This protein is coupled to a G protein and evokes a variety of functions by mediating intracellular signal transduction.

CLASSIFICATION #superfamily metabotropic glutamate receptor 4

KEYWORDS G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

FEATURE 1-32

33-912

588-610 #domain signal sequence #status predicted #label SIG\

625-645 #product metabotropic glutamate receptor 4 #status predicted #label MET\

657-675 #domain transmembrane #status predicted #label T11\

700-720 #domain transmembrane #status predicted #label T11\

751-772 #domain transmembrane #status predicted #label T11\

786-807 #domain transmembrane #status predicted #label T11\

822-847 #domain transmembrane #status predicted #label T11\

98,301,454,484, #binding_site carbonydrate (Asn) (covalent) #status predicted\

621,689,695,859, #binding_site phosphate (Ser) (covalent) #status predicted

870

SUMMARY #length 912 #molecular_weight 101818 #checksum 808

Query Match 12.6%; Score 799; DB 2; Length 912;

Best Local Similarity 25.98; Pred. No. 2.81e+126;

Matches 206; Conservative 222; Mismatches 307; Indels 59; Gaps 50;

Db 75 GHRLEAMFALDRINNDLLPNITLGARILDTCGRDTHALEQSLTFVQALIEKGTIEV 134

QY 73 GYHLFQAMRTYVEINNSALLPNITLGEIVDYCS-ESSNYYATLR-VPA--Q-QGTG- 126

GENETICS	#cross=	references	CB:M90518;	NID:g205400;	PID:g205401
CLASSIFICATION	GLUR4	#superfamily	metabotropic	glutamate	receptor 4
KEYWORDS		neurotransmitter	receptor		
SUMMARY		#length 912	#molecular-weight 101846	#checksum 818	
Query Match		12.5%;	Score 798;	DB 2;	Length 912;
Best Local Similarity		25.9%;	Pred. No. 4,45e-126;		
Matches		206;	Conservative 222;	Mismatches 307;	Indels 59; Gaps 5
Db	75	GIRHLEAMFLALDRINDDPLNPITLGARLIDTCSRDTALHESGLTFRVALIEKDGTEV	134		
Qy	73	GYNHFOAMRFTVEEINNSTALPNIITGLGYELDVCS--ESSNYATLRL-VPA-Q-QGTG	126		
Db	135	RCGGSGPRITTKPRVYGVGASGSVSIMVANIILRFIPIDISASTAPLDSNRDF	194		
Qy	127	H-LEMQDLRNHSSKRYVALGPDNTHAYTALASPILMPVSTEASVILSKRKP	185		
Db	195	FSRVPSDITYQAQAMVDYALAKMNVSTLASBSYSGSEVAFIQKRENGGVICA-QS	253		
Qy	186	FLRTIPSDKQVEYVIALDGSFGWMSILVSGSYGDYQGLGVALBELATPRG-ICVAFKD	244		
Db	254	VKTREREKTEGFDKIKRLLETSNAG--IIFANEDDIRVLEAKRANQGTGHTFMGS	311		
Qy	245	V-VPLISAQAD-PRMQXMLRLARARTVYVVSNNHLAGVFRFSVALNTLGRV-WIAS	301		
Db	312	DSMGSKAPVRLLEEVE-GAV-TILPKRMSVGEFRYSSTLLNNRNITFAFEWDN	369		
Qy	302	EDM-AISTYITNPVGIGIGTGVALAIQROVPGI-KEEESYQAVNGAPRTCP--EGS	357		
Db	370	FHCKLSRHALKGSHIKCTNRISIQDSATYDEGKVQFVIDAVTAMGHALAHNRDLP	429		
Qy	358	W-CG-TNQ-LCRECHA--FTTNW-MELAFMSAAYN-VYDAVVAVAGHQDL-G-CT	408		
Db	430	GRVGLCPMPDVGDTOLKIRIVNVNSGIAGNVTFENGDAPGRDIYQOLNRGSA-E	488		
Qy	409	S--GTGAR-GRVYPMQLQIYKYNL-LHKRTVARDKDGDLGYDIIDAMD-WNGPWT	463		
Db	489	YKVTGSMT-DHLHLIER--MOWPGSGQOLPSISGLPCQGERKKYKGMACWCEPC	545		
Qy	464	FEVIGSASLSPVHDIKTKIQWGNKNNOVPVSVCTRDLEGHRLVMGSHHCEPCMC	523		
Db	546	-TG-YQOVQRYCKTCQPYMRTERNTSQRPPIYKLEMSPMANVLPFLAVGIANLT	603		
Qy	524	EAGFLTSLSEHTQPCGTEWAPBESSACFSKTYEELGMBP-ISLV-LAANTLILL	581		
Db	604	FVVVT--FVRINDPIYKASGRELSTVLLAGIFLCATITFLMAEPDGTCSRIFGL	661		
Qy	582	LIGTAGFLAMRLHTPVYRSAGRLCFLMLGSLVAGSCLSYSPFGKPYACLLRPPLSL	641		
Db	662	GMSISYALLLTKIRIKYRIFEDQKRSVSAPRFTSPASQALITFILISDL-LGICV-WFV	719		
Qy	642	GFAFLFSLDIRSQVLITIKFKST-VPEFFHTMAONHAGLFVVSIVHLFLLTWLA	700		
Db	720	VDPSSHVYDPODQTLDPFRARGVLC-DISDSLICLLGYSMILMVTCTYAAIKTRVP	778		
Qy	701	MTPTREPREYO-R-F-PHY--ILECTEVNSGFLVPAFAHMLILSISFVSYIGKRLP	754		
Db	779	ETFEAKRIGETMTTICVIALEPIFEFGTSQADKLYIQTTTLTVSVLSASVSLGMLY	838		
Qy	755	ENYNEAKCVFSLHLHFVSVIAFFTWS-siyQSSY-L-PAVNVLAGLALTISGGS-G-YF	809		
Db	839	MPKYIILFHPEON 852			
Qy	810	LPKCVIILCREPLN 823			
RESULT	12				
ENTRY	S71376	#type complete			
TITLE	glutamate receptor homolog - cherry salmon				
ORGANISM	#formal_name Oncorhynchus masou #common_name cherry salmon				
DATE	11-Mar-1998	#sequence_revision 17-Apr-1998	#text_change		

01-May-1998
#71376
#authors Kibokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.
#journal FEBS Lett. (1996) 392:71-76
#title Cloning and characterization of a bifunctional metabotropic receptor activated by both extracellular calcium and glutamate.
#cross-references MUID:96354880
#accession #71376
#status not compared with conceptual translation
#molecule-type mRNA
#residues 1-1218 #label K0B
#glycoprotein: phosphoprotein
KEYWORDS
FEATURE
603-625 #domain transmembrane #status predicted #label TM1
640-660 #domain transmembrane #status predicted #label TM2
672-680 #domain transmembrane #status predicted #label TM3
717-737 #domain transmembrane #status predicted #label TM4
761-782 #domain transmembrane #status predicted #label TM5
795-817 #domain transmembrane #status predicted #label TM6
826-850 #domain transmembrane #status predicted #label TM7
104,223,403,525,
757 #binding-site carbohydrate (Asn) (covalent) #status predicted
636,699,961 #binding-site phosphate (Ser) (covalent) (by protein kinase C) #status predicted
705 #binding-site phosphate (Thr) (covalent) (by protein kinase C) #status predicted
892 #binding-site phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predicted
SUMMARY #length 1218 #molecular-weight 136838 #checksum 1674
Query Match 12.5%; Score 797; DB 2; Length 1218;
Best Local Similarity 27.8%; Pred. No. 7,046-126;
Matches 201; Conservative 195; Mismatches 271; Indels 55; Gaps 44;
Db 166 IAGVIGPGSSVAIQVQLFNIPQIAYSAISIDSKTFFKYLVRVPSDIIQARAI 225
QY 141 VVALIGPNDIDAVITALLSPFLMPLVSEASSVLSKRRFPSTLRITPSDKVOEVI 200
Db 226 LDIVKRYNTYVSAVTEGSEGAERKELASOGLIAHSDKI-VSN-AGEKHFDRL 283
QY 201 VLLQSGFWWVILSVGYDYGQLGVALLELATPRGICVARKDYVPLSAQAGDPRMQM 260
Db 284 LRLKLERLPKAVYVCFGCGMTVRGLMAMRLG-VAGEFLIGSGMADRDREVEGYEO 342
QY 261 MLRL-AR-ARTIVVYVFN-RRLAGVFFRSVYLANLTGK-VWIASEDMAISTYITVPGI 316
Db 343 EAVGGI-TVKLSEEVTSFDDYFLKRLNTNRPWF-PE-FMQHRFO-CRIPGHPLEHM 398
QY 317 QGIGIVLGVAITQROVPGIKE-FEESYVQAVMGAPRTCEGSGMGINOLCREC-NAFTTW 374
Db 399 NYRKNCSGESLEDNVYDQSKMGFVINAAYMAOGLHDMHSLCPGHVGLCKAMPIDGS 458
QY 375 NPPEL-GAF-SMSAAV-N-V-Y-EAVYVAVHGLHQLLG-CIS-CATC-ARGPVPM 420
Db 459 QLEFLMRLSFVGSSEVDYWFDENGDTPRGYELMNTQIYEPG-AFPIYINGSHESQLSI 517
QY 421 QLLQIYKYNFL-LHKRTYAFDDKGPDLGYDIIADWMGPEFTFEVISASISLPYHDI 479
Db 518 DDYMQO-IRSRMV-LSVCEPSCSGEIVIRKGEVSCWICITACQDNBIYO-DEF-TCT 573
QY 480 NKTIKIOWHKNNOVPYVCTRDCLBEGHRLV-MGSHHCFCFCMPCAGAGFLINTSEIHTQ 538
Db 574 ACDDGMPDPELEGEPIITLRYLEWGNPESIVQVFAACGLIVTSFVTEIFVLYR-DTPV 632
QY 539 PGCTREMAPEGSSACFSRTVEFLGHEPISIVLLANTLLLLISTAGLFA-WRLHTPV 597
Db 633 VSSSRRLCYIILAGIFLGIYICP-FTLIMOPTYASCYIDRLVLGSLATGACSLVLTXTNR 691
QY 598 VRSAGRCLCEMLGLVAG-SCSLYSFEGKPTVPACLLRPLFSLGFAIFLSCLTIRSFQ 656

Db 692 IARIAGSKKKICTRRKPREMSAMQVLAGLVSYOLTLEVT-II-LE--PPMPKSP 747
QY 657 LVITF-----KSTKVPFPEYHWAQNHGIGIVSYVHLFLCLTWLAMPRRPTREQ 711
Db 748 SIRE-VFLIC-NTSTVGMVAPLGIYGLIMCTY-YAKTRVNPANNEAKIATMTYT 804
QY 712 RPHVILIECTEVNSGVGLVAFANHLLIS-TEVCYSLGKELPENYNEAKVFTSLH 770
Db 805 CLIMLAF--VP-IYFGSNKITTTSFVSLSYTVLGMCFSPKIYIILLAKPRENRSAT 861
QY 771 FVSWIAFTMTSSIIYGS-VLPAVNVLAGLATLDSGSGFYFLPKCYVILCRPELNTHEQ 829
Db 862 TS 863
QY 830 AS 831
RESULT 13
ENTRY JH0561 #type complete
TITLE metabotropic glutamate receptor 2 precursor - rat
ORGANISM Rattus norvegicus #common_name Norway rat
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998
ACCESSIONS JH0561
REFERENCE JH0561
#authors Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
#journal Neuron (1992) 8:169-179
#title A family of metabotropic glutamate receptors.
#cross-references MUID:92110002
#accession JH0561
#molecule-type mRNA
#residues 1-872 #label TAN
#experimental_source brain
COMMENT This protein is coupled to a G protein and evokes a variety of functions by mediating intracellular signal transduction.
CLASSIFICATION #superfamily metabotropic glutamate receptor 4
KEYWORDS G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
FEATURE
1-18 #domain signal sequence #status predicted #label SIG
19-872 #product metabotropic glutamate receptor 2 #status predicted #label MET
568-590 #domain transmembrane #status predicted #label TM1
605-625 #domain transmembrane #status predicted #label TM2
637-665 #domain transmembrane #status predicted #label TM3
680-700 #domain transmembrane #status predicted #label TM4
726-747 #domain transmembrane #status predicted #label TM5
761-782 #domain transmembrane #status predicted #label TM6
795-819 #domain transmembrane #status predicted #label TM7
203,286,338,402,
547 #binding-site carbohydrate (Asn) (covalent) #status predicted
601,675,827,837,
843 #binding-site phosphate (Ser) (covalent) #status predicted
832 #binding-site phosphate (Thr) (covalent) #status predicted
SUMMARY #length 872 #molecular-weight 95773 #checksum 5740
Query Match 12.1%; Score 769; DB 2; Length 872;
Best Local Similarity 25.4%; Pred. No. 2,646-120;
Matches 210; Conservative 218; Mismatches 343; Indels 56; Gaps 43;
Db 26 LTLBBDVLVIGGLFPPVH----Q-KGCP-AEEGCPVVE-H-RGIQRLKAMFLALDRINRDPH 77
QY 33 FSLPDPFLIAGLFLSHADCIQVRRHPDYVTSQDRSPSFGHGHLPAQARFTVEEENNSIA 92
Db 78 LTPGVRLGHMIDDSKDPHLEQALDVFRAISRGAGSGRIICPDGASVATSDAPVATV 137
QY 93 LIPNTILGELIDVCSSESNVYA-TL--RVPAQOGT-G--HL--EMQBDLRNHSKSYVA 143
Db 138 GVIIGSYSDVSIVQVNLRLFOIPQISYASTAKLSDSKRYDYFARTVPPDFQAKAAE 197

Qy 144 -LIGPNDTHAVTAALLSPFLMPLVSYEASVYLSGKRRFPSELTITPSDKYQVEIVR 202
 Db 198 ILRFEMWTVSTVASEGDYGETGIEAFELARARNICVATSEKVGSRAMRAAFEGVVAL 257
 Qy 203 LQSFQFWMSISLVGSDYGGQVQALBELATPRGICVAFKQVPLS-AQAGPRKQRM 261
 Db 258 LQPSAR--VANVLFPSDEARELLAATQRLN-ASFTWASDGMGALESYVAGSERAAEA 314
 Qy 262 LRLARATVVVVVFSNRHLAGVFFRSVLANLKGKWIASEDAIATYITNPAGIIGT 321
 Db 315 I-TIELASTPISDFASFPQSLDPMNNSRNPWFEEFEHFHCFRQ--RDCAHSRAVP 371
 Qy 322 VLGVAIQKQVQVQKFEESYVQ-AVMGAP--RTCEGSH-CGTNOLCBECAFTTWNP 377
 Db 372 FEQSKIMEVNVAVYAMAHAL--HNMHRL-CPNTTHLCDAMRPVNRRLTKDFLVNKEP 429
 Qy 378 -ELGASMSAAVNVAVYAVAGHLQGLGCTSGT--C-ARGVYVWQQLQ-ITYVNF- 431
 Db 430 APPRPADTDEVRDFRFGGICGRYNTFTYLRAGSGR-YR-YQKVGYSWABGLTIDTSFIW 487
 Qy 432 L-LHK-KT--VAFDQKGPGLGYDIIAMDWNGPEWTFEYIGSASLSPYHLIDINKTIOM 486
 Db 488 ASPSAGPLRASRSEPCLONEVYSGVPGECWLCIPQPYEY-RIDEF--TCADGLGYW 545
 Qy 487 HG-KNNQVAVSVCTRDCLSGHRLVMSHHCCEPCPCGATPLNTSELTCOPCTEEM 545
 Db 546 PNASLTGCFELPOEYTRMGDAMAVGVTIACIGALATLFLVGVFNHNAIPYKASGREI 605
 Qy 546 ADEGSSACSRVTEFEGWHEPISLVLLANTLILLLIGAGLFAHRLHTPVRSAGRL 605
 Db 606 CYILGGLVLCYMTFVFAKSTAVCTLRGLGTAFCVYSAITLTKNRLARIFG-GA 664
 Qy 606 CRLMGLSLVAGSCSLSTFGFKPTVPACLLRQPLFSGLGFALISCLTIRSFQVLIIFKST 665
 Db 665 REGA-QRPPEFISPASOVALICLISGOLLIVAMLYVAEPCTEKAPRERREYVLRCH 723
 Qy 666 KPTPEYTHAONHAGIYIVS-STVHLFLCTLWLMKMPRPTREORPH-LVILECTE 723
 Db 724 RDA-SMGLSLAVNVLIALCTL-YAEKTRCPENFENAFICGTTTTCIIMLAFPIFY 781
 Qy 724 VMSVGLVAFANHLL-SISTFVCSYLKELPENYENACVFTSLHLHVSVAFTTMS 782
 Db 782 VMSDVRVQTTMVCVSVLSGVVGLCLPAKLIHLLFOPQKNVSH 828
 Qy 783 IYQGYLPAVNVLAGLALISGFS-GY-FLPKCYILCRBELNTEH 827

RESULT 14
 ENTRY JH0562 #type complete
 TITLE metabotropic glutamate receptor 3 precursor - rat
 ORGANISM Rattus norvegicus #common_name Norway rat
 DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998

ACCESSIONS
 REFERENCE JH0562
 #authors Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
 #journal Neuron (1992) 8:169-179
 #title A family of metabotropic glutamate receptors.
 #cross-references WJID:92110002
 #accession JH0562

#molecule_type mRNA
 #residues 1-879 #label TAN
 #experimental_source brain
 COMMENT This protein is coupled to a G protein and evokes a variety of functions by mediating intracellular signal transduction.
 CLASSIFICATION #superfamily metabotropic glutamate receptor 4
 KEYWORDS G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

FEATURE
 1-72 #domain signal sequence #status predicted #label SIG\
 23-879 #product metabotropic glutamate receptor 3 #status predicted #label MTR\
 577-599 #domain transmembrane #status predicted #label TRI\
 577-599

614-634 #domain transmembrane #status predicted #label TRI\
 646-664 #domain transmembrane #status predicted #label TRI\
 689-709 #domain transmembrane #status predicted #label TRI\
 735-756 #domain transmembrane #status predicted #label TRI\
 770-791 #domain transmembrane #status predicted #label TRI\
 804-828 #domain transmembrane #status predicted #label TRI\
 209,292,414,439 #binding_site carbohydrate (Asn) (covalent) #status predicted
 610,845 #binding_site phosphate (ser) (covalent) #status predicted

SUMMARY #length 879 #molecular_weight 98959 #checksum 5581

Query Match 11.9%; Score 759; DB 2; Length 879;
 Best Local Similarity 25.8%; Pred. No. 2,56e-118;
 Matches 206; Conservative 202; Mismatches 340; Indels 50; Gaps 44;

Db 57 GCRINE-D-RGQRLDAMFAIDELINKDNYLLPGKLGVLHIDTOSRQTYALEQLEVR 114
 Qy 63 CDRSDFNGHGHRLQARFVEEINNSTALLPNTLLEYLYDVS-ESSNYATLR-VP 120
 Db 115 ASLTRYDEAEYPCPGSYAIOENIPLLAGVIGSYSSVSIQVANTLRFOIPISTAST 174
 Qy 121 AQGGT-GHLE-X-Q-R-DLRHSSKYVA-LIGPNDTHAVTAALLSPFLMPLVSYEAS 173
 Db 175 SAKLSDKSRDYFAVTPDPDYQAAMAEILRFEMWTVSTVASEGDYGETGIEAFQEA 234
 Qy 174 SVLSGKRKFPFLRTITPSDKYQVEIVRLQSFQFWMSISLVGSDYGGQVQALFEIA 233
 Db 235 RLNRICIAEYVGSNIRKSDSYIRELQKPNR--VYVLFMSDSDSRELLAANRYN 292
 Qy 234 PRGICVAFKDVPLISA-QAGPRKQRMRLARATVVVFSNRHLAGVFFRSVLAN 292
 Db 293 -ASFVWASDGMGAOESYKSGSEHYAGAITLEASHVRODFRQSLNPNRNPNWF 351
 Qy 293 LIGKWIASEDAIATYITNPAGIIGT-VGVAIQ-RQVPLGKEFEESVQVAMGAP 350
 Db 352 RQFWBOKFOCSLQNK-RNHQVCDXHLAIDSSNYDOESKIMEVNVAVYAMAHALHKMOT 410
 Qy 351 RCPREGSW-CGTNOLCBECAFTTWNP-ELGAFMSAAVN-VYBAVYAVAGHLQGL-G 406
 Db 411 LCPNTTKLCDANKIIDGKLYEYLKINTAPRPNKGADSYAFDFPGDGMGXNPNF 470
 Qy 407 -CTSGT-C-A-R--GP-VYPMQLQIYKVNFLHK-KTVA-FDQKGPGLGYDIIA 454
 Db 471 LQOTGKSYLKVGHMA-ETLSLDV-D-S-IHW-SRNS-VPTSOCSDPAPNEMKNMOPGD 525
 Qy 455 WDMNGPEWTFEYIGSASLSPYHLIDINKTIOMKGNQVPVSVCTRDCLSGHRLVMSH 514
 Db 526 VCCWICICEPEYEY-VDEF-TCMDCGPGQWFTADLSCYNLPEDYIKMEDAMAIQVYI 583
 Qy 515 HCCFECMCEAGTFLNTSELHCOGTEEMAPDEGSSACFSRTVEFLGWHEPISLVLLA 574
 Db 584 AGLGFLCIVITVPIKNNMPLVNASGRELCYLLFVSVLSYCTFTFFIKRSPVICAL 643
 Qy 575 NTLLELLIGTAGLPAHRLHTPVVNSAGGRCLCELMGLSVAGSCSLYFFGKPTVPACLL 634
 Db 644 RLIGTSPFAICYALLTKTNCIARIP-GVYNGAQORPKFI-SPSSQVFCIGLILVIV 701
 Qy 635 RQPLSLSGAIFLSCLTIRSPOLVLIIFKSTKVPFFHTHMQNHAGIFVYVSSR-VHLE 693
 Db 702 MYSVLLIETP-GTRRYLPEKRETVILK-NVQDSKEISITVDVVLVILCTVYAFKTR 759
 Qy 694 LCLTWLAWMTPRPTREYO-RFPH-LVILECEVNSVGLVFAFANHLLISIFVCSYLGK 751
 Db 760 KCPENFNEKFGFMNTTCIWLAFLIYVTSDDYVQTTMKISLSGFFVLGCLF 819
 Qy 752 ELPENYENACVFTSLHLHVSVAFTTMSIYQGYLPAVNVLAGLALISGFS-GY-F 809
 Db 820 APKVHIVLEOPQKNVYTH 837
 Qy 810 LPKCYIILCRBELNTEH 827


```
RESULT 15
ENTRY 149142 #type complete
TITLE metabotropic glutamate receptor 8 - mouse
ORGANISM Mus musculus #common name house mouse
DATE 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change
13-Sep-1998

ACCESSIONS
REFERENCE 149142
#authors Duvoisin, R.M.; Zhang, C.; Ramonell, K.
#journal J. Neurosci. (1995) 15:3075-3083
#title A novel metabotropic glutamate receptor expressed in the
#refina and olfactory bulb.
#cross-references MIMD:95239344
#accession 149142
#status preliminary: translated from GB/EMBL/DBJ
#molecule_type mRNA
##residues 1-908 ##label RES
##cross-references EMBL:U17252; NID:g854728; PID:g854729

GENETICS
#gene mGluR8
CLASSIFICATION #superfamily metabotropic glutamate receptor 4
KEYWORDS neurotransmitter receptor
SUMMARY #length 908 #molecular_weight 101413 #checksum 2996

Query Match 11.6%; Score 740; DB 2; Length 908;
Best Local Similarity 24.6%; Pred. No. 1,51e-114;
Matches 210; Conservative 246; Mismatches 332; Indels 66; Gaps 52;

Db 17 LIAKFWILTMORTHQOEYAHSLRLDGIILGGLFPVHA---KG-ERG-V-PC--GDLK 68
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
14 LAVAYCWFASC-ORTES---SPGFSLPDGLAGLFLSHADCLQVRHRPLVTSQCRSDSF 69
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
69 KKGHLEMLVAIDQTNKDELSTLGVRIIDTCSDRTALAESITFVQALIEKDA 128
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
70 NGHGTHLFQAMRTVEEDINNSTALPNTILGELYDVCS--ESSNVATLR-VPA--OQGT 125
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
129 SDVKCANGDPPIFTKPKDISGIVGAASVSIMVANIILRFKIPDISASTAPELSDNTR 188
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
126 GHLE-MQRD--LRNHSSKVVALIGPDNTDHAVTALALSPMLPLVGYEASSVILSGRRK 182
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
189 YDFFSRVPPDSIQAMVDIVTALGNVYSTLASGNGYSGEYEAFTQISREIGVCIA 248
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
183 FPFSLRTIPSDKYQVEYIVRLQSFQWVWISLVGSDYQQLGVQALDELATPRG-ICVA 241
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
249 QSQKIPREPRGEFEKIKRLTFPNARA--VIMEFANEDDIRGILEAAKKL--NOSGHFIW 305
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
242 FKDVPLSAQAGD-PRQRMALRLARARITVYVFSNRH--LAGVFERSVVLANTLTKG-VW 298
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
306 IGSDSWG-SK-IAPVYQOEIEAGAVTILPKRASIDGFRYFRSRTLANNRRNWFAPFS 363
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
299 IASDEMAISTYITNPQIGIGTVLGAIOQRQ-VPLG-KEFEESYQAVMGAPR-T-CP 354
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
364 EGNFGCKSGSHGKRNHIKCTGLERIARDSSYEQSKVOFIDAVYSMAVALHMHKEL 423
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
355 EGSW-C-GTNQLCRECHAF-T-WN-MPELGAFMSAAYN-VYEAVYVAHGLHQLL-G- 406
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
424 CPQYIGLCPMWTIDGKELGYIRAVNENGSAGTPVTENNGDAPGRDIFQYQINNKT 483
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
407 CTS--GTCAR-GPYVPMQLLOQTKVNFLLHAKT-VAFDDKGDPLGYDITIAMDNQPEW 462
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
484 EYKLIQHMT-NOLHLKVED--MOWANREHTHPASVCSLPCKPGRKRTVKGVPCCMHGCR 540
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
463 TFEVIGSASLPYHLDINKIKIQHGKKNQVPVSCVTRDCLEGHRLVMGSHHCCFEQMP 522
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
541 CEGYNT-QVDEL-SCETLCPLDQRPINRTGCGQRLPIIKLEHSPAVAVPVLAIIIGIAT 598
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
523 CEAGTFLNTSELHTQCPGTEEMAPEGSSACFSRTVEFLGHEPISLVLLAANTLLDLLL 582
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
599 TFLVITFVRNDPTPIVASGRELSTVLTGFLCYSTIFLMAADPTIICSFRRIIFLIG 658
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
583 IGTAGLFAMRLHTPVVASAGRLCFLMLGSLVAGSCSLYSPFGKPTVPACLLRQPLFSLG 642
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
659 MCFSYALLTKTRNIRHIFQGGKSVTAPKFIIPASQLVITFSLIS--VOLLGVFWFVV 716
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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QY 643 FAIFLSCLTIRSFQVLIIEFKSTK-VPTFYHTWAQNHGAGIFVYSSVHFLCLTWLAM 701
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 717 DPHHTIIDYGEORTLPDENRAGYLKC-DISDLSLISGSIILMTYCTYAAIKTRGYPE 775
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 702 WTPPTREY--QR-F-P-HL-VIECTEVNSVGFVAFANILLISTFVCSYLGKELPE 755
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 776 TENEAKPIGFTWYTTCTIWLAFPIFEFGTAQSAEKMYIOTTTLTVSMS-LSASVSLGLY 834
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 756 NYNDAKCVTSLLHFPYSWLAFTMS-SIYQGS---YLPAVNVLAGIATLSGGS-G-YF 809
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 835 MPKVYIIIFHPEQN 848
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 810 LPKCYVILCRPELN 823
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Search completed: Fri Mar 17 13:16:00 2000
Job time : 48 secs.

CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SO SEQUENCE 1085 AA: 121170 MW: 6189757 CN:

Query Match 20.7%; Score 1316; DB 2; Length 1085;
Best Local Similarity 31.9%; Pred. No. 1.69e-100;
Matches 272; Conservative 234; Mismatches 273; Indels 73; Gaps 51;

DB 31 GDILGTFPIHFG-VAAKDDOLKSRPSEVCIRYNFRGFQMLAMFAIREINSPALL 89
QY 37 GDFLLAGFSIHADCIQVRRHPLVTSCDRSDS--FNGHYILFOAKRTVEINNSTALL 94
DB 90 PNMILGRIPIPTCNVSKALEATLSFAQNKIDSLNDEFNCSEHPISTIAVAGATGSG 149
QY 95 PNILGVELYOVCESSNVY-ATLRPAQOQTGHEMR--DLNHSKXVALLGPDTD 151
DB 150 ISTAVANLGLFIYPOVSYASSSRLSKNOFKSFLRTIPDEHQATMADITFYFRMW 209
QY 152 HAVTTAALLSPFLMPLVSYEASVILSGKRKPSFLRTIPSDKYQVEIYVRLQSGVWV 211
DB 210 VGTIAADDDVGRPGIEKREAEERDIDFSELSIQVSD-E-KIQVYVIONSTAKV 267
QY 212 ISLVGSGDYGQQLGVQALEELATPGICVARKDVVPLSAQGDPRMQRMLRARTV 271
DB 268 IVVSSGPDLEPLI-KEIVRRNITGRILWASEAMASSSLIMPEYFHYVGGTIGFGLKAG 326
QY 272 VVYFSN-RHLAGVFFRSVYLANLGKVAIASEDMA---IS-T-YITNVPG-IQ-GI--G 320
DB 327 QIPGFRFLQVHPRKSVHNGFAKEFMEETFNCHLQECAGKPLVDVFLRGHEGGARLS 386
QY 321 TVLVV-A-IQ--Q-RQ--VP-GL-KEF-EESY--VQ-AVMGA-P-----RTCPGEG-SW-C 359
DB 387 NSPTAFRLCGEENISSVERPYMDYTHLRISYVYLAVYSIAHALODIYICIGRGIFT 446
QY 360 -G-TN-O-LCECHAFITWNPPELGAFSMAVYVEVAVAHGLQLLC-----T 408
DB 447 NGSCADIKKVEAMQVLAHLRLHNTSNAGEVTEDECGLAGNSIINHLSPEDEGSI 506
QY 409 SGTA-RGPYPMQLLOQIYKVNFLHK-KVAFDDKDPGLGYDITIAMDNNGE-WT-F 464
DB 507 KEVGYVYVAKKGERLINDEKILMSGFSREVPSPNSRDLACTRGKIGIEPTCCFEC 566
QY 465 EVIS--SA-SLSPVHLIDINKTKIOMHGKNNQVPSVCTRDCEGHHR-LVYSGSHCCFEC 520
DB 567 VECGDGYSODETADACKDDDEMSNENHTSCIAKEIEPSTWEPGICATLNAVIGIF 626
QY 521 MPCBAGFLNLTSELHTQPCGTEEMAPEGSSACFSRTVEFLGWHPEISLVLLANTLL 580
DB 627 LTAFLVGVFIKFR-NPIVAKTNRELSYLLFSLCCFSSSLF-FIGEPQDMTRLROPA 684
QY 581 LLITGALFA-WRLHTPVVRAGRGLCFMLGSLVAG-SCGLYSFFGKPTYPALLLOPL 638
DB 685 FGISFVUCISCIWKNRVLVFE--AKIPTSEHRKMGWLOFLVFLCTEQVICA 742
QY 639 FSLQFAIFLSCLIRFSLQVLIIFKFSKVPF-FYHTWAQNHGACIFVIVSVTHVLC 697
DB 743 WLNAPPSRYRNHLEDEIIFITCHEGSLMALGFLIGTC-LLAICGFF-AFSSRLPE 800
QY 698 WLAAMTRPREFORPHPLVLECTEVN--SVGFLVAFAHNILLISTIFVCSYGLKEP 755
DB 801 NFNEAKFIITSMILFIIVMISFIPAYASTY-GKPVSAEVAITLAASGLLACIFFNKV 859
QY 756 NYNKAQVTSLLHFWSWIAFFTM-SSTYGSLPAVNVLAGLATLSGGISGIFLRKY 814
DB 860 ILFKPSRNTIE 871
QY 815 VILCRPELNTE 826

RESULT 5 STANDARD: PRT: 1085 AA.
ID US-08-353-784-5
XX

AC xxxxxx

DT

XX

DE

Sequence 5, Application US/08353784

Sequence 5, Application US/08353784

Patent No. 6011068

GENERAL INFORMATION:

APPLICANT: Edward F. Nemetz, Edward M.

APPLICANT: Brown, Steven C. Hebert, Manuel

APPLICANT: Bradford C. Van Wageningen, Manuel

APPLICANT: F. Balandrin, Forrest H. Fuller,

APPLICANT: Eric G. Delmar, and Scott T. Moe

TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE

MOLECULES

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: First Interstate World Center

STREET: Suite 4700

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: FASTSEQ

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/353,784

FILING DATE: 9 December, 1994

CLASSIFICATION: 514

Prior Application DATA:

Prior Application DATA: including application

Prior Application DATA: described below: 8

APPLICATION NUMBER: PCT/US/94/12117

FILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 23 August, 1994

APPLICATION NUMBER: U.S. 08/141,248

FILING DATE: 22 October, 1993

APPLICATION NUMBER: U.S. 08/009,389

FILING DATE: 23 February, 1993

APPLICATION NUMBER: U.S. 08/017,127

FILING DATE: 12 February, 1993

APPLICATION NUMBER: U.S. 07/934,161

FILING DATE: 21 August, 1992

APPLICATION NUMBER: U.S. 07/834,044

FILING DATE: 11 February, 1992

APPLICATION NUMBER: U.S. 07/749,451

FILING DATE: 23 August, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Hebert, Sheldon O.

REGISTRATION NUMBER: 38,179

REFERENCE/DOCKET NUMBER: 209/069

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1085 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 1085 AA: 121170 MW: 6189757 CN:

Query Match 20.7%; Score 1316; DB 3; Length 1035;
Best Local Similarity 31.9%; Pred. No. 1.69e-100;
Matches 272; Conservative 234; Mismatches 273; Indels 73; Gaps 51;

D	b	267	IIVNSGGDLEPLI-KETVLRNINIGKIMLASEAMSSSLIMPQYFNHYGCTIGFALAK	322
O	y	272	VWFSN-RHLGVEFRSRYVLNLGKWIASEDMA----IS-T-YTNVP-G-IO-GI--G	320
D	b	326	QIPGEFREFLKVHPKSYHNGFAKEFWETRNCHLOEGCAKGPLVDITFLRGHESGDRFS	385
O	y	321	TVLG-----VA-IQQHQ--VP-GI-KEF-BESY-----VO-AVMGA-P-----RCPPE-GSM--	358
D	b	386	NSSIAFRPLCLGDENISSVEPRPIDTYLRLSTNYVLYAIAARLDITYCLEGRGLFT	445
O	y	359	-CGTN-Q-LCEBCHAFTTMNPBELGAFMSAANYTEAVYAAGLMOL--L-GC--T	408
D	b	446	NGSCADIKKYAAOVILKRLRHNFNTNNNGEQVTDECCDLVGANSIIWHLSPPDGSIWF	505
O	y	409	SCTCA-RKPYPVPMQLOOIYYKNFLHR-KTVAPDDKGDPGLGYDIIDAMDNGPE-WT-F	466
D	b	506	KEYGVYNYAKKERLFINEEKILMSGSRVFPSPNCSDRCAGTRKGIIERGEPTCCFEC	565
O	y	465	EVIQ--SA-SISPVLHDINKTKIQHGKGNNOVPVSVCRTDLCGHHR-LVWGSHCCFEC	520
D	b	566	VECPDGEISDETASACKPCDDFMSENHNHSCIAREEFISTEPFGIALTLPAVLGI	622
O	y	521	MPCAGTFLMNTSELTQPCPGCTEEMAPGSACSCEFRTVEFLGMHBPISTVLANTLL	580
D	b	626	LTAFLVGFIRKFR-NTPVKATNRSLSTLLFLSLCCFSSSLF-FIGPODWTCRLROPA	683
O	y	581	LLIAGAGIFA-WRLHTPYVRBSAGGLCTLMLGSLVAG-SCILYSFPGKPTYPACILNQPL	633
D	b	684	FGISFVLCISCIILVKTNRVLLVF-E-AKIPTSFRKKMGWLQELVFLCTFMOIVICI	743
O	y	639	FSLGAIPLSCLITTSIFSOVLIIFFKSTKVPF-FYHTMAQNHGAGIFIVSSTVHLFCLT	697
D	b	742	WLYTAPPSYINGOELEDIIFITCHESSLMLGLPITGC-LLAICIFF-AFSCRULPE	799
O	y	698	WLAMTPTPTREYOEPFHLVILECTEVN-SVGLVAHAHHLLISITFYCSYLKLEPE	755
D	b	800	NFNKAFTTFMLLFEFIYMWISFIPAYASTY-GKFVASVEYTAIIAASRGLACIFFNKY	858
O	y	756	NYNEMKCTVELLLHFWSMIAFFTW-SSIYGSYLPANVYLAGLATLSGSGIFLPCXY	814
D	b	859	IILFKPSRNTIE 870	
O	y	815	VILCRPELNTE 826	
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ID		US-08-485-588-7		
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AC				
XX				
XX				
XX				
DE		Sequence 7, Application US/08485588		
XX				
XX		Sequence 7, Application US/08485588		
CC		Patent No. 5688938		
CC		GENERAL INFORMATION:		
CC		APPLICANT: Edward M. Brown		
CC		APPLICANT: Steven C. Hebert		
CC		APPLICANT: Forrest H. Fuller		
CC		APPLICANT: James B. Garrett, Jr.		
CC		TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE		
CC		TITLE OF INVENTION: MOLECULES		
CC		NUMBER OF SEQUENCES: 20		
CC		CORRESPONDENCE ADDRESS:		
CC		ADDRESSEE: Lyon & Lyon		
CC		STREET: First Interstate World Center		
CC		STREET: Suite 4700		
CC		STREET: 633 West Fifth Street		
CC		CITY: Los Angeles		
CC		STATE: California		
CC		COUNTRY: USA		

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CC      ZIP: 90071
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: FASTSEQ
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/485,588
CC      FILING DATE: 7 June, 1995
CC      CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:
CC      PRIOR APPLICATION DATA: including application
CC      PRIOR APPLICATION DATA: described below: 9
CC      APPLICATION NUMBER: 08/353,784
CC      FILING DATE: 9 December, 1994
CC      APPLICATION NUMBER: PCT/US/94/12117
CC      FILING DATE: 21 October, 1994
CC      APPLICATION NUMBER: U.S. 08/292,827
CC      FILING DATE: 23 August, 1994
CC      APPLICATION NUMBER: U.S. 08/141,248
CC      FILING DATE: 22 October, 1993
CC      APPLICATION NUMBER: U.S. 08/009,389
CC      FILING DATE: 23 February, 1993
CC      APPLICATION NUMBER: U.S. 08/017,127
CC      FILING DATE: 12 February, 1993
CC      APPLICATION NUMBER: U.S. 07/934,161
CC      FILING DATE: 21 August, 1992
CC      APPLICATION NUMBER: U.S. 07/834,044
CC      FILING DATE: 11 February, 1992
CC      APPLICATION NUMBER: U.S. 07/749,451
CC      FILING DATE: 23 August, 1991
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Heber, Sheldon O.
CC      REGISTRATION NUMBER: 38,179
CC      REFERENCE/DOCKET NUMBER: 213/005
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (213) 489-1600
CC      TELEFAX: (213) 955-0440
CC      TELEX: 67-3510
CC      INFORMATION FOR SEQ ID NO: 7:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 1078 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 1078 AA; 120573 MW; 6153012 CN;
SQ
Query Match          20.3%; Score 1293; DB I; Length 1078;
Best Local Similarity 31.8%; Pred. No. 1.70e-98;
Matches 271; Conservative 224; Mismatches 274; Indels 73; Gaps 48
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QY 409 SGTCA-RGVPYMWQLQOIKYKNFLHK-KTVAFDKGDPLGYDIAMDNGPE-WT-F 464
 DB 506 KEVGYNYAKKGERLFINNEKILMSGFSREVPFNSRDCIAGTRKGIIEGPPCCFEC 565
 QY 465 EVIG--SA-SLSPVHLDINKTKIOWHGKNNQVPVSVCTRDCEGHR-LVMSGHCCFEC 520
 DB 566 VECDEYDETDASACNCPDDFMSNENHTSCIAKEIEFLSWTEPFGALTLFAVLGIF 625
 QY 521 MCEAGTFINTSELHTCOGCTEEMAPDESSACFSRTVELGWHERPISLVLAANLULL 580
 DB 626 LTAFLVGVITKR-NTPYKATNRELSTLLSLCCFSSSLF-PIGEPODWTCLRQRA 683
 QY 581 LIGTAGLFA-WRLHTPVRSAGRCLFLMGLSLAG-SCSLSPFGKPTVPACLLRPL 638
 DB 684 FGISEVLCISLIVKTNRLVLEVE-AKIPTSRHRKMWGLQFLVPLCTEFOIYCVI 741
 QY 639 FSGGFIFISCLTRFQVLYIKFESTKVPF-FYHTMAONHGAGIVVSYVHLELCLT 697
 DB 742 WDTAPSSYRNOELDEDEIFITCHEGSLMALGFLGYTC-LMAACFFP-AFKSRKLE 799
 QY 698 WLAAMTPTREYQRPPLVILECTEVN--SVGFLVAFANHLISITFCVSLGKLEPE 755
 DB 800 NNEAKFTFMSLIFIVISFIPAASTY-GKFSVAVEYIALAASFGILACIFPNKIY 858
 QY 756 NYNEACVTFSLHLFVSIAFPTM-SIYQSGYLPAVNYLAGLATLSGGFSGYFLPKCY 814
 DB 859 ILFKPSRTIE 870
 QY 815 VILCREPLNTE 826

RESULT 10
 ID US-08-480-751-7 STANDARD; PRt: 1078 AA.

AC xxxxxx

DE Sequence 7, Application US/08480751

CC Sequence 7, Application US/08480751

CC Patent No. 5858684

CC GENERAL INFORMATION:

CC APPLICANT: Edward F. Nemeth

CC APPLICANT: Edward M. Brown

CC APPLICANT: Steven C. Hebert

CC APPLICANT: Forrest H. Fuller

CC APPLICANT: James E. Garrett, Jr.

CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE

CC NUMBER OF SEQUENCES: 20

CC CORRESPONDENCE ADDRESS:

CC ADDRESS: Lyon & Lyon

CC STREET: First Interstate World Center

CC STREET: Suite 4700

CC STREET: 633 West Fifth Street

CC CITY: Los Angeles

CC STATE: California

CC COUNTRY: USA

CC ZIP: 90071

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: FASTSEQ

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/480.751

CC FILING DATE: 7 June, 1995

CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:

CC PRIOR APPLICATION DATA: Including application

CC PRIOR APPLICATION DATA: described below: 9

CC APPLICATION NUMBER: 08/353.784

CC FILING DATE: 9 December, 1994
 CC APPLICATION NUMBER: PCT/US/94/12117
 CC FILING DATE: 21 October, 1994
 CC APPLICATION NUMBER: U.S. 08/292,827
 CC FILING DATE: 23 August, 1994
 CC APPLICATION NUMBER: U.S. 08/141,248
 CC FILING DATE: 22 October, 1993
 CC APPLICATION NUMBER: U.S. 08/009,389
 CC FILING DATE: 23 February, 1993
 CC APPLICATION NUMBER: U.S. 08/017,127
 CC FILING DATE: 12 February, 1993
 CC APPLICATION NUMBER: U.S. 07/934,161
 CC FILING DATE: 21 August, 1992
 CC APPLICATION NUMBER: U.S. 07/834,044
 CC FILING DATE: 11 February, 1992
 CC APPLICATION NUMBER: U.S. 07/749,451
 CC FILING DATE: 23 August, 1991
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Heber, Sheldon O.
 CC REGISTRATION NUMBER: 38,179
 CC REFERENCE/DOCKET NUMBER: 213/004
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (213) 489-1600
 CC TELEFAX: (213) 955-0440
 CC TELEX: 67-3510
 CC INFORMATION FOR SEQ ID NO: 7:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 1078 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 1078 AA; 120573 MW; 6153012 CN;

Query Match 20.3%; Score 1293; DB 2; Length 1078;
 Best Local Similarity 31.8%; Pred. No. 1,70e-98;
 Matches 271; Conservative 234; Mismatches 274; Indels 73; Gaps 48;

DB 30 GDIIIGLEPIIFG-VAAKDDLKSPESVEICIRNFGFMLOAMPAIEEINSPALL 88
 QY 37 GDFLAGLFSIADLCQVRRHPLVYSCDRSDS-FNGSGYHIFQAMRTVEEINNSTALL 94
 DB 89 PNLITGRIPTCNTVSKALEATLSFVAONKIDSLNLDFFCSEHIPSITIAVVGATSG 148
 QY 95 PNITGELYDYCVSSSNVY-ATLRVPAQGGHLEMR-DLRHSSKVALIIPDNTD 151
 DB 149 VSTANLILGLYIPQVSYASSSLSKNOFKSLRTIPNDEHQTAMADIIEFRNMW 208
 QY 152 HAVTTAALLSPMLPLVSYEASSVILSGKRKFPFLRTIIPSDKYOVEIVRLLOSFGWV 211
 DB 209 VGTIADDDYGRPGIEKREAEEDICIDFSELISQYDEE--IQHVEYIQNSTAKV 266
 QY 212 ISLVSYGDYGLQVQALELATPRTGICVARKDVPLAQAGDPMMQMLRLAARTTV 271
 DB 267 IVFSSGPDLEPI-KEIVRRNITKILWASEWASSSLIAMPQYFHVGGTIGPALAG 325
 QY 272 VVFFSN-RHLAGVFRSYVLANLTGKWIASEDMA---IS-T-YITNVP-GI-G 320
 DB 326 QIPGREFPLAKYHPKRSVHNGFAKEFMEETPCHQDEAKGRLPYDTLRLGHESGDFS 385
 QY 321 TVLG---VA-IQORQ-VP-GI-KEF-BESY--VQ-AVMA-GP-----RCPE-GSW-- 358
 DB 386 NSSTFRPLCTGDEMISSETPYIDYTHLRISYNYLVAVYSIAHLDIYCLPQGLFT 445
 QY 359 -CGTN-Q-LRCRCHAFFTWNPDELGAFMSAANYEAVYAVAGLHDJ---L-GC---T 408
 DB 446 NSCADIRKVEAMOVLLKHLRLNFTNNMGEQVTEDECGDLGVNTSIIMHLSPEDESVF 505
 QY 409 SGTCA-RGVPYMWQLQOIKYKNFLHK-KTVAFDKGDPLGYDIAMDNGPE-WT-F 464
 DB 506 KEVGYNYAKKGERLFINNEKILMSGFSREVPFNSRDCIAGTRKGIIEGPPCCFEC 565
 QY 465 EVIG--SA-SLSPVHLDINKTKIOWHGKNNQVPVSVCTRDCEGHR-LVMSGHCCFEC 520

QY	698	WLMWTPPTREYQEPHVLILECTEVN-VSGFLVFAHNLISSTFWOSYLGKDLPE	754
Db	800	NFNENKFTFSFLIFWISFIPRYASTY-KREVSANEVATLAASEGLACIFENKRY	858
QY	756	NYNENKCYTFSLHLFEVMAFFTM-SSYOGSYLPAVNVLAGLATLSGSPGYFLPKCY	814
Db	859	IILFKSRNTIEEVRSSATAHA	880
QY	815	VILCRPELNTNEHFOASIQDYT	836
RESULT	13		
ID	US-08-353-784-8	STANDARD:	PRT: 1079 AA.
XX	xxxxxx		
DE	Sequence 8, Application US/08353784		
XX			
CC	Sequence 8, Application US/08353784		
CC	Patent No. 6011068		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Edward F. Nemeth, Edward M.		
CC	APPLICANT: Brown, Steven C, Hebert,		
CC	APPLICANT: Bradford C. Van Wageningen, Manuel		
CC	APPLICANT: F. Balandrin, Forrest H. Fuller,		
CC	APPLICANT: Eric G. Delmar, and Scott T. Moe		
CC	TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE		
CC	TITLE OF INVENTION: MOLECULES		
CC	NUMBER OF SEQUENCES: 20		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: Lyon & Lyon		
CC	STREET: First Interstate World Center		
CC	STREET: Suite 4700		
CC	STREET: 633 West Fifth Street		
CC	CITY: Los Angeles		
CC	STATE: California		
CC	COUNTRY: USA		
CC	ZIP: 90071		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage		
CC	COMPUTER: IBM PC compatible		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	SOFTWARE: FASTSEQ		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/08/353,784		
CC	FILING DATE: 9 December, 1994		
CC	CLASSIFICATION: 514		
CC	PRIOR APPLICATION DATA:		
CC	PRIOR APPLICATION DATA: including application		
CC	PRIOR APPLICATION DATA: described below: 8		
CC	APPLICATION NUMBER: PCT/US/94/12117		
CC	FILING DATE: 21 October, 1994		
CC	APPLICATION NUMBER: U.S. 08/292,827		
CC	FILING DATE: 23 August, 1994		
CC	APPLICATION NUMBER: U.S. 08/141,248		
CC	FILING DATE: 22 October, 1993		
CC	APPLICATION NUMBER: U.S. 08/009,389		
CC	FILING DATE: 23 February, 1993		
CC	APPLICATION NUMBER: U.S. 08/017,127		
CC	FILING DATE: 12 February, 1993		
CC	APPLICATION NUMBER: U.S. 07/934,161		
CC	FILING DATE: 21 August, 1992		
CC	APPLICATION NUMBER: U.S. 07/834,044		
CC	FILING DATE: 11 February, 1992		
CC	APPLICATION NUMBER: U.S. 07/749,451		
CC	FILING DATE: 23 August, 1991		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Heber, Sheldon O.		
CC	REGISTRATION NUMBER: 38,179		
CC	REFERENCE/DOCKET NUMBER: 209/069		
CC	TELECOMMUNICATION INFORMATION:		

CC	TELEPHONE: (213) 489-1600
CC	TELEFAX: (213) 955-0440
CC	TELEX: 67-3510
CC	INFORMATION FOR SEQ ID NO: 8:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 1079 amino acids
CC	Type: amino acid
CC	TOPOLOGY: linear
CC	MOLECULE TYPE: protein
CC	SEQUENCE 1079 AA: 120867 MW: 6054255 CN:
Query Match	20.1%; Score 1282; DB 3; Length 1079;
Best Local Similarity	31.2%; Pred. No. 1,54e-97;
Matches 269; Conservative	240; Mismatches 280; Indels 73; Gaps 50;
Db	30 GDIIIGGFLPFFHFQ-VAAKDQDLKSRDEVEECIRYNEGRFWIQAMIFAIEEINSSPRL 88
Oy	37 GDPLLAGIFSLHACQLQRRHPRYLTSCDSDSDS--FNCHGHLQAMRYEEELNNSTALL 94
Db	89 PNMILGRIFEDTCTVSKALEPATISFYAQNKIDSINDEFCONSEHIPPSTIAVVGATGSG 148
Oy	95 PNILGLYGLYDVCCSESSNV-ATLRPAQCGTGHEWQR--DLRNNHSSKVALIGPDND 151
Db	149 VSTAVANLIGFIYPOVSYASSSKSLNKNQOYSFLRTINDEHQATAMDIETFRMKN 208
Oy	152 HAVTTAALSLFLMPDVSEASVILSGKKRPFELTIPSDKYQVEVIRLLQSGWGW 211
Db	209 VGTIAADDDYRPGIEKFEFEAEERDQIDFSELSQSPDEE-VIOUYEVQNSAKY 266
Oy	212 ISLVGYSDYQQLGVALSELATRGICVAFKDYVPLSAGQDPFRQRMRLARARTIV 271
Db	267 IVTFSSGDDLEPLI-KEIVRRNYTGRIWLASEMAWASSSLIAMEEYFHVYGGTIGFLKAG 325
Oy	272 VVFESEN-RHLAGVFFR3SVLANLTKGWKIASEDMA---IS-T-YITNPG-IQ-GI-G 320
Db	326 QIQGFREFLOVHRKSYVHNGFAKEFEFEETFNCHDQAGPLPVDTFYRSHDEGNRL 385
Oy	321 TVLGV-A-IQ--Q-RQ--VP-GI-KEF-EERY--VQ-AVWGA-P-----RTCEGS-W-- 358
Db	386 NSTAFREPLCTGDEINISVEFPYDYDEHLISYVAVYSIAHALODITYCIPGRGLFT 445
Oy	359 -CGIN-Q-LCECHAFPTWNNPELGASMSAAINVEAYVAVHGHQL--L-GC--T 408
Db	446 NGSCADIKKYEAMQVLKHLRLNFTNNMGBOVTFDECGDLVGVYSIIMHLSPEDSIVF 505
Oy	409 SGCTA-RGPVYPQGLQIYKVNLLHK-KTVAFDKQDGLPYGDIIMDMWNPE-WT-F 464
Db	506 KEVGYYNVYAKKGERLTINEBKILMSGFSSEVPSPNCSRDDCAQIRKGIIEGPTCCFEC 565
Oy	455 EVIG--SA-SLSPHLDINKTKIDMGHKNQVPSVCTRCLEIGHNR-IVMGSHHCCFEC 520
Db	566 VECDDGEVSGSDASADCKCPDDPWSXENNTSCIAKEIEFLATTEPFGIALTFAYLGI 625
Oy	521 MCPDAGTFLNTSELHTQPCGTETEMAEQSSACFSKVEFLGMEHPISTVLANTLTL 580
Db	626 LTAFLVGLVFIKFR-NPIYKATNRELSYLLLFGLLCCFSSSLF-FIGEPQDMTCRLRPA 683
Oy	581 LLITAGIGFA-WRIHTVVSAGRGCLCFMLGSLVAG-SCSLSPFGKRPVPRACILRQL 638
Db	684 FGISFVLCISCIILKRVZLVFE-AKIDTSFRKMWGINOLFVLCFQEMQLICIT 741
Oy	639 FSLGFAIFLSCLTIRSPOLVIEKFSIKVPT-FYHTMAQHGAGIFIVASSVTHFLCLT 697
Db	742 WLYTAPSSSYNNHLEDEIFITICBESLMALSLIGYTC-LLAALCFPP-AKSKLPE 799
Oy	698 WLAMTRPFRPREYORPFDHILLECTEVN--SVGFLVAFANILLSTIVCSYIGLELPE 755
Db	800 NFENAKEITEEMLFIFWIMISFIPAYSTR-GKVSAAVEVITAIASFGIACIFENKY 858
Oy	756 NYNNAKCVTSILHHEWYIAFLFM-SSTIQSGILPRAVNYLAGLATLISGFSGYFLPKCY 814
Db	859 IILFSPRNTIEVRSIAAHA 880


```

XX DE Sequence 8, Application US/00485588
XX CC Sequence 8, Application US/00485588
XX CC Patent No. 5688938
CC GENERAL INFORMATION:
CC APPLICANT: Edward M. Brown
CC APPLICANT: Steven C. Hebert
CC APPLICANT: Forrest R. Fuller
CC APPLICANT: James E. Garrett, Jr.
CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
CC TITLE OF INVENTION: MOLECULES
CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: First Interstate World Center
CC STREET: Suite 4700
CC STREET: 633 West Fifth Street
CC City: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: FASTSEQ
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/485,588
CC FILING DATE: 7 June, 1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC PRIOR APPLICATION DATA: including application
CC PRIOR APPLICATION DATA: described below: 9
CC APPLICATION NUMBER: 08/353,784
CC FILING DATE: 9 December, 1994
CC APPLICATION NUMBER: PCT/US/94/12117
CC FILING DATE: 21 October, 1994
CC APPLICATION NUMBER: U.S. 08/292,827
CC FILING DATE: 23 August, 1994
CC APPLICATION NUMBER: U.S. 08/141,248
CC FILING DATE: 22 October, 1993
CC APPLICATION NUMBER: U.S. 08/009,389
CC FILING DATE: 23 February, 1993
CC APPLICATION NUMBER: U.S. 08/017,127
CC FILING DATE: 12 February, 1993
CC APPLICATION NUMBER: U.S. 07/934,161
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CC APPLICATION NUMBER: U.S. 07/834,044
CC FILING DATE: 11 February, 1992
CC APPLICATION NUMBER: U.S. 07/749,451
CC FILING DATE: 23 August, 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hebert, Sheldon O.
CC REGISTRATION NUMBER: 38,179
CC REFERENCE/DOCKET NUMBER: 213/005
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1079 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQ SEQUENCE 1079 AA: 120867 MW: 6054255 CN:

Query Match 20.1%; Score 1282; DA 1; Length 1079;
Best Local Similarity 31.2%; Pred. No.1,54e-97;
Matches 269; Conservative 240; Mismatches 280; Indels 73; Gaps 50.

```

Dh	30	GDILIGLFPHFG-VAAKODDKSRESVBCIYNRGRGRMLOAMIFALEEINSSSLL	88
Oy	37	GDFLLAGFSLHADLOVRRHPRPLVTSODRSDS--FNHGYSILQVQMPFVTEINNSTALL	94
Dh	89	PNMTIGRIFPDCTVSKALPATLSPFAONKIDSLNDFEONCSSEHPISTIAVYGATSG	148
Oy	95	PNITIGLYLVYCESSSVNY-ATLRVAQOOGTGHLEQOR--DLRNHSSKVALIGPNTD	151
Dh	149	VSTAVANLLGLFPIPOVSYASSSSRLSNKOYSFLETPINDENHOATMADIIEFRMN	208
Oy	152	HAVTAAULSPFLMPLVSYEASVSLSGKRFPSEFLTIPSDKQVEIVIRLLQSPGMW	211
Dh	209	VGTIADDDYRPRGIEKFEFEAEERDICIDFSELISQSBEEF--IOQVEVIONSTAKY	266
Oy	212	ISLVSYDYQDQLQVQALEELATPRGICIVAFKDVYP--SAQAGPRMQRMMLRLARARTY	271
Dh	267	IYVESSGDLEPLI-KEIVRNITIGRMIMASEMASSSLAMPREYHVAGGTIAGFKAG	325
Oy	272	IYVESN-RHLGVEFFRSVLANLIGKWMISEDA---IS-T-YITNVG-IQ-G--G	320
Dh	326	QIPGREFLQVYHRKSYHNGFAKEFMEEFENCHLOEGAKGPLVDPTFVSHEEGNRLL	389
Oy	321	TYLGV-A-IQ--Q-RQ-VP-GL-KEF-EBSY---VQ-AWGA-F-----KTCPRGS-W--	358
Dh	386	NSSTAFRLCTGDENINSVETPYMDYEHRLISYNVLYAVYSIAHALODIYTCPLRGFLT	445
Oy	359	-CGTN-Q-ICRECHAFITMNPBELGAFSMAAYVYEAUYAAVAHGLHQL--L-GC--T	408
Dh	446	NGSCADIKYVAMOVAKHLRLNTNNKGEBYTFDECGDLVGNSTIINHLSPPDSIVF	505
Oy	409	SGTCA-RGPVPMOOLQOIKYVNFLLHR-KTVAEDDGDPLGYDIIAMOMNGPE-WT-F	464
Dh	506	KEVGYNYVYAKGGERLFINKEKILMSGFSREVPFNSRQOQATRKGIIEGEPTCFEC	565
Oy	465	EYIG--SA-SLSPYHLDIKTKIOMHGKNQVPYVCTRDLSEBHR-LVMGSHCCFEC	520
Dh	556	VECPDGEVSGETDASACDKCPDDEFSWSEKNT--SCIAKSEFELAWTEPGIALTLFVGLIF	625
Oy	521	MPCEGTFPLNTSELHQPOCTGEWAPRGSACSRTVEFGLWHEPISTIVLANTLTLL	580
Dh	626	LTAFLVGLFIFR-NTPIYKATNELLSLLFSLCCFSSLP-FIEPDQMTCLRQPA	683
Oy	581	LLIGTAGLFA-WRHTHPVVRAGRGLOFLMIGSLVAG-SCLXSFEKRPVPAOLHQPL	638
Dh	684	FGISVLCISCIKTNVLLVFE--AKIPSEFRKMGNLQELFLEFCTFMOLICII	741
Oy	639	FSLGAIFLSCCT--SFOVLIIFFSTKVP-PTHYTAONHGAGIYIVASYVHLFCLT	697
Dh	742	WLTYAPPSYRNHELEDIIFITHEGSLMALGSLIYTC-LLAALOFFF-AFKSRKLP	799
Oy	658	WLAMTTPRPTSEYQRPFLVILLECTEVN--SVGLVFAHNHLLISTIFVCSYIGKLP	755
Dh	800	NFNEAKPTFSMLFFIYWISFIDAVASTY-GRFVSAVEYAIATIASGGLACIFENKY	858
Oy	756	NYNEAKCTFESLLHFVSMIAFFTM--SSIYGSYLPAVNVNLAGIATISGSGSYFLPKCY	814
Dh	859	IILFKPSKNTIEVRSSTAAHA	880
Oy	815	VILCRPELNTNEHFOADYOT	836

Search completed: Fri Mar 17 13:23:19 2000
Job time : 32 secs.

 WISEWISER (TM)

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MPearch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:13:13 2000; Maspar time 39.37 Seconds

Tabular output not generated. 506,520 Million cell updates/sec

Title: >US-09-361-652-2
 Description: (1-842) from US09361652.pep
 Perfect Score: 6366
 Sequence: 1 MLFWAHLHLJSLQLAAYCW.....NTEHFOASIDYTRCGTT 842

Scoring table: PAM 150
 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq36
 1:geneseqp

Statistics: Mean 38.664; Variance 175.009; scale 0.221

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description	Pred. No.
1	1316	20.7	1085	Bovine parathyroid cal	2.60e-107
2	1316	20.7	1085	Bovine parathyroid cal	2.60e-107
3	1316	20.7	1085	Bovine parathyroid cal	2.60e-107
4	1293	20.3	1078	Human parathyroid calc	3.67e-105
5	1293	20.3	1078	Human parathyroid calc	3.67e-105
6	1293	20.3	1078	Human parathyroid calc	3.67e-105
7	1293	20.3	1078	Human parathyroid calc	3.67e-105
8	1282	20.1	1079	Rat kidney extracellular	3.91e-104
9	1282	20.1	1079	Rat kidney extracellular	3.91e-104
10	1282	20.1	1079	Rat kidney extracellular	3.91e-104
11	1282	20.1	1079	Rat kidney extracellular	3.91e-104
12	1204	18.9	1088	Dogfish shark kidney c	7.44e-97
13	1202	18.9	1088	Human parathyroid cell	1.14e-96
14	1201	18.9	1088	Human parathyroid cell	1.14e-96
15	1201	18.9	1088	Human parathyroid cell	1.14e-96
16	1201	18.9	1088	Human parathyroid cell	1.14e-96
17	1069	15.6	1058	Amino acid sequence of	2.73e-84
18	993	15.6	1058	Amino acid sequence of	2.73e-84
19	974	15.3	850	Rat pheromone receptor	1.77e-75
20	832	13.1	850	Mouse pheromone recept	2.29e-62
21	814	12.8	1056	Amino acid sequence of	1.03e-60
22	810	12.7	906	GUO-G-R subtype 1b.	2.41e-60
23	806	12.7	1180	Human mcgJUR5a.	5.63e-60

ALIGNMENTS

RESULT 1
 ID W89563 standard; Protein: 1085 AA.
 AC W89563;
 DT 19-MAR-1999 (first entry)
 DE Bovine parathyroid calcium receptor BopCar 1.
 KW calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;
 KW spinal cord injury; hypoxia induced nerve cell damage; cardiac arrest;
 KW neonatal distress; neurodegenerative disease; Alzheimer's disease;
 KW Huntington's disease; Parkinson's disease; dementia; muscle tension;
 KW depression; anxiety.
 OS Bos sp.
 PN US5658684-A.
 PD 12-JAN-1999.
 PF 07-JUN-1995; 480751.
 PR 23-AUG-1991; US-749451.
 PR 11-FEB-1992; US-834044.
 PR 21-AUG-1993; US-934161.
 PR 12-FEB-1993; US-017127.
 PR 23-FEB-1993; US-009389.
 PR 22-OCT-1993; US-141248.
 PR 19-AUG-1994; US-292827.
 PR 21-OCT-1994; WO-012117.
 PR 08-DEC-1994; US-353784.
 PA (BGM) BRIGHAM & WOMENS HOSPITAL.
 PA (NPSF-) NPS PHARM INC.
 PI Balandrin MF, Brown EM, Del Mar EG, Garrett JE,
 PI Hebert SC, Nemeth EF, Van Wagenen BC;
 DR WPI: 99-119871/10.
 DR N-PDB: V82483.
 PT Screening for calcium receptor-active compounds - by recombinant
 PT expression of nucleic acid encoding calcium receptor and determining
 PT the effect of compounds on calcium receptor activity
 PT Claim 1; Fig 47; 176pp; English.
 CC A method has been developed of screening for a compound able to affect
 CC one or more activities of a calcium receptor (CR) comprises: (A)
 CC contacting a recombinant cell with a test compound, where the
 CC recombinant cell comprises a recombinant nucleic acid expressing the CR,
 CC provided that the cell does not have functional CR expression from
 CC endogenous nucleic acid; (B) determining the ability of the test
 CC compound to affect one or more activities of the calcium receptor; and
 CC (C) comparing the ability with the ability of the test compound to
 CC affect the one or more CR activities in a cell not comprising the
 CC recombinant nucleic acid. The present sequence represents bovine
 CC parathyroid CR, designated a BopCar 1. The nucleic acid sequence of
 CC BopCar 1 can be used as part of the recombinant nucleic acid in the

24	810	12.7	1199	1	R25080	GUO-G-R subtype 1a.	2.41e-60
25	807	12.7	1212	1	R64254	Human mcgJUR5b.	4.55e-50
26	800	12.6	877	1	R64255	Human mcgJUR5c.	2.00e-50
27	802	12.6	906	1	R64250	Human mcgJUR1B.	1.31e-50
28	804	12.6	912	1	R82658	Human mcgJUR4.	8.55e-50
29	801	12.6	912	1	R72092	Human mcgJUR4.	1.62e-50
30	800	12.6	1056	1	W25765	Amino acid sequence of	2.00e-50
31	800	12.6	1194	1	R42199	HsmGJUR1.	2.00e-50
32	798	12.5	803	1	W94920	Mouse pheromone recept	3.06e-50
33	785	12.3	865	1	W94920	Rat pheromone receptor	4.70e-50
34	778	12.2	872	1	R95052	Human metabotropic glu	2.10e-50
35	764	12.0	877	1	R82657	Human mcgJUR3.	4.03e-50
36	757	11.9	872	1	R89580	Metabotropic glutamate	1.77e-55
37	760	11.9	879	1	R64252	Human mcgJUR3.	9.39e-56
38	741	11.6	877	1	W01099	Metabotropic glutamate	5.16e-54
39	734	11.5	867	1	R72093	Human mcgJUR4.	2.26e-53
40	732	11.5	915	1	R72097	Human mcgJUR4.	3.44e-53
41	730	11.5	915	1	R80479	Rat metabotropic gluta	5.25e-53
42	734	11.5	922	1	R72098	Human mcgJUR7b.	2.26e-53
43	727	11.4	657	1	W94919	Rat pheromone receptor	9.87e-53
44	718	11.3	908	1	W41568	Human metabotropic glu	6.56e-52
45	717	11.3	908	1	W49928	Human metabotropic glu	8.10e-52

DE Human parathyroid calcium receptor 4.0 protein 4kb fragment.
 KW Calcium ion concentration; parathyroid hormone; homeostasis;
 KW Kidney; calcium receptor; detection.
 OS Homo sapiens.
 PN US5763569-A.
 PD 09-JUN-1998.
 PF 07-JUN-1995; 484565.
 PR 07-JUN-1995; US-484565.
 PR 23-AUG-1991; US-749451.
 PR 11-FEB-1992; US-834044.
 PR 21-AUG-1992; US-934161.
 PR 12-FEB-1993; US-017127.
 PR 23-FEB-1993; US-009389.
 PR 22-OCT-1993; US-141248.
 PR 19-AUG-1994; US-292827.
 PR 21-OCT-1994; WO-012117.
 PR 08-DEC-1994; US-353784.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PA (NPSF-) NPS PHARM INC.
 PI Brown EM, Garrett JE, Hebert SC;
 DR MPI: 98-347412/30.
 DR N-PSDB: V26964.
 PT Calcium receptor poly(peptide)s - useful for drug screening or
 PT antibody production
 PS Claim 7; Fig 49; 174pp; English.
 CC The tissue from which the human parathyroid calcium receptor and
 CC receptors from bovine parathyroid and rat kidney are derived, respond to
 CC changes, and control changes, in calcium ion concentration,
 CC e.g. parathyroid hormone regulates Ca2+ homeostasis in blood and
 CC extracellular fluid, and kidney function alters through changes in Ca2+
 CC levels in juxtaglomerular and proximal tubule cells in the kidney. The
 CC purified receptors (produced recombinantly) can be used to screen for
 CC compounds that modulate calcium receptor activity, especially those that
 CC can be used to treat diseases associated with the receptors in these
 CC tissues. They can also be used to raise antibodies for use in detection
 CC assays.
 SQ Sequence 1078 AA;

Query Match 20.3%; Score 1293; DB 1; Length 1078;
 Best Local Similarity 31.8%; Pred. No. 3,67e-105;
 Matches 271; Conservative 234; Mismatches 274; Indels 73; Gaps 48;

DB 30 GDIIIGLGFPIHFV-VAAKQDKSPRESVEICIRYNGFGRMLQAMIFAEINSSPALL 88
 QY 37 GDFLLAGLFLSHADLOVHRPLVTSQDRSDS--FNGHGHLFOARFVEEINNSTALL 94
 DB 89 PULTIGRFDICNTVSKALFATLSVAQNKIDSLNDFCNSSEIPISTIYVATGSG 148
 QY 95 PULTIGRFDICNTVSKALFATLSVAQNKIDSLNDFCNSSEIPISTIYVATGSG 151
 DB 149 VSTAVANLGLFYIPQVSYASSSRLSNKQKSPFLRTIPNDEHONTATADIIIEFRNM 208
 QY 152 HAVTAAALISPLMLPYEASVLSGKRKPSFRTIPSKYQVEYVRLQSGW 211
 DB 209 VGTIADDDYGPPIEKEPREAEENDICIDSELSISQYDEEB--IQHVEVYINSTAKV 266
 QY 212 ISLVSSYSGYGGOLGOALELATPRGICVAFKDVVPLSQADDPKQRMRLARARTIV 271
 DB 267 IYVSSGPDLELI-KEIYRNRITGKIWASSEAMSSSIAMPOFYHYVGGIIGFALKG 325
 QY 272 VVVFEN-RHLACVFRSVYLANLTKGWTASDWA---IS-T-YITNPG-IQ-GI-G 320
 DB 326 QIPGREFELKHPKRSYVANGFAKEWETFNCHLOEGAKGFLPYDTFLRHEESGDRFS 385
 QY 321 TVLG-----VA-IQQRH-VF-GL-KEF-ESY---VQ-AVMA-G-P-----RTPE-GSW-- 358
 DB 386 NSSTAFRLPCTDENISSVETPYIDYTHLRISYNYVLAAYSIAHALQDIYTCPLRGLETF 445
 QY 359 -GGTN-Q-LCRCHAFATWMMPELGAFSMAAYNYEAVYVAHGHQ--L-GC--T 408
 DB 446 NSSCADIKKVEAWOYLKHLRHLNFTNNMGEQYTFDECGVLGVNYSIIMHLSPEGSGIYF 505
 QY 409 SGTCA-RGPIYPMOLLQOYIKVNFLLHK-KTVAFDKGDPLGYDIIADWNGPE-WT-F 464

DB 506 KEVGYNYAKKGERLFINEEKILMSGFREVPSNCSRDCLAGTRKGIIEGPTCFEC 565
 QY 465 EVIG--SA-SLSPVHLINKIRIQHGNNOVPYSVCTRDCLGHR-LVMSHHCCFEC 520
 DB 566 VECPDGEYSDETDASACNKPDDFWSNENHTSIAKEIEFLSWTEPFGIALTLFAVLGIF 625
 QY 521 MPCENGTFLNTESELTQPCGTEBMAPGSSACFSRTVEPLGWHPEISLVLAANTLL 580
 DB 626 LTAFLVGFPIKR-NTPIYKATNRELSTLLFSLCCSSSLF-FIGEPDMTCRLRPA 683
 QY 581 ILIGTAGLFA-WRLHTPVRSAGRLCLMLGSLVAG--SCSLYSPFGKPTAPACILRPL 638
 DB 684 FGISFVLICSLIVTNNVLVEF--AKIPISFHKMGWLNQFLVLCFMOVICVI 741
 QY 639 FSLGFAIFLSCITLIRSFQVLIIFKSTKVPF-FYTHMONGAGITFVASSVHLPLCLT 697
 DB 742 WLTPAPSSYRNOLEDELIIFITCHEGSLMALGFLIGYTC-LLAICPF-AFKSRKLP 799
 QY 698 WLAMTPRPTREYQRFPHLVILECTEVN--SVGFLVAFANHILISIFVCSYLKELPE 755
 DB 800 NNEAKFITFSLLIFFIYISIPAYASTY-GKFSANVEVAILAASGLACIFPNKIT 858
 QY 756 NNEAKCVTFSLILHFVSMIAFTW-SSLYGSLPAAVNLAGLTLISGFGSYFLPCY 814
 DB 859 IILFKPSRTIE 870
 QY 815 VILCRPELNTE 826

RESULT
 5
 ID M89565 standard; Protein; 1078 AA.
 AC M89565;
 DT 19-MAR-1999 (first entry)
 DE Human parathyroid calcium receptor PHUPCAR 4.0.
 KW Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;
 KW Calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;
 KW spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;
 KW neonatal distress; neurodegenerative disease; Alzheimer's disease;
 KW Huntington's disease; Parkinson's disease; dementia; muscle tension;
 KW depression; anxiety.
 OS Homo sapiens.
 PN US5858684-A.
 PD 12-JAN-1999.
 PF 07-JUN-1995; 480751.
 PR 07-JUN-1995; US-480751.
 PR 23-AUG-1991; US-749451.
 PR 11-FEB-1992; US-834044.
 PR 21-AUG-1992; US-934161.
 PR 12-FEB-1993; US-017127.
 PR 23-FEB-1993; US-009389.
 PR 22-OCT-1993; US-141248.
 PR 19-AUG-1994; US-292827.
 PR 21-OCT-1994; WO-012117.
 PR 08-DEC-1994; US-353784.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PA (NPSF-) NPS PHARM INC.
 PI Balandrin MF, Brown EM, Del Mar EG, Garrett JE,
 PI Hebert SC, Nemeth EF, Van Wagenen BC;
 DR MPI: 99-119871/10.
 DR N-PSDB: V82485.
 PT Screening for calcium receptor-active compounds - by recombinant
 PT expression of nucleic acid encoding calcium receptor and determining
 PT the effect of compounds on calcium receptor activity
 PS Claim 1; Fig 49; 176pp; English.
 CC A method has been developed of screening for a compound able to affect
 CC one or more activities of a calcium receptor (CR) comprises: (A)
 CC contacting a recombinant cell with a test compound, where the
 CC recombinant cell comprises a recombinant nucleic acid expressing the CR,
 CC provided that the cell does not have functional CR expression from
 CC endogenous nucleic acid; (B) determining the ability of the test
 CC compound to affect one or more activities of the calcium receptor; and
 CC (C) comparing the ability with the ability of the test compound to

CC affect the one or more CR activities in a cell not comprising the
CC recombinant nucleic acid. The present sequence represents human
CC parathyroid CR, designated a pHPCar 4.0. The nucleic acid sequence of
CC pHPCar 4.0 can be used as part of the recombinant nucleic acid in the
CC method described above. The compounds identified can be used to treat
CC diseases or disorders characterised by abnormal calcium homeostasis, e.g.
CC hyperparathyroidism, osteoporosis and other bone and mineral-related
CC disorders. They can also be used for the treatment of diseases and
CC disorders associated with disrupted Ca²⁺ responses, e.g. seizures,
CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in
CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative
CC diseases such as Alzheimer's disease, Huntington's disease and
CC Parkinson's disease, dementia, muscle tension, depression, and anxiety.
SQ Sequence 1078 AA:

Query Match 20.3%; Score 1293; DB 1; Length 1078;
Best Local Similarity 31.8%; Pred. No. 3,67e-105;
Matches 271; Conservative 234; Mismatches 274; Indels 73; Gaps 48;

```
Db 30 GDIILGLFPIHFG-VAAKDQDKSRPSEVCEIRYNGRFRMLOAMFAEEINSSPALL 88
QY 37 GDFLALGLFLHADCLQVRRHPLVTSCDRSDS--FNGHGHLPLAMFYEINNTALL 94
Db 89 PNILGRIFDTCNTVSKALEATLSFVAQNKIDSLNDEFCNCSEHIPSTIAVVGATGSG 148
QY 95 PNILGRIELVDCSESSSNV-ATLRVPAQOGTGHLEMQR--DLNHSKVALIGPNTD 151
Db 149 VSTRANALLGLFIYPOYSYSSSSRLSNKNOFKFLRTIPDEHQARAMDITFEFKNW 208
QY 152 HAVTALALSPFLMPLVTSYASVILSGKRKFPFLRTIPSDKQVEIVRLLSFGMW 211
Db 209 VGTIADDDGPRGPIKEKFEAREEDICIDPSELSISQYSDPEE--IOHVEVIONSTAKY 266
QY 212 ISLVSGIDGQLOVQLLELATRGICVAFKDVVPLSAQAGDRMRMRMLKARATTV 271
Db 267 IVVFSSPDLEPLI-KEIVRRNITGKIWLASEAWASSSLIAMPQYFHYVGTTIGFALAKG 325
QY 272 VVVFESN-RHLAGVFFRSVLANLTGKWIASEDMA---IS-T-YITNVRG-IG-GI- -G 320
Db 326 QIGGFRFLKKVHPKRVNHGFAKEFEWETFNCHLOGACGRLPVDFLGHESGGRFS 385
QY 321 TVG-VA-IOQR-V-P-GL-KEF-EESY--VQ-AVMKA-P-----RTCPG-GSM-- 358
Db 386 NSSTAFRLCTGDENISSEVETPYDYTHLRISYVWYLAIVSAIALODITYCLGRGLT 445
QY 359 -CGTN-Q-LRECHAFETTKMNPGLGATSKMAVYVAIVAGLQL---L-GC---T 408
Db 446 NSGCAIRKVEANQVLLKHLNLTNNMGQVTFDECGDLVGNSTIINHLSPEDGSI 505
QY 409 SGTCG-RGPVPMQLLOQIKVNFLLHK-KTVAEDDKGDPGLGYDIIAMDNGPE-WT-F 464
Db 506 KEYGVYVWAKKGERFLINEKILMSGFSRVPPNSRCDLAGTRGIIIEGPTCCFEC 565
QY 465 EVIG--SA-SLSPVHLIDINTKIQMHKKNQVPVYCTRDLECHNR-LVWGSHHCCFEC 520
Db 566 VECDEGYSSETDASACNKPDPDEWSNENHTSCAKETIEFLSTPEPGIATLPAVIGIF 625
QY 521 MPCEAGFLTLTSELHTQCPGTEMAEGSSACSRIVEFLGMEHPISLVLLANTLLIL 580
Db 626 LIAFVLGVFIKFR-NPIVATNRELISYLLSLCCFSSSL-FIGEPDWTQRLROPA 683
QY 581 LLIGTAGLFA-WRLHTPVVSAGRLCLFMLGSLVAG-SCSLYFFGKPYPAACLLNOLP 638
Db 684 FGISFVLCISGLVTKNRVLVFE--AKIPTSFHRKMWGLNOLVFLCLFMOIVLCVI 741
QY 639 FSLGFAFLSCILTRISQVLIIFEFSTRKVP-FYHTWAQNNGAIFIVISVTLFLCLT 697
Db 742 WLVTAPSSYRNOLEDEIIFITCHEGSLMALGFLIGYTC-LIAAICFF-AFKSRKPE 799
QY 698 WLAMMTPRPREYORPHVLVECTEVN--SVGLVFAFHILLISITFYCSYGLKELE 755
Db 800 NFNEAKFTTSMELFIWISIFIPAYASTY-GKFSVAVEVIAIIAASFGLLACIFENKIY 858
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QY 756 NYNEAKCVTFSLILHFWSWIAFFTM--SSIIQSYLPAVNVLAGIATLDSGSGCYFLPKY 814
Db 859 IILFKPSPNTIE 870
QY 815 VILDRPELNTIE 826

RESULT 6
ID W1889 standard; Protein; 1078 AA.

DT 22-APR-1997 (first entry)
DE Parathyroid calcium receptor encoded by clone pHPCar4.0.
KW Calcium receptor; human parathyroid gland adenoma tumour; pBOPCar1;
KW primary hyperparathyroidism; Xenopus oocyte; alternative splicing;
KW calcium-activated chloride current; agonist; NPS R-467; NPS R-568;
KW variant; untranslated region; alternative polyadenylation; probe;
KW alternative transcription initiation; pHPCar5.2; pHPCar4.0;
KW human Car gene; isoform.
OS Homo sapiens.
PN W09612697-A2.
PD 02-MAY-1996.
PF 23-OCT-1995; U13704.
PR 21-OCT-1994; WO-U12117.
PR 08-DEC-1994; US-353784.
PA (NPSP-) NPS PHARM INC.
PI Balandrin MF, Delmar EG, Moe ST, Nemeth EF, Van Wagenen BC;
DR WPI: 96-230520/23.
DR N-PSDB; T61862.

PT New di:arylalkyl amine cpds. useful for modulating inorganic ion
PT receptor activities - esp. for modulating effect of extracellular
PT calcium on cell surface calcium receptors, useful for treating e.g.
PT hyperparathyroidism, Paget's disease or osteoporosis
PS Example 1, Page 93-100; 231pp; English.
CC The sequences given in W1888-89 represent functional calcium receptors.
CC The cDNAs encoding these sequences were isolated from human parathyroid
CC gland adenoma tumour using pBOPCar1 as a hybridisation probe. mRNA was
CC isolated from a 39 year old caucasian male diagnosed with primary
CC hyperparathyroidism and two clones of approx. 5 and 4 kb were
CC identified. These cDNAs were injected into Xenopus oocytes which were
CC assayed for the presence of functional calcium receptors. Both clone
CC types gave rise to functional calcium receptors as assessed by the
CC stimulation of calcium-activated chloride currents upon addition of
CC appropriate calcium receptor agonists, e.g. NPS R-467 and NPS R-568.
CC Sequence analysis of the two cDNA clones indicated the existence of at
CC least two sequence variants differing in the 3' untranslated region and
CC which may result from alternative polyadenylation. Sequence variation
CC also exists in the 5' end of the inserts. These sequence differences may
CC have arisen due to alternative transcription initiation and/or splicing.
CC Three additional sites of sequence variation occur within the coding
CC regions of cDNA clones pHPCar5.2 and pHPCar4.0 demonstrating that they
CC encode distinct proteins. Sequence analysis of the human Car gene
CC indicates that the additional 30 bp in clone pHPCar5.2 as compared to
CC pHPCar4.0, results from alternative mRNA splicing. This alternative
CC splicing is predicted to insert 10 additional amino acids into the Car
CC protein encoded by pHPCar5.2 between residues 536 and 537 of the protein
CC encoded by pHPCar4.0. In addition pHPCar4.0 encodes Gln at position
CC 925 and Gly at position 990, whereas pHPCar5.2 encodes Arg at both
CC equivalent positions. The human Car gene encodes for Gln and Arg
CC respectively at these positions. These two receptor isoforms may be
CC functionally and/or pharmacologically distinct. Pages 94-95 are
CC missing from the specification, sequence information was obtained
CC from the EPO.

SQ Sequence 1078 AA:

Query Match 20.3%; Score 1293; DB 1; Length 1078;
Best Local Similarity 31.8%; Pred. No. 3,67e-105;
Matches 271; Conservative 234; Mismatches 274; Indels 73; Gaps 48;

```
Db 30 GDIILGLFPIHFG-VAAKDQDKSRPSEVCEIRYNGRFRMLOAMFAEEINSSPALL 88
QY 37 GDFLALGLFLHADCLQVRRHPLVTSCDRSDS--FNGHGHLPLAMFYEINNTALL 94
Db 89 PNILGRIFDTCNTVSKALEATLSFVAQNKIDSLNDEFCNCSEHIPSTIAVVGATGSG 148
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QY 95 PNTLGLGVCESSSNVY-ATLRVPAQOCTGHELMQR--DLRNHSSKVALIGPNTD 151
DB 149 VSTAVANLGLFTIPQVYSSASSRLSKNOFSEFLRTIPNDEQATAMADIIEYFRMW 208
QY 152 HAVTATALLSPFLMPVSYEASSVILSGKRKFPFLRTIPSDKQVEYVRLLOSFGMW 211
DB 209 VGTIADDDYGRPGIEKFRFEAEERDIDSELSISQDEE--IQHVEVIONSTAKV 266
QY 212 ISLVGSYGDYGOALVELELATRGICVAFKDYAPLSAQGDPRMQRMRLARARTV 271
DB 267 IYVSSSPDLEPL-KEIVRNITGKTIWASEMASSSLAMPYFVVGSTIGFALKAG 325
QY 272 VVVFESN-RHLAGVFRSVLANLIGKWLASEDA---IS-T-YITNVPG-IQ-GI-G 320
DB 326 QIDPREFELKVVHPRKSVHNGFAKEFWEETFNCHLOGAKGPLPVDTFLRGHESSGDRS 385
QY 321 TVLG---VA-IDQRQ-VP-GL-KEF-EESY---VQ-AVMGA-P-----RTCPD-GSW-- 358
DB 386 NSSTAFRPLCTGDNISSEVETPYIDYTHLRISVNVYLAVYSIAHALODITYCTLRGRLFT 445
QY 359 -CGTN-Q-LCRECHAFITTMNPELGAFSMSAAVYEAAYVAHAGHLQL--L-GC---T 408
DB 446 NSGADIKKYEAMQVYLKRLNFTNNMGEVYTFDECGDLVGNYSIINMHLSPEDGSIVF 505
QY 409 SGTCG-RGPYPMQLQOIKVNFLLK-KTVAEDDKGDPGLGYDIIAMPNGPE-WT-F 464
DB 506 KEYGVYVYAKKGERLFINEKILMSGFSEVPFNSCRDCLAGTRKGIIEGPTCCFEC 565
QY 465 EVIG--SA-SLSPVHLDINKTKIOMHGKNNQVPSVCTROCLBGRHR-LVMGSHCCFEC 520
DB 566 VECPDGEYSDETDASACNCPDDEFSNENHTSCIAKEIEFLSTWEPFGIALTFVAVLGIF 625
QY 521 MPEAGTFELTSELHTQPCGTEEMAEBSGACFSRTVEFGHEPISLVLAANTLL 580
DB 626 LTFVGLGVFIKFR-NTEPIVATNELSYLLLSLCCFSSSLF-FIGEPQDWTGRLQPA 683
QY 581 LLIGTAGLFA-WRLHFPVRSAGRCLFELMGLSVAG-SCSLYSEFKRPVACLLRQPL 638
DB 684 FGISFVLCISCIIVKTNRLVLFVE--AKIPTSEFRKMGMLQFLVFLCTFMQIVCVI 741
QY 639 FSLGFAFLSCLTRFSQOLVYIFKFSKVPRT-FYHTAQNHGAGIPIYVSVAHLEFCLT 697
DB 742 WLYTAPSSYRNOLEDEIIFITCHEGSLMALGFLIYTC-LLAALCFE-APKSRMLPE 799
QY 698 WLMAMTPRTPREYORFPHLVILECTEYV--SVGFLVAFAHNILLISTFVCSYLGKELPE 755
DB 800 NPEAKITESMILFEIIVWISFIPAVASTY-GKRVSAVEYAIILAAFGLLACIFENKIY 858
QY 756 NYNEAKCVTSLHLHFVSMIAFFTM-SITIGSITLPAVNVLAGLATLSGGSGYFLPKCY 814
DB 859 IILFKPSRNTIE 870
QY 815 VILCRPELNTE 826

RESULT
ID W38274 standard; Protein: 1078 AA.
AC W38274;
DT 08-MAY-1998 (first entry)
DE Human parathyroid cell calcium receptor 4.0 (Hupcar 4.0).
KW Human parathyroid cell calcium receptor 4.0; Hupcar 4.0;
KW calcium homeostasis; hyperparathyroidism; osteoporosis.
OS Homo sapiens.
PN US568938-A.
PD 18-NOV-1997.
PF 07-JUN-1995; 485588.
PR 07-JUN-1995; US-485588.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-017127.
PR 23-FEB-1993; US-009389.

PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (BGM) BRIGHAM & WOMEN'S HOSPITAL.
PA (NPS-) NPS PHARM INC.
PI Brown EM, Fuller FH, Garrett JE, Hebert SC;
DR MPI: 98-008040/01.
PT DNA encoding calcium receptor polypeptide(s) - useful for
N-PSDB: T95859.
PT therapeutic purposes, e.g. hyperparathyroidism and osteoporosis
PS Claim 20; Columns 125-134; 14pp; English.
CC The present sequence is human parathyroid cell calcium
CC receptor 4.0 (Hupcar 4.0).
CC The specification includes details of molecules that can modulate
CC one or more inorganic ion receptor activities, and antibodies and
CC antibody fragments targeted to inorganic ion receptor proteins. The
CC proteins, nucleic acids and antibodies may be used to treat
CC disorders by modulating one or more inorganic ion receptor
CC activities, preferably disorders of calcium homeostasis, e.g.
CC hyperparathyroidism and osteoporosis.
SQ Sequence 1078 AA;

Query Match 20.3%; Score 1293; DB 1; Length 1078;
Best Local Similarity 31.8%; Pred. No. 3,67e-105;
Matches 271; Conservative 234; Mismatches 274; Indels 73; Gaps 48;

DB 30 GDIILGLPIFHG-AAACDQCKSRSEVECTRYNFGFRMTOAMIFAEIINSSPALL 88
QY 37 GDIILGLPIFHG-AAACDQCKSRSEVECTRYNFGFRMTOAMIFAEIINSSPALL 94
DB 89 PNTLGLGVCESSSNVY-ATLRVPAQOCTGHELMQR--DLRNHSSKVALIGPNTD 151
QY 95 PNTLGLGVCESSSNVY-ATLRVPAQOCTGHELMQR--DLRNHSSKVALIGPNTD 151
DB 149 VSTAVANLGLFTIPQVYSSASSRLSKNOFSEFLRTIPNDEQATAMADIIEYFRMW 208
QY 152 HAVTATALLSPFLMPVSYEASSVILSGKRKFPFLRTIPSDKQVEYVRLLOSFGMW 211
DB 209 VGTIADDDYGRPGIEKFRFEAEERDIDSELSISQDEE--IQHVEVIONSTAKV 266
QY 212 ISLVGSYGDYGOALVELELATRGICVAFKDYAPLSAQGDPRMQRMRLARARTV 271
DB 267 IYVSSSPDLEPL-KEIVRNITGKTIWASEMASSSLAMPYFVVGSTIGFALKAG 325
QY 272 VVVFESN-RHLAGVFRSVLANLIGKWLASEDA---IS-T-YITNVPG-IQ-GI-G 320
DB 326 QIDPREFELKVVHPRKSVHNGFAKEFWEETFNCHLOGAKGPLPVDTFLRGHESSGDRS 385
QY 321 TVLG---VA-IDQRQ-VP-GL-KEF-EESY---VQ-AVMGA-P-----RTCPD-GSW-- 358
DB 386 NSSTAFRPLCTGDNISSEVETPYIDYTHLRISVNVYLAVYSIAHALODITYCTLRGRLFT 445
QY 359 -CGTN-Q-LCRECHAFITTMNPELGAFSMSAAVYEAAYVAHAGHLQL--L-GC---T 408
DB 446 NSGADIKKYEAMQVYLKRLNFTNNMGEVYTFDECGDLVGNYSIINMHLSPEDGSIVF 505
QY 409 SGTCG-RGPYPMQLQOIKVNFLLK-KTVAEDDKGDPGLGYDIIAMPNGPE-WT-F 464
DB 506 KEYGVYVYAKKGERLFINEKILMSGFSEVPFNSCRDCLAGTRKGIIEGPTCCFEC 565
QY 465 EVIG--SA-SLSPVHLDINKTKIOMHGKNNQVPSVCTROCLBGRHR-LVMGSHCCFEC 520
DB 566 VECPDGEYSDETDASACNCPDDEFSNENHTSCIAKEIEFLSTWEPFGIALTFVAVLGIF 625
QY 521 MPEAGTFELTSELHTQPCGTEEMAEBSGACFSRTVEFGHEPISLVLAANTLL 580
DB 626 LTFVGLGVFIKFR-NTEPIVATNELSYLLLSLCCFSSSLF-FIGEPQDWTGRLQPA 683
QY 581 LLIGTAGLFA-WRLHFPVRSAGRCLFELMGLSVAG-SCSLYSEFKRPVACLLRQPL 638
DB 684 FGISFVLCISCIIVKTNRLVLFVE--AKIPTSEFRKMGMLQFLVFLCTFMQIVCVI 741

PI Calcimimetic receptor polypeptide(s) - useful for drug screening or
PT antibody production
PS Claim 8; Fig 50; 174pp; English
CC The tissues from which the rat kidney calcium receptor and receptors from
CC bovine parathyroid and rat kidney are derived, respond to changes, and
CC control changes, in calcium ion concentration, e.g. parathyroid hormone
CC regulates Ca^{2+} homeostasis in blood and extracellular fluid, and kidney
CC function alters through changes in Ca^{2+} levels in juxtaglomerular and


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OY 756 NNEACVFTSLHFRVSWIAFPTM-SSITYGSLPAVNVLAGLATLSGSGSYFLPKCY 814
DB 859 IILFKPSRTIEVRSSSTAHA 880
OY 815 VILCRPELNTEHFQASIODYT 836

RESULT 12
M32059 standard; Protein: 1026 AA.
AC M32059;
DE 27-MAR-1998 (first entry)
DB Dogfish shark kidney calcium receptor related protein (SKCAR-RP).
KW Calcium receptor related protein; Car-RP; dogfish shark; SKCAR-RP;
KW polyclonal-sensing receptor; aquaculture; fish farming;
OS Salinity tolerance.
FH Squalus acanthias.
FH Key Location/Qualifiers
FT Region 351..395
FT /note= "region in extracellular domain that is highly divergent from mammalian PVCR"
FT Region 870
FT /note= "region in C-terminal domain that is highly divergent from mammalian PVCR"
FT Region 870
FT /note= "region in C-terminal domain that is highly divergent from mammalian PVCR"
PD WO9735977-1.
PN 02-OCT-1997.
PF 27-MAR-1997; U05031.
PR 27-MAR-1996; US-622738.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PI Brown E, Harris HW, Hebert S;
DR N-PSDB: T89290.
PT New isolated Aquatic polyvalent cation-sensing receptor - used to
PT develop products for increasing or decreasing the salinity tolerance
PT of fish for use in aquaculture.
PS Clam 9; Fig 5A-B; 5/PP: English.
CC This protein comprises dogfish shark kidney calcium receptor
CC related protein (SKCAR-RP), an aquatic polyvalent cation-sensing
CC receptor (PVCR). Its amino acid sequence was deduced from a kidney
CC cDNA clone (see T89290). It shows 74% homology to rat kidney
CC PCVR and bovine parathyroid PVCR and possesses general features
CC that are homologous to PVCR proteins, including a large
CC C-terminal domain, 7 transmembrane domains and a cytoplasmic
CC membrane of epithelial cells of elasmobranch fish particularly
CC from cells found in the collecting duct or late distal tubule in
CC the kidney, intestine, gill, rectal gland, gonad or brain; an
CC antibody that specifically binds to a PVCR; and a method of
CC screening for aquatic PVCR agonists and antagonists. Modulation of
CC the expression of the aquatic PVCR activates or inhibits aquatic
CC PVCR mediated ion transport and endocrine changes that permit fish
CC to adapt to fresh or salt water. The method facilitates the
CC aquaculture of marine fish and can provide for the development of
CC marine fish that are easily adaptable to fresh water aquaculture.
SQ Sequence 1026 AA;

Query Match 18.9%; Score 1204; DB 1; Length 1026;
Best Local Similarity 31.0%; Pired. No. 7.44e-97;
Matches 263; Conservative 237; Mismatches 273; Indels 76; Gaps 47;
DB 34 GDIIIGLPIIFHG-VAADQDLKSPREATKIRYFRGFRMLQAMIFAIIEINSMTEFL 92
OY 37 GDFLAGLGLSHADLCQVHHRPLVTSDD--RDSFNGHGTHLQFAARFVEEINNTALL 94
DB 93 PNTTLCYRIFDTCNTVSKALEATLSTVAONKIDSLNLDFFCNSDHPITIAVVGATGSG 152
OY 95 PNTTLCYRIFDTCNTVSKALEATLSTVAONKIDSLNLDFFCNSDHPITIAVVGATGSG 151
DB 153 ISAVANLGLPIFYOVYASSSRLLSNKREYKAFRTIPNDEQQAATAEITENHQNMW 212
OY 152 HAVTALLSPFLMPLVYSEASSVILSGRRKPFSLRTIPSDKYQVEYIVRLLSGGWMW 211

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DB 213 VGLTAAADDYGRGIDKREAVKRDICIDFSEMIQYV-T-QKOLEPIADYONSSAKV 270
OY 212 ISLVGSYGDGLGVQALBELATPRGICVAFKDYVPLSQAQADPMQOMRLAARTV 271
DB 271 IYVFSNGDLEPLI-OELVRNITDRIMLASEAMASSLIAPKPEYFHVGGTIGFALRAG 329
OY 272 VYVFSN-RHLAGVFFRSVLANLTGKWIASEDMAISTYITNVPISIQIG-TV--L-G 324
DB 330 RIGFNKFLKEVHPAGPPTMGSRSSGRLOLLHREDLTQKNSKVPSHGPAAGDSK 389
OY 325 -VA-10Q--KQV---P--GL-----K-EF--E-ESTVQ--A-VMG-ARTCPDSW 358
DB 390 AGNSRTALRHHCTGEENITSVETPLDYTHLRISYNYVAVYSAHAADODHSCPGTG 449
OY 359 GCTNQ---LCRC--HAFITWMPDELGAFSMAKYNYEAVYANAHLLHQLGCG---T- 408
DB 450 IFANSCADIKKVEAMQVNLHLHKLFTNSMGEQVDPDQGLKGNITTIKMQLSAEDS 509
OY 409 --S-GTCA-RGFVYPMOQLQIKYVFLHK-KTVAFDKGDPLGYDIAMDWNGP-EW 462
DB 510 VLFHEGYNNAKPSDRLNINEKILMSGFSKYVPFNSGSDCVPRGKIIEBPTCC 569
OY 463 T-FEYVIGS-ASLS-PV-HUDINKTKIOWHGKNOVPVSVCTDCIEGHR-LVMGSHHC 517
DB 570 FEOMACAESEFSDENDASACTKCPNDFWSENHTSCIAKEIEYLSWTPPGIATLIFAVL 629
OY 518 FEOMCEAGTFLNTESELTCCQCGTEEMAPBESSACFRTEFLQWHPISLVLAANTL 577
DB 630 GLITSEVYLGVFIKFR-NPIYKATNRELSTYLLFSLICFSSSLI-FIGEDRWTCRLR 687
OY 578 LLLLLIGTAGLEA-WRLHPTVVRASAGRLCFMLSLGSLVAG-SCSLYSFPGKPYACILR 635
DB 688 OPAGFISFLCISCTIVTNRVLVEE--AKPTSLHKKWGLNQGLFLFCLIMQVLT 745
OY 636 QLFSLGFAIFLSCLTINSFQVITFKSTKVP-FTYTMQNHAGLFIYSSVTHLFL 694
DB 746 CILMYTAPSSRYRHEDEVEIFITCDEGSLMAGFLIGYTC-LIAAICFF-AFKSRK 803
OY 695 CILWLAAMTPRTRTQYQPHVILTECEVN--SVGLVAFANHLTSLISFVCSLKE 752
DB 804 LPENNEAKFTFSMLIFFIWISFIPAVSYI-GKEYSAVEVILIASGGLCITFN 862
OY 753 LPENNEACVFTSLHFRVSWIAFPTM-SSITYGSLPAVNVLAGLATLSGSGSYFLP 811
DB 863 KCYILFKP 871
OY 812 KCYVILCRP 820

RESULT 13
M38273 standard; Protein: 1088 AA.
AC M38273;
DE 08-MAY-1998 (first entry)
DB Human parathyroid cell calcium receptor 5.2 (hUPCAR 5.2).
KW Human parathyroid cell calcium receptor 5.2; hUPCAR 5.2;
KW calcium homeostasis; hyperparathyroidism; osteoporosis.
OS Homo sapiens.
PN US5688938-A.
PD 18-NOV-1997.
PF 07-JUN-1995; 485588.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-834161.
PR 12-FEB-1993; US-017127.
PR 23-FEB-1993; US-009389.
PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PI (NPS-) NPS PHARM INC.
PI Brown EM, Fuller FH, Garrett JE, Hebert SC;

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QY 571 LLAANTLLLLLIGTAGLFA-WRLHTPVVRSAGGRCLFLMLGSLVAG-SCSLYSFPGKPT 628
Db 684 DWTGRLROPAFGISFVLCISCLIVKTNRLVFE--AKTPTSHRKKWGLNLQFLLVFLC 741
QY 629 VPACLRQPLFSUGFAIFLSCLTIRSFQVLITFKESTKVPT-FYHTWAQNHGAGIFVIVS 687
Db 742 TFMQIVICVIMLYTAPSSYRNOLEDEIIFITCHEGSLMALGFLIGYTC-LLAICPFF 800
QY 688 STVHLEFLCLTWLAWTPRPTREYQRFPHLVILECTEVN--SVGFLVAFANHTLSTFTV 745
Db 801 -AFKSRKLPENNEAKFITFSMLIEFTIVISFIPAYASTY-GKVSASVEVIAIILAASTGL 858
QY 746 CSYLGKELEPENNEAKCYTFSLLHFVSWIAEFTM-SIYOGSYLPANVYLAGLATLSSG 804
Db 859 LACIFFNKIYIILFKPSRNTIE 880
QY 805 FSGYFLPKCYVILCRPELNNT 826

Search completed: Fri Mar 17 13:14:52 2000
Job time : 99 secs.

[illegible]

RESULT	2			
ID	O9ZOR7	PRELIMINARY;	PRT:	843 AA.
AC	O9ZOR7;			
DT	01-MAY-1999	(TREMBLrel. 10,		
DT	01-MAY-1999	(TREMBLrel. 10,		
DT	01-MAY-1999	(TREMBLrel. 10,		
DE	PUTATIVE TASTE RECEPTOR TR2	(FRAGMENT).		
OS	Rattus norvegicus (Rat).			
CC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=MISTAR;			
RC	MEDLINE: 99159821.			
RX	HOON M.A., ADLER E., LINDEMAYER J., BATTERY J.F., RYBA N.J.P.,			
RA	ZUKER C.S.;			
RT	"Putative mammalian taste receptors: a class of taste-specific GPCRs			
RT	with distinct topographic selectivity.";			
RL	Cell 96:541-551(1999)			
DR	EMBL: AF127390; AAD18070.1; -.			
NW	Receptor.			
FT	NON-TER			
SO	SEQUENCE	843	843	
		843 AA;	95799 MW;	6B0AE9EE CRC32;
Query Match		31.7%;	Score 1848;	DB 11;
Best Local Similarity		37.5%;	Pred. NO. 0.00e+00;	
Matches	293;	Conservative	193;	Mismatches 269;
			Indels	26;
			Gaps	22;

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Db 71 GYNLMQARFVPEEELNNNSLSLLPGVGEWVDVCYLSNNHPELXYFLA-QDDDLLEILK 123
QY 9 GYHLPGARLGEVEELNNSTALLPNTLTGQLXDVCSDSANVATLRSLSPGQHIIETGG 68
Db 130 DYSQMPHYAVIGPDNESAITYLSNIISHLLPQIITYSAISDKLRDRHFPMSLRTVPS 188
QY 69 DLMHSPVYLAVIGDSTNNRATNALSPFLV-HISTAAASELLSVKRRPSSLRIIPN 127

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Dd	190	ATHHLEAVOLMWHFQWMMIVLVVSDDDYGHRENNHLSQRLKTSIDCIPAEVLPPIES	249
OY	128	DKYQVEIVVLLQKFGWMTISLVSSDDYQGLQVQALENO-ALVRGICIFKIDMPF--S	184
Dd	250	SOVMSEBROLDNIDLRKRTSARVVVESP-ELSYSEFHEVLRNFGFWIASSEW	308
OY	185	AQV--GDE-R-MOCIMRLHAQAGATVYVVSRRQAR-VFESVVLNLTGKMWASSEM	239
Dd	309	AIDPLVHLUDELKRTGFFLGTIGORVSIPEFSQR--VRRDKPGYVVPNTMLRTTCNO	365
OY	240	ALSRHITVPGIQIRIGVLAIOKRAVPGIKAEFEAYAAKDEA-PRCHKMSWSSNO	298
Dd	366	DDADALN-TKSFNNILITSEGERVYVUYSAVVAHARILRLGCNVRCTOKKYPMOL	424
OY	239	LCRQEQANMATMRKIAFAFSMSSA-YANARAVAVANGHOLLGCASELCSRRRYPMOL	357
Dd	425	LRFTVHVFITLGNRLFFDQOGDKPML-LDIOMQWDLSONPQOSIASVSPISKRLTYIN	483
OY	358	LEQIHKVFELHAKDTVAFENDNRD-PLSSYNIAMDWNGPKMTFTVLGSSFTWSVQOLINE	416
Dd	484	NVSWYGTNTNTVPVSMKSSKQOPOMKSGVLHPCCECDKMGPTYLINSADPEFNLSC	542
OY	417	TKIQHGNHNGHPVSSVSSDCEBHQVNTVGFHHCCCECPGACAGTIFLANK-ELYKQPC	475
Dd	543	PGSMKSYKNDITCFORRPTELEWHEVPTIVAILAALGFESTLALDFTF-WRHFOQPMYR	601
OY	476	GTEWAPRGSGOTCEPRVVFETALREHSTWILLANLTLTLTLTLGTAGLEFAM-HLDPPYVR	534
Dd	602	SAGSGMCGMLMVEPLLAFWGVVYVSGPTVFCGCRQAFTEVFCISLQITRSPQIYC	661
OY	535	SAGGICLCTLMGSLAASSGSIYGFGEPTRPACILROALFDLFTFPLSLIYKRSQLLI	594
Dd	662	VFKMARLPSAYSEFWMRVHGPVYFAETAIKVALVGNMLATTINPIGRTDPPDENIMI	721
OY	595	IFKSTKATPEYHAMOVONHGAGLEFVMSAAOILICTLMTLVMTPLP-AREYORPFLVW	653
Dd	722	LSCHPNRNGLLFMTSDMLLSVYGSEFAFMGKELPNTYNEARFITLSMTFSTTSSISC	781
OY	654	LECTETNSLGITLFLYNGLSLSTAFACSLTGLDPLNENEAQCVFSLFENVSIAIEF	713
Dd	782	TFMSVHDDVLTINDLIVTYNLPLALIG-YFPGCKMILFEYERNTSAYFNSMIGYTM	840
OY	714	TTASVYDGRKYLPAANNMAG-LSSIASSGFGYFLPKCVYLICRPDLNSTEHPQASIODYR	772
Dd	841	R 841	
OY	773	R 773	

ID	RESULT	3	PRELIMINARY;	PRT;	848 AA.
AC	093553;				
DT	01-NOV-1998	(TrEMBLrel. 08, Created)			
DT	01-NOV-1998	(TrEMBLrel. 08, Last sequence update)			
DT	01-NOV-1999	(TrEMBLrel. 12, Last annotation update)			
DE	PUTATIVE ODORANT RECEPTOR.				
GN	GPR8.				
OS	Carassius auratus (Goldfish).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;				
OC	Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;				
OC	Cyprinoidae; Cyprinidae; Cyprininae;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=OLFACTORY EPITHELIUM;				
RX	MEDLINE; 98426265.				
RA	CAO Y., OH B.C., STRYER L.;				
RT	"Cloning and localization of two multigene receptor families in				
RT	goldfish olfactory epithelium";				
RL	Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).				
DR	EMBL; AF083081; AAC64076.1;				
DR	PFAM; PF00003; 7tm3; 1.				
DR	PFAM; PF01094; ANF-receptor; 1.				
DR	PRINTS; PR00248; GPCRNGR.				

[illegible]

OC Neopterygii, Teleostei, Euteleostei, Acanthopterygii, Percormorpha;
 OC Tetraodoniformes, Tetraodoncoidei, Tetraodontidae, Fugu.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98226788.
 RA NAITO T., SATO Y., YAMAMOTO T., NOZAKI Y., TOMURA K., HAZAMA M.,
 RA MAKANISHI S., BENNER S.;
 RI 'Putative pheromone receptors related to the Ca2+-sensing receptor in
 RT Fugu'.
 RL Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).
 DR EMBL: AB008858; BAA26123.1; .
 DR PFAM: PF000003; 7tm_3; 1.
 DR PFAM: PF01094; ANF_receptor; 1.
 DR PRINTS: PRO0248; GPCRMR.
 KW Pheromone.
 SQ SEQUENCE 868 AA; 95531 MW; DA037862 CRC32;
 Query Match 22.0%; Score 1286; DB 13; Length 858;
 Best Local Similarity 30.5%; Pred. No. 4.2e-241;
 Matches 239; Conservative 197; Mismatches 312; Indels 36; Gaps 30;
 Db 94 CRVIDHEELQASHAVFAIEBINNSTELLEPGIKLGYIHDSCAVPIANVVAEQ-L-LNT 151
 QY CS-FNEHGHLFQAMRIGVEINNSTALPTLTGQYLVDCSD-SANVYATLRSLSPG 60
 Db 152 LDPVVTVDNCSQSGKVAAYVSGSGTSPSSISINVISFDPILVSHRATACISDKQKP 211
 QY 61 QHHELEQSDLLHYSPVLAIVGDPISIRRAATTALESFELVH-ISTYASSETLSVKRYP 119
 Db 212 SFERTIPSDQFQAQALYKLIKHFQMTWIGAVCSQSDSGNGMAFLIAAQKEGICVEYSE 271
 QY 120 SFRLRIPMDKQVETWMLLOKFGMTWISLVGSSDDYGLQGLQALEQALVRGICIAFKD 179
 Db 272 SF-YRTH-PSRIKRVADVIRRSSTAVVVAFTASTEXMILLEELSHEDSPROMIGSESW 329
 QY 180 IMPFSAQYQDERMOCMLKRLHQAQATVYVVFSSKQLARVFESVLTNLGKTVASSEAW 239
 Db 330 VTDPDLLEFS-F-CAGTI-GPAIDRSVIRPGLRDLDLSPS-KVASSPVLTFFMEDSFC 385
 QY 240 ALSRIITGVPEIQIKGKLVGAIDKRAVPGLKAFEEAYARADKADAPRCHKGSW----C 294
 Db 386 RLNGKERKDCDSESDIT-QSPYDTSELRTLNMYKAVYIAIAHINAVQDINATRCSS 445
 QY 295 S-SN-Q-LCRGCAQFMAHTMPKCLAFMSASYANAYRAVVAHGHQLL--GC-ASLICS 348
 Db 446 KFTTINPKKVTLTQIKYVNSONGIAVSFPDQPVASTELYNNKKSGSGSIEVVPQGYD 505
 QY 349 R-GRYVPMQLLEQIHKHVFLLHKTKTVAFNNRNPDLSSYNTIADMDNPKPTFTV-DGS-S 405
 Db 506 ASLPGQGEFRLFQDIITWWDGRVQVYVSCDSQCGRKYRLQKGRPLCCYDCVQCEGET 565
 QY 406 TWSPQQLININTK-IQMHGKNHVPKSKVCSDDLIEGHQRYV-IGFHHCCECPCCGAGTF 463
 Db 566 SNVTDSPEDICLDDFNPENRNACFPKPEYFELSFNEVLG-IILAVFSVAGACIAVITTA 624
 QY 464 LKNSLRYKQCGCFHEMABEGSQCEPRTVYVFLALREHTSMVLLAANTLL-LLGTVG 522
 Db 625 VPFHRTSPRIYRANNSLSFLLESLLCLCLSTFGAASHLSCHMRHATBSITVLCI 664
 QY 523 LEAMHLDLPVYRSAGGRCLFMLGSLAAGSGSLYGFGEPTRACCLROLALGFETIFL 582
 Db 685 SCVLGKT--VVVLAAFRATLDGSVVMKMFQPPDOORMVVFETSIQVLCIYVILVWPNPP 742
 QY 583 SCLVRSQQLIIITKFKSVPTFPHA-WYONHGAGLFVYLSSAOLLICLTLLVWATPLP 641
 Db 743 VRLTTYKERIILECALGSSVGFMAVLGYTGLLAAYCLAVLARKLPDNFNDAKITFS 802
 QY 642 AREYQRFELHMLTECTETNSIGFIATFLAYNGLLISAFACSYLGKLDPENYNAKCVTFS 701
 Db 803 MLI-FCAMWIFIFIAVYVSPGKFTVAEIPAILAS-SFGILCIPAKCIIILFKREKKS 860
 QY 702 LLENFVS-WIAFFTASVQDKYIPRANMAGLSLSSGSGY-FLPKCVIILCRDLNS 759

Db 861 KHL 864
Y 760 TEHF 763

RESULT 5
ID 073637 PRELIMINARY; PRT: 864 AA.

AC 073637;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE PHEROMONE RECEPTOR.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.

RM [1]
RP SEQUENCE FROM N.A.

RX MEDLINE; 98226788.

RA NAKANO T., SATO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,

RT "Putative pheromone receptors related to the Ca2+-sensing receptor in

RT Fugu".

RL Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).

DR EMBL; AB008859; BAA26124.1; -.

DR PFAM; PF00003; 7tm_3; 1.

DR PFAM; PF01094; ANF_receptor; 1.

DR PRINTS; PR00248; GPCRMR.

KW Pheromone.

SEQUENCE 864 AA; 96216 MW; E26A0114 CRC32;

Query Match 21.8%; Score 1270; DB 13; Length 864;
Best Local Similarity 30.6%; Pred. No. 1,33e-237;
Matches 243; Conservative 216; Mismatches 287; Indels 48; Gaps 37;

Db 75 CTRFDLGFHMAWMAFAVOEINKNPDLPLNLTGLRGLYDNCGLAVGFSGLALA-SGQ 133
Y 3 CS-FNEHGYHFLQAMRLGVEEINNSTALPNTLGLYQYDVCSDSANYATRLVSLPQ 61

Db 134 EEAALOGGCGG-SPVVGIVGDSITSTIASAVLGKIKPMVSFYATCGLTRKQFP 192
Y 62 HH-TELQDHLHYSPVLAIVIGPDSINRAATTAALLSPFLVH-ISAASSSETLSVKRQYP 119

Db 193 SFRRTIPSDDFOVAMIOILKHFQWTWGLVSDDDYGLHYVASQSD-LVOSGGGCIAY 251
Y 120 SFLTIPDKYQVETWVLLQKFGMTWISLVGSSDDYQGLQVQALBNALVR-GI-CIAF 177

Db 252 LEVLPMDNYLSENR-R-IVHVIKESTAVLVFAHOSHIMLM-BEYVRQVATGLQWLAS 308
Y 178 KDIMPFSQVODERMOCIMRLHAQAGATVVVSSR-QLARVFEFSVLTJLTGKRVVAS 236

Db 309 EAMVGTITLQ-TPDPMPLNTGLTGLIRGELTGRLDLRLRPOSSNNTSYDVQPF 367
Y 237 EAMLSRHTITVPISQIR-IGVILGVALIQRAVPGIKAFEEAARADKAPRCHGGS--W 293

Db 368 EYSQCKGAGSAGACTGDNIOQVDAEFLDVSNLRPEYNIYKAVYLAALADMLQCE 427
Y 294 -----CS-SNOLCRE-C-QAFMAHTMK-LKAFMSASAYNAYRAVAVAGSHRLDLC- 342

Db 428 PGRPFSGGSCADILKLEPMQFVHYLVHNTTTFGGVSDENGDLVPIYDILMOWLP 487
Y 343 AS-E-L---CS-RGRVYPMOLLQIHVYFLH-KDTVAFNDNDPLSSNIILMDWG 394

Db 488 DGRVQVAVGVKSPSGEELQIHEDKIFNFEENKRPVSHVSCSCPPGRMRKKQOP 547
Y 395 PKMT-FTVLGSGTSPV--OLNINETRIOWGNKNOVPKSVSCSSDCLEGHRRVYT-CFH 449

Db 548 VCCPDLCSGKISNTDSMECTSCPEDWSSPQRDHCVPKRTBELSYHEPLG-ICLTA 606
Y 450 HCCFECVCGAGTFLNKSELRQCPGTEBNAPESQTCFPTVYFLRLREITSVNLAA 509

Db 607 ASLGTIVSVVVLGFIHHRSTPVVRRANSELFLVLSKLCLFCLSL-FIGRRLWTC 665

Y 510 NTL-LILLIGTAGLFAWMDTPVRSAGRGCLFMGLSAGS-SLYGFFGPTPAC 567
Db 666 QLRNAGISIVLCVSCILKTKMYLVAVFRASKGGATLTKFCAVQORGT-VLGTSIQ 724
Y 568 LLRQALFALGFTIFLSCLTVRSFOLIIIFKSTVPPTFYHAMWON-IGAGIFVMISSAQ 626
Db 725 AAFICFAMLLSSPKPHNIOYHKDIVECVGSGTGFVAVLSTYGLLAILFLPLAR 784
Y 627 LLICLTLVMTPTLPAREYQRFHLVMECTEINSLSFLIAFLYNGLISAFACSTLKG 686
Db 785 NLPDNEAKLITPSMLI-FCVAVVAFVPAVYNSPGYADAVEFAITSSFGLLVAFG 843
Y 687 DLPENYDAKCVTSLSLFNEVS-WIAFFTASYVDGYLPAANMAGLSSISGCGYFL 745
Db 844 PKCYIIIFRPERNT 857
Y 746 PKCYVILCRPDLNS 759

RESULT 6
ID 073639 PRELIMINARY; PRT: 880 AA.

AC 073639;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE PHEROMONE RECEPTOR.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.

RM [1]
RP SEQUENCE FROM N.A.

RX MEDLINE; 98226788.

RA NAKANO T., SATO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,

RT "Putative pheromone receptors related to the Ca2+-sensing receptor in

RT Fugu".

RL Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).

DR EMBL; AB008861; BAA26126.1; -.

DR PFAM; PF00003; 7tm_3; 1.

DR PFAM; PF01094; ANF_receptor; 1.

DR PRINTS; PR00248; GPCRMR.

KW Pheromone.

SEQUENCE 880 AA; 97464 MW; 91D72807 CRC32;

Query Match 21.8%; Score 1271; DB 13; Length 880;
Best Local Similarity 30.6%; Pred. No. 8.07e-238;
Matches 247; Conservative 214; Mismatches 298; Indels 48; Gaps 40;

Db 83 CTRSFTRFMOMMIFAVEINNAELIPNTLGYIKIYDSCSPHOSIKRAIDL-MGSE 141
Y 3 CS-FNEHGYHFLQAMRLGVEEINNSTALPNTLGLYQYDVCSDSANYATRLVSLPQ 61

Db 142 KDSQFEGKLRGCGDGNVAVYIGDGSSTOSLVARFLGVFHVPOVSFYSSCACTSDKTOF 201
Y 62 HHIELQGLHLH-YSPVYLVAVIGPDSINRAATTAALLSPFLV-HISVAASSETLSVKRQY 118

Db 202 PAFILRMPDLEVOYVALQVLYKYGWTVGYIAGDDAYRGGAALFANEVRRLLACIALY 261
Y 119 PSFLRTIPDKYQVETWVLLQKFGMTWISLVGSSDDYQGLQVQALBNALVRGICIAFK 178

Db 262 EMIR-KTQ-SQAAISSIISNRSSGAVLVAVNEQVAVRLF-DEAVRQKITGLQWLASE 318
Y 179 DIMPFSQVODERMOCIMRLHAQAGATVVVSSRQ-LARVFEFSVLTJLTGKRVWASE 237

Db 319 AMSTAAILSTPKRYHILQSGMGFAIRRADIPGQDPLRLRHPSSAADDPFLIPWEE 378
Y 238 AVALSRHTITVPISQIR-IGVILGVALIQRAVPGIKAF-EAY-ARAD-KEAP--RPHKG 291

Db 379 VFOCSLDPHGHSEAKRPGSGTEELRSVKNIYSDVQSOLRISYVYKAYAYALAKAMRSC 438

OY	292	SW-CS--SN-OL-C-RECOAFMA-HIWPKL-KAFS-MSSAYNAYRAYAAHGLHOLLGC	342
Db	439	EKSGSPSOACPDLDNIHWMOLHHYIKOYNYTRFDEKIDENGPAAWYDLINMOLT	498
OY	343	---A---SEL-CGR-GVYVWOLLEOHKXVFLH-KDYAFNDNRPLSYNIANDWN	393
Db	499	PGGDMFVTYVKGEDDIAGTRKNLHIEEKIYVNGNTOVPLSVCSICPPGTRKAIKRN	558
OY	394	-GPKMFE-TV--LGS-STWSPVOLINETKIOWHGNHQVPKSVCSDDCLEGHORVY-TG	447
Db	559	YPLCHDCVCTGAEISNQDIAECARCLEPFENSNADRTACVROVEFLSGDTIGALL	618
OY	448	FHHCCEPCVCGAGTFLNKSSELYRCQPCGTEWMAPECSQCFPRTVFLALREHTSVLL	507
Db	619	VV-SLIGSEFTCAVALVEFHRTPSPIRANNSDSELLLSLICEFSLFISPPQWS	677
OY	508	AAITLLELLGLTAGL-FANHLDTPVRSAGRLCFMLGSLAAGSGLYGFGEPTIPA	566
Db	678	CMLRHAFGITFVLICISLIGKTIIVLMAFRALPGSDVMK-WFGPKOKAILITFTLVQ	736
OY	567	CLLRQALFALGFTIFLSCLVRSFOLLIFKSTKVPTFHAWQNGAGLFWMISSAQ	626
Db	737	VVICVWLVV-APPTPOQYPPRESAIIILLCDEGSTAIFSLVGYIGVLAOCMFLAFLA	795
OY	627	ILILCTMLVWYTPDPAEY-QREFPHLVMECTEINSLGFLAFLYNGLLISAFACSYLG	685
Db	796	RKIDPNENEARLIAFSLI-FCAMVMAFVPAVYISSPGKYSTLIEIFAILAS-SVGLIGCI	853
OY	686	KDLPENENKCYFSLFENFVS-WIAFTTASVYDGKYLPAANMAGLSLSSGFGGY-743	
Db	854	FAPKCYIILMKSEKNTKHLMSKSEF 880	
OY	744	FLPKCYIILCRPDLNSTEHQASIQDY 770	
RESULT	7	PRELIMINARY: PRT: 844 AA.	
ID	093552		
AC	093552		
DT	01-NOV-1998 (TEMBLrel. 08, Created)		
DT	01-NOV-1998 (TEMBLrel. 08, Last sequence update)		
DT	01-NOV-1999 (TEMBLrel. 12, Last annotation update)		
DE	PUTATIVE ODOURANT RECEPTOR.		
GN	GEBL.		
OS	Carassius auratus (Goldfish).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;		
OC	Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinidae; Cyprinidae; Cyprinidae; Carassius.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-OLFACTORY EPITHELIUM;		
RX	MEDLINE: 98426265		
RA	CAO Y., OH B.C., STRYER L.;		
RT	"Cloning and localization of two multigene receptor families in		
RT	goldfish olfactory epithelium."		
RL	Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).		
DR	EMBL: AF083080; AAC64075.1;		
DR	PFAM: PF00003; 7tm_3.1;		
DR	PFAM: PF01094; ANF_receptor.1;		
DR	PRINTS: PR00248; GPCRNGR.		
SQ	SEQUENCE 844 AA: 94599 MW: 7A84F7AC CRC32:		
Query Match	20.8%; Score 1217; DB 13; Length 844;		
Best Local Similarity	29.2%; Pred. No. 5,15e-226;		
Matches	227: Conservative 209; Mismatches 312; Indels 30; Gaps 30;		
Db	67	SCSSVNLDRFLAQTIFAIOENKNEILLPNISIGYIIVDTGSRSLT-MTA-TMGIMN 124	
OY	2	SCS-FNEHGHLFOAMRLGVEEINNSTALLPNITLGYQLDYVDCSDANVYATLRLVSLPG 60	
Db	125	SQDFG-PGNICNGSPHAIIGSETSATYILSTTGPFKIPVISHSSCECISNRKNYP 183	
OY	61	QHIEILOGDLHRSPTLAVIGPDSINRAATIALSLPFLVH-ISTYASSETLSVKRQYP 119	

Db	184	SFFRTISSDYHOSRALASIVKHFQWGVAVNSDNDYGNNGMAIFLTKVOEGICVEY-S	242
OY	120	SFLRTINDKXYQETWYLLQKQWMTYISLVGSSDDYGGQVQALENQALVRGICLAFKD	179
Db	243	VK-FY-RTETEKLRKVDITIKGTAKYVAFISFVNG-ILIEQLSIONITGQMIGVER	299
OY	180	IMFSAQVDEBQMCLMRHLQAQATVAVVFS-RQLARVFESVLTNLTKWVAVASEA	238
Db	300	MIANTFTKSLHMGSGIFAM-KK-I-NISGFAL-YAMKFPMDIATFCSSEGNYSK	355
OY	239	WALSRIITGVPGIQRIGWLVGAIQKRAVGLAFEBAY-RADKREPRCHAG-SWCS	296
Db	356	YALSCSYEEELAKXVNEVETERYSSVYKAVAAHSLKIKOEGCEKPIQ 415	
OY	297	NOL-CRECOAFMAHTMKLAFSSSAYNAYRAYAAHGLHOLLGAS-ELCSRG-RVY	353
Db	416	POOVETFLKINFAIKTDRWFDSTGTVALYEVVNMOODSDGTQFQSVGYDASLPT	475
OY	354	PMOLLEQIHKVHFLLHK-DYAFENDNRDPLSYNIIMDWNNGP-KMTFTVLGS-STWSPV	410
Db	476	YQNHILNVENTIINAGGHLERPRASCSCEPPTKKA-QKGRPCYCIPTCAGSEISNET	535
OY	411	-Q-LNIEIKIOWHGNHQVPKSVCSDDCLEGHORVY-TGFHHCCEPCVCGAGTFLNKS	467
Db	536	REINCKPCPEWYSNAEKNKCVLKAVEFLSFTETMG-VLVFSLPGVGLLVAILFYN	594
OY	468	ELTRPCQCEIEWAPESQCFPRIVYFLALREHTSVYLAANTLLIL-LILGAGLFAW	526
Db	595	KDTPYKANNSEIFLLFLSLFCLSLFTIGRPTWSCMLCHAFGITFVLICISVL	654
OY	527	HLDPVYRSAGRLCFMLGSLAAGSGLYGFGEPTRPACLLRQALFALGFTIFLSCLT	586
Db	655	GKTIIVLMAKATLPNGNIMK-WGPAQOQLSVAFETLVYTCVLMITISPPPYNNMK	713
OY	587	VRSFQLIIFKSTKVPTFHAWQNGAGLFWISSAOLILCLVWLVWYTPDPAEYQ	646
Db	714	YKKEIILFECISLSTIGFVWLVYISLAFPLCFILAFARTLPDKNEAKFITFSMLI-F	772
OY	647	RPHLVMECTEINSLGFLAFLYNGLLISAFACSYLGDLDBENYEAACVIFSLFNF	706
Db	773	CAYWITFIPAYVSSPKFTVAVEIFAILSSFGLFGIFAPKCYIILKPEQNTKQL 830	
OY	707	VS-WIAFTTASVYDGKYLPAANMAGLSLSSGFGGYFLPKCYIILCRPDLNSTEHF	763
RESULT	8	PRELIMINARY: PRT: 940 AA.	
ID	073635		
AC	073635		
DT	01-AUG-1998 (TEMBLrel. 07, Created)		
DT	01-AUG-1998 (TEMBLrel. 07, Last sequence update)		
DT	01-NOV-1999 (TEMBLrel. 12, Last annotation update)		
DE	CALCULON+ SENSING RECEPTOR.		
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;		
OC	Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;		
OC	Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	MEDLINE: 98226788.		
RA	NAITO T., SAITO Y., YAMAMOTO J., NOZAKI Y., TOKURA K., HAZAMA M.,		
RT	"Putative pheromone receptors related to the Ca2+-sensing receptor in		
RT	Fugu."		
RL	Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).		
DR	EMBL: AB008857; BAA26122.1;		
DR	PFAM: PF00003; 7tm_3.1;		
DR	PFAM: PF01094; ANF_receptor.1;		
DR	PRINTS: PR00248; GPCRNGR.		
SQ	SEQUENCE 940 AA: 105814 MW: 034CB09E CRC32:		
Query Match	20.8%; Score 1216; DB 13; Length 940;		
Best Local Similarity	30.7%; Pred. No. 8,51e-226;		

[illegible]

QY	575	ALGFTFLSCUTSVSPFQIIIFIKFKSTAVPFPEYHAMV-QNNGAG-LFPMISSAAQILLCLT	632
Db	742	WLSISPPVQADDD-VGLOYTTECCAMASVYGSVLYGYIGLLACTCLLLAFARKIPDN	800
QY	633	WLVMVTPLPAAEYORFPHL-VMECTETNSLGFLLAFLYNGLLSISAFASYSIGKDPEN	691
Db	801	FNEAKLIFSLSLI-FCVWVAFAVAVYISSQGSVAVEIFAILAS-SYGLFCIFAPKCF	858
QY	692	YNEKCYTFSLFLEFVVS-WIAFFITASVYCGKILPAAANNAGSLSSSGGGr-FLPKCY	749
Db	859	IILLRPEKNTKKHL	872
QY	750	VILCRPDLSNTEHR	763
RESULT	11		
ID	070410	PRELIMINARY;	PRT; 912 AA.
AC	070410;		
DT	01-AUG-1998 (TEMBREL. 07, Created)		
DT	01-AUG-1998 (TEMBREL. 07, Last sequence update)		
DT	01-NOV-1999 (TEMBREL. 12, Last annotation update)		
DE	POTATIVE PHEROMONE RECEPTOR V2R2.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-VOMERONASAL NEURONS;		
RA	RYBA N.J.P., TIRINDELLI R.;		
RL	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF053986; AAC08413.1; -		
DR	PFAM; PF00003; Tm_3; 1.		
DR	PFAM; PF01094; ANF_receptor; 1.		
DR	PRINTS; PR00248; GPCRMR.		
SO	SEQUENCE 912 AA; 102348 MW; 35AEB35A CRC32;		
Query Match	17.0%; Score 994; DB 11; Length 912;		
Best Local Similarity	28.4%; Pred. No. 1,59e-177;		
Matches	231; Conservative 224; Mismatches 291; Indels 68; Gaps 51;		
Db	77	CEGNFRGFRRMKMTIKTKEINRKDLNHTLGYOIFPSCYTISKAMSSSL-VF-LTG	134
QY	3	C-STENEGYHLPQMRIGVEEINNSTLNPNTLGVOYDVC-SDSNVATLRVLSLPG	60
Db	135	QE--EKKPNFRNSGTSLIALVSGSGSSLSVAASRIILGYMPOVGYTSSCSLSDFOF	192
QY	61	QHHTELGDLHRSPTVLA-VIGPDSINRAATTAALLSP-LVHISVAASSELUSVKROY	118
Db	193	PSYLRVLPNDLQSEALVNLKHKGYWGAIALAADYCGYGYKTFREKKESANLCVAFS	252
QY	119	PSFRLIRIPNDKYQYETVWLLQKFGWMISSVSSDDYGGDGLQADLENQALVAGICIAFK	178
Db	253	ETIP-KV-YSEKKQKAVKAVKSTAKVIVLYSDIDLS-LFVLEMIHNHTDRTWATE	309
QY	179	DIMFSSQVQDEDRQCLMRHLAOGATVVVYFSS-ROLAVFVESVYLTMLTGKVVASE	237
Db	310	AMITSALIANPEYFPYFGGTIGFATPSPVIGLKEFLYDVHPKKDPNDVLTIEFWQTAFN	369
QY	238	AMALSRHITGPQIGRIQGMVLGVAIOKRAVPGLKAEF-EAYARAD-KEA-PRPC-HKG--	291
Db	370	CWPMNSVPPNVNDRVMTGKEDRLYMSQOLGTGEKKEDLKNYLYDTSQLLITQCKQ	429
QY	292	-SWC-SS--N--O--L-C-RECOAF-MA-H--T--MFKLK-AF-SWS--SAYNAIR	327
Db	430	AVVAIAHGLDHLSCQGGPFGSGNOCAIIPFDFEWQWLYYUKEIKFKSHEDKAWILLD	489


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QY 328 AYAVAGLHQLGQC-ASE--LCSGRG-VY-P---WQLEQIHKVHFLHKDT-VAFND 377
DB 490 NGDKNHYDVLMMHLDDEGEISFVTVGRNFRSTNFEVLPTNSTLFTMTESRRRDSF 549
QY 378 NRDLSS-YNLIADWNGP-KWITTVLGSSST-WSPV-QLN-NEKTIQMGKNQVRSV 432
DB 550 CTQVCPGRTKRGNOGPICCFDCPCADGVSEKSGQRECDPCGEDMWSNAGSKCVPK 609
QY 433 CSSQCLEGHQRYVGFHH-CQFECVPGAGVFLNKSSELYRQPGCTEMMAPESSQTCFPR 491
DB 610 LVEFLANGELGFLTVLSTFGALVYLAIVYVYIHHRTPLVYKANDRELSTLQMSLVT 669
QY 492 TVYFLALREHSTVWLLAANTLLLLGLTGLTGFAMHLDTPVRSAGRLCTFLMGSLAAG 551
DB 670 VLSLU-FIKPCWMSMAROITLALGCPCLSLISLCKTISLEFARISYKTRLI-S-M 726,
QY 552 S-GSLVGFEEPRPACLRALFALGFTTLFSLCTVRSFOLLITFEKSTVPTFYHAMV 610
DB 727 HPIFRKLIVCVVGEIGVCAAYLVLEPPRMFKNE-IQWYKILFECNE-GSVFELCSIF 784
QY 611 QNNGAGLFVWISSAQLICLTWLVWTPPLPAREYQRFPHL-VMLECTETNSLGFT-LAF 668
DB 785 GFDVRLALFLFTTVARQDPNDYBCKCTFGMLVFPIYVWISFVPAVYSTGKFKYAVE 844
QY 669 LYNGLSISAFACSYLCKDLPENYNEAKCVFSLFNFVSIATFTASVYDGKYLPAAN 728
DB 845 IFALIAS-SYGLGCLFLPFCITILPKRNTDE 877
QY 729 MMAGLSLSSGFGY-FLPKCYILCRDLNSTE 761

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RESULT 12
AC 070409: PRELIMINARY: PRT: 855 AA.
DT 01-AGC-1998 (Tremblrel. 07, Created)
DT 01-AGC-1998 (Tremblrel. 07, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE PUTATIVE PHEROMONE RECEPTOR V2R1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-VOMERONASAL NEURONS;
RX MEDLINE: 97436753.
RA RYBA N.J., TIRINDELLI R.;
RT "A new multigene family of putative pheromone receptors.";
RL Neuron 19:371-379(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-VOMERONASAL NEURONS;
RA RYBA N.J.P., TIRINDELLI R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF053385; AAC08412.1; -
DR PFAM: PF00003; 7tm_3; 1.
DR PFAM: PF01094; ANF_receptor; 1.
SQ SEQUENCE 855 AA; 96215 MW; C8389BJC CRC32;

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Query Match 16.2%; Score 946; DB 11; Length 855;
Best Local Similarity 28.3%; Pred. No. 3,72e-167;
Matches 223; Conservative 204; Mismatches 313; Indels 49; Gaps 45;

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DB 79 YOHILAVFAIEKINKPDLFNKSLGFFLVNFIMKAAEGSMAL-LGESPPIPNYS 137
QY 10 YHFOAMRLVEELINNTALPNTLTGLQYDVCSDSANVYATLRKVLSTFGQ-HHILQG 68
DB 138 CREPTDKLAVIGISTSIQISRYLSYVPOISYAFPDQILGTQVLOQSPQFSMH 197
QY 69 DLHYSPTVALVIGSDSTNRATTAALLSPVLY-HISYASSSELVSKRQYF-FLATIP 126
DB 198 TAAIYQ-GIVOLLV-FTWIVGLVPPDDMRGELYLRDITKEMISHGICFAFAKVEYS 255

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QY 127 NDK-YOYETVALLQKFGWTWISLVGSSDDYDGLGVQALENOALVIGICIAFKD-IMPFS 184
DB 256 SMDTVMMKH-FMERLPLT-PVITVGDTHSLRIYV-FVYFVLGSGWTTSDWITTL 312
QY 185 AQYDGERMOCIMHHLAQAGATVYVVSROLARVFESVLTITLTKVWASAMLSRH 244
DB 313 PFONLTYTHFGGSLFSPFMEDELIGFKDPLRSQVPRKYPHDFIRHVSLSLGCCHYQ 372
QY 245 ITGVPGI-QRIGVAVLQKRAVPGLKAFEEAY-ARA-DKEA-PRPKHGSN-CSSN-Q 298
DB 373 HRMLDSQCEPNSSLTSPRLHAMDNTSPYKYVYAAVTAIAQALHEELSRREGSSNK 432
QY 299 -L-C-RECOFAHATMPKLAFSM-SS-AYNAYRAYVAVAGHLQ-L-L--GCASEL 346
DB 433 CLLOAPLPWKHLPFOQKAO-IGRSTNEENTVNE-VSALKLDIFNYSQISQSGTEAHVKV 490
QY 347 CSRGRTYPMOLLEQIHKVHFLHKDTVAERNDNDPLSTNITAMDNGPRW-TFT-V-IG 403
DB 491 EFVDSHVSQHLSLNDKILTW-GKHSQTPLSVCSQCFEFSKTAVEGKPFCCPCVPC 549
QY 404 SSTW-S-PVQ-LNINTEKIQMGKNH-QYPKSVCSDDCLEGHQRY-VTGFHCCFCVPC 458
DB 550 PDEIANKTDMHOCICPEQYFNKQKNOCPLKTIILFLAHEDPLGVLYSLAISAFSA 609
QY 459 GAGTFNKSSELYRCQCGTEEMAPBESSQTCFRTVFLALRETSVWLLAANTLLILL 518
DB 610 MTLGLFCYAREPIYVANNRNLSTYLLISLKLCFCSLI-FIQGPRTVCULRQIFGIY 668
QY 519 GTAGLFRMHLDTPVVSAGRLCFMLGSLAAGS-SLGFEEPRPACLRALFALG 577
QY 578 FTIFLSCLTVRSFOLLITFEKSTVPTFYHAMVQNGAGLFWISSAQLICLTWLVW 637
DB 728 PPPDDVMHSEFQIILM-CNESTIATFCVGLYGLFPLSLILFLARLPDSNEAK 786
QY 638 TPLPAREYQ-FPHLVMLECTETNSLGFTLAFLYNLSTISAPACSYLCKDLPENYNEK 696
DB 787 TIFSMUV-FCSWISFVPAVYISSKGTMYAVELISLAS-SAGLGCFLPCKYILK 844
QY 697 CVFSLFNFVS-WLAFITASYDGKLYPLAANMAGLSLSSGFGY-FLPKCYILCR 754
DB 845 SGGHSRRKF 853
QY 755 PDLNSTEHF 763

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RESULT 13
AC 035269: PRELIMINARY: PRT: 779 AA.
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE PUTATIVE PHEROMONE RECEPTOR.
GN GO-VNS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE: 97433086.
RA HERRADA G., DUDAC C.;
RT "A novel family of putative pheromone receptors in mammals with a
RT topographically organized and sexually dimorphic distribution.";
RL Cell 90:763-773(1997).
DR EMBL: AF016182; AAC53329.1; -
DR PFAM: PF00003; 7tm_3; 1.
DR PFAM: PF01094; ANF_receptor; 1.
SQ SEQUENCE 779 AA; 88036 MW; B89CEAD5 CRC32;

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Query Match 15.7%; Score 915; DB 11; Length 779;
Best Local Similarity 25.5%; Pred. No. 1,79e-160;

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Matches 198; Conservative 223; Mismatches 310; Indels 45; Gaps 40;	
Db	1 MRFAIEEINSPHLPNTSLGFEINNV-PHGOR-YTLVKLFSSLSGSNY-DIPNYSASE 57
Qy	16 MRLGVEEENNTALLPNTLTGQLYDYVSDSANYATIRYLS-LPGQHIEQSLHYS 74
Db	58 SNSAAVLTPSWTI-SECVGTLDDLKFPQTLFGPFDLSLEQRSSLYOAPKDFLT 116
Qy	75 PTYLAIV-GPDSIRNAATALLSPF-LVHISYASSETLSVSRQYPSFLRTIPNDKQY 132
Db	117 PGISLMHFHMNVGFLIIDDDKGAQTLSDLRNEMKNGCTAVEIPVIGSFFTKS 176
Qy	133 ETMYLLQKFGFWTISLVGSSDDYQGLGVALENQALVYICIAKDKIMP-FSAQV-CDE 190
Db	177 WKN-HVQIL-ESSSNVLIYGDSDLSLIYNIKQLTMYWVLIQMDVSK-FDDYEM 233
Qy	191 RMQCLMRLAAGATVYVVFSSRQIARVFFESVYLTNLTKWVASEMALSRLHTGPG 250
Db	234 VDSLHGLIFSHAREEIPNFTDFMOKYNSPKYPEDTYLHVIMHYFNSFYKDKCIYHN 293
Qy	251 IORIGMVLGVALOKRAVYGLKAFEEAYARAD-KEAP-RPC--HKGSMCS-SNOJCREQA 305
Db	294 CLPNASLGFLPGNIFDAMSEESTNVNAVVAHSHLHMLNOVQPTHEKCKKMPFP 353
Qy	306 FMAHT-MPKL-KAFSMS-S--AYNAVAYVAHGLHQL-LG-CASELCSRG-R-VY-P 354
Db	354 WQLPFLERROLINONGANEDLCTRKSHVEYDILNF-WNPKGLGLWYKYGIFSPAPK 412
Qy	355 WQLLEQIHKVFLHKLQVYA-FNDNRDPLSSYNIITAMWNGPK-WTFYV-LGS-STWSP- 409
Db	413 EOKLSSNMLOMATGSTIEIPQSVCSCHAPFRKTHOEGVACFDICPENEISNET 472
Qy	410 VQ-LININEKIQMHGKNHQVKSVSSDCLGSHQVYT-GRHOCFECVPCGAGFLNKS 467
Db	473 DVDQVCPCPEHYANIEKIHLOKTYTFLYYDDPLGKTL-CFMSIGESLSLAAYLVFLK 531
Qy	468 ELYRCQPCGTEWAPESQTCFPRTVFLALREHTSWLLAANTLLLLLLGTA-GLFAM 526
Db	532 NRDPPIVANKALASYTLITLMLCFLCPLIFIGRPTASCILOONIFGLFTVALSTVL 591
Qy	527 HLDPPVRSAGRCFLMLGSLAGSGSLYGFGEPTPACILRLQALALGFTITLSCLT 586
Db	592 AKITTVIAFKITS--PGRIIRWLLISAPNFIIPLCTLLQVFLSGVLTSPPIDXA 649
Qy	587 VRSQOLIIEFESTKVPFEYHAMVQ-NHGAGLEWISSAQLLCLMLVMTPLPAREY 645
Db	650 HSEGHIIIT-CNKGSAVAFHONIGYCALALVSTFMAFLSRNLPDITNEAKFLAFSLV 708
Qy	646 QR-PPHVLMECTETNSIGFLIAYLNGLLISAFACSYLGDKDPENYNEAKCVTFSLF 704
Db	709 -FCSVWVTELPVYHSTGKNVAMEVPSILASSSTSLGIIIFAPKCYLLLRPERNS 763
Qy	705 NFVS-WIAFFTASYDGKTYLPAANMMAGLSLSSGFGYLPKCYVILCRPDLNS 759
RESULT 14	
ID	062916 PRELIMINARY; PRT; 983 AA.
AC	062916;
DT	01-NOV-1996 (TEMBLrel. 01, Created)
DT	01-NOV-1996 (TEMBLrel. 01, last sequence update)
DE	01-NOV-1999 (TEMBLrel. 12, last annotation update)
DE	METABOTROPIC GLUTAMATE RECEPTOR 4B.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN	[1]
RP	SEQUENCE FROM N.A.
RA	O'HARA P.J.;
RL	Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR	EMBL: U47331; AAA88788.1;
DR	PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR	PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR	PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.

DR	PFAM; PF00003; 7tm_3; 1.
DR	PFAM; PF01094; ANF_receptor; 1.
DR	PRINTS; PR00248; GPCBR.
DR	PRINTS; PR00593; MTABOTROPICR.
SO	SEQUENCE 983 AA; 109276 MW; E4209F27 CRC32;
Query Match	
Best Local Similarity 27.3%; Pred. No.3,21e-145;	
Matches 217; Conservative 223; Mismatches 287; Indels 68; Gaps 54;	
Db	72 KEKGIRLEAMLPALDRINDPDLIPNTLTGACRLDTCSTHABDGLTVRALIEKD 131
Qy	6 NEHGHLQAMRLGVEEENNTALLPNTLTGQLYDYVCS-DSANVATYLR-VLSIPGQH 63
Db	132 TEVCGSGCPPIILKPEYVGVIGASGSSVIMANIRKEKIQIQAASAPRLSDSR 191
Qy	64 IELQ---GDL-LHYSPT-VLAVIPDSTNRATTAALLSPFLV-HISYASSETLSVKRQ 117
Db	192 YDFSRVPSDTYOQAMVDIVRALKMYVSTLASGSGSEGYEAFIOKRENGVCIA 251
Qy	118 YPSFLRTIPNDKYQVETMVLLQKFGWTVISVSSDDYQGLGVALENQALVYRG-ICIA 176
Db	252 QSVKIPREPRTGEEDKT--IKRLIETSNAGIIFANEDJIRVLEAARRANOTGHEFWX 309
Qy	177 FKDIMPSAQVD-ERMQCLMRLAAGATVYVVFSSRQIARVFFESVYLTNLTKGY-WV 234
Db	310 GSDSMG-SKS-APLRLIEVNEG-AVITLPRKMS-VRGEDYFESSRTLDNRRNIWFAEF 365
Qy	235 ASEAMALSRHITGVPGIORIGMVLGVALOKRAVYGLKAFEEAYV-RDKKEAPRPC-HKGS 292
Db	366 W-EDNFHCKLSRHALKKGSHIKCTNREIRIGDSAYE2QGVQVVIDAVYAMGALHAMH 424
Qy	293 WCSSNOJCREC-QAFM-AHTMP-KLKA-FSMSAYN-A---Y-R-AVYVAHGLHQL 340
Db	425 RDLCPRGVGLCPRMDPDVDTGLKYIRNVNFSGLAGNVTFNENGADAGRDYIYOQLRN 484
Qy	341 -G-CAS-ELCSR-GRAYPMQLEQIHKVHPL-LHKDVAANDNRDPLSSYNIITAMD-WN 393
Db	485 GSA-EYKYIGS--MTD-HLHRIERMQWPGSGOOLPRISGLPCQPGRKKTVMGMA-CC 539
Qy	394 GKMTFTVLSSTSPVOLNINETKIOMHGKNHGVPSVCSDCLEG-HQHVYTGFFHCC 452
Db	540 WHCEPC-TG-YOYQVDRYCTXCTPYDMRPTENRTSCOPIPVKLE-MD-SPWAVLPFLA 595
Qy	453 FECVPCGAGTFLNKSELYRQPCGTBEWAPBSQTCFPRTVFLALRHRTGM-VL-LAAN 510
Db	596 VVGIAATLVVVTVRYNDPIYKASGRELSYVLLAGIFLCYATTFILMAIPDLGTSGLR 655
Qy	511 TLLLLLTGTAGLPAMHLDTPVRSAGRCFLMLGSLAGSGSLYGFGEPTPACILR 570
Db	656 RIFGLGNSISYALLIKINRYKIFEDGKRSVAPRISASQALITFIIS--LQLLG 713
Qy	571 QALPALGFTIFLSGLTVRSFQLIITFEFSTK-VPTFYHAMVQNGAGLEVVISSAQLL- 628
Db	714 ICV-WFVVDPSHSYVDDODRTLDPRFARGYLK-DISDLSLIGLIGSLMYNTCYVA 771
Qy	629 ICLTWLVMTPLPAREYO-R-F-PHLV--MDECTENSLGFIILAYLNGLLISAFACS 682
Db	772 IKIRGVPEPTEAKPIGFTMYTCIWLAFIPFGISQSAKLYIOTTLTVSVSISAS 831
Qy	683 YLGDLDPENYNEAKCVFSLFNVSWIAF--FTIASVYDGK-YLPAANMMAGHS-SLS 737
Db	832 VSLGMKVPKYIITL 845
Qy	738 SGFGYLPKCYVIL 752
RESULT 15	
ID	093555 PRELIMINARY; PRT; 458 AA.
AC	093555;
DT	01-NOV-1998 (TEMBLrel. 08, Created)
DT	01-NOV-1998 (TEMBLrel. 08, last sequence update)
DT	01-MAY-1999 (TEMBLrel. 10, last annotation update)

 WISE (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:29:20 2000; Maspar time 43.87 Seconds

Tabular output not generated. 528,906 Million cell updates/sec

Title: >US-09-361-652-3
 Description: (1-777) from US09361652.pep
 Perfect Score: 5838
 Sequence: 1 RSCSFNHHGYHLFQAMRLGV.....NSTHFQASIDQYTRCGST 777

Scoring table: PAM 150
 Gap 11

Searched: 82229 seqs, 29854866 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot38
 1:swissprot

Statistics: Mean 53.443; Variance 92.251; scale 0.579

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1170	20.0	1085	1	CASR_BOVIN	1.05e-237
2	1160	19.9	1078	1	CASR_HUMAN	2.67e-235
3	1158	19.8	1079	1	CASR_RAT	8.09e-235
4	856	14.7	912	1	MGR4_RAT	9.24e-163
5	846	14.5	912	1	MGR4_HUMAN	2.13e-160
6	798	13.7	1203	1	MGR5_RAT	4.44e-149
7	796	13.6	1199	1	MGR1_RAT	1.31e-148
8	786	13.6	1212	1	MGR5_HUMAN	1.31e-148
9	789	13.5	872	1	MGR2_RAT	5.82e-147
10	787	13.5	1194	1	MGR1_HUMAN	1.72e-146
11	772	13.2	908	1	MGR8_MOUSE	5.74e-143
12	768	13.0	908	1	MGR8_RAT	4.99e-142
13	761	13.0	872	1	MGR2_HUMAN	2.19e-140
14	757	13.0	908	1	MGR8_HUMAN	1.90e-139
15	729	12.5	871	1	MGR6_RAT	6.82e-133
16	731	12.5	877	1	MGR6_HUMAN	2.32e-133
17	718	12.3	879	1	MGR3_RAT	2.54e-130
18	714	12.3	877	1	MGR3_HUMAN	2.18e-129
19	675	11.6	915	1	MGR7_HUMAN	2.64e-120
20	674	11.5	915	1	MGR7_RAT	4.50e-120
21	452	7.7	976	1	MGR_DOME	2.12e-69
22	333	5.7	999	1	MGR1_CAELI	2.05e-43
23	150	2.6	986	1	CYGR_ARABU	1.21e-07

RESULT ID	1	STANDARD:	PTI:	1085 AA.	ALIGNMENTS
AC	P35384;				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	01-OCT-1996 (Rel. 34, Last annotation update)				
DE	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR).				
GN	CASR OR PCAR1.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;				
OC	Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.				
OC	Bovinae; Bos.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=PARATHYROID.				
RX	MEDLINE: 94077182.				
RA	BROWN E.M., GAMBA G., RICCARDI D., LOMBARDI M., BUTTERS R., KIFOR O., SUN A., HEDIGER M.A., LYTON J., HEBER S.C.;				
RA	"Cloning and characterization of an extracellular Ca(2+)-sensing receptor from bovine parathyroid."				
RT	Nature 366:575-580(1993).				
RL	Nature 366:575-580(1993).				
CC	-1- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.				
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
DR	EMBL: S67307; AAB29171.1; -.				
DR	PIR: S40476; S40476.				
DR	GCORDB: GCR_0900; -.				
DR	PROSITE: PS00979; G-PROTEIN RECP_F3.1; 1.				
DR	PROSITE: PS00980; G-PROTEIN RECP_F3.2; 1.				
DR	PROSITE: PS00981; G-PROTEIN RECP_F3.3; 1.				
DR	PRAM: PF00003; 7tm_3; 1.				
DR	PRAM: PF01094; ANF_receptor; 1.				
KW	G-protein coupled receptor; Transmembrane; glycoprotein; signal.				
FT	SIGNAL 1 19				

FT	CHAIN	20	1085	EXTRACELLULAR CALCIUM-SENSING RECEPTOR
FT	DOMAIN	20	613	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	614	636	I (POTENTIAL).
FT	DOMAIN	637	650	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	651	671	II (POTENTIAL).
FT	DOMAIN	672	682	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	683	701	III (POTENTIAL).
FT	DOMAIN	702	725	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	726	746	IV (POTENTIAL).
FT	DOMAIN	747	770	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	771	793	V (POTENTIAL).
FT	DOMAIN	794	806	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	807	829	VI (POTENTIAL).
FT	DOMAIN	830	837	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	838	863	VII (POTENTIAL).
FT	DOMAIN	864	1085	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	91	91	POTENTIAL.
FT	CARBOHYD	131	131	POTENTIAL.
FT	CARBOHYD	262	262	POTENTIAL.
FT	CARBOHYD	288	288	POTENTIAL.
FT	CARBOHYD	401	401	POTENTIAL.
FT	CARBOHYD	447	447	POTENTIAL.
FT	CARBOHYD	469	469	POTENTIAL.
FT	CARBOHYD	489	489	POTENTIAL.
FT	CARBOHYD	542	542	POTENTIAL.
FT	CARBOHYD	595	595	POTENTIAL.
EQ	SEQUENCE	1085 AA:	121170 MW: 501kD	CRG32;

Query Match 20.08; Score 1170; DB 1; Length 1085;

2007 LOCAL SIMILARITY 21.50, FREQ. NO. 1.00E 207,
 Matches 263; Conservative 227; Mismatches 256; Indels 78; Gaps 56;

[illegible][illegible]

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ID RESULT 2 CASR HUMAN STANDARD; PRT: 1078 AA.
AC P41180; Q133912; Q16379; Q16108; Q16109; Q16110;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID
DE CELL CALCIUM-SENSING RECEPTOR).
CN CASR OR PCAR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA PEARCE S.H.S., THARKER R.V.:
RL submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-PARATHYROID;
RX MEDLINE: 95279439.
RA GARRETT J.E., CAPUANO I.V., HAMMERLAND L.G., HUNS B.C., BROWN E.M.,
RA HEBERT S.C., NEMETH E.F., FULLER F.;
RT "Molecular cloning and functional expression of human parathyroid
RT calcium receptor cDNAs.";
RL J. Biol. Chem. 270:12919-12925(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RX MEDLINE: 95408281.
RA AIDA K., KOISHI S., TAMATA M., ONAYA T.;
RT "Molecular cloning of a putative Ca(2+)-sensing receptor cDNA from
RT human kidney.";
RL Biochem. Biophys. Res. Commun. 214:524-529(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96343808.
RA FRIGHEL M., ZINK-LORENZ A., HOLLOSCHI A., HAFNER M., FLOCKERZI V.,
RA RAUE F.;
RT "Expression of a calcium-sensing receptor in a human medullary
RT thyroid carcinoma cell line and its contribution to calciumln
RT secretion.";
RL Endocrinology 137:3842-3848(1996).
RN [5]
RP VARIANTS FHH GLU-185; LYS-297 AND TRP-795.
RX MEDLINE: 94094324.
RA POLLAK M.R., BROWN E.M., CHOI Y.H., HEBERT S.C., MAXX S.J.,
RA STEINMANN B., LEVI T., SEIDMAN C.E., SEIDMAN J.G.;
RT "Mutations in the human Ca(2+)-sensing receptor gene cause familial
RT hypocalcaemic hypercalcaemia and neonatal severe
RT hyperparathyroidism.";
RL Cell 75:1297-1303(1993).
RN [6]
RP VARIANT ADH ALA-127.
RX MEDLINE: 95179179.
RA POLLAK M.R., BROWN E.M., ESTEP H.L., MCILAIN P.N., KIFOR O., PARK J.,
RA HEBERT S.C., SEIDMAN C.E., SEIDMAN J.G.;
RT "Autosomal dominant hypercalcaemia caused by a Ca(2+)-sensing receptor

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RT gene mutation.";
 RL Nat. Genet. 8:303-307(1994).
 [17]
 RP VARIANTS FHH MET-62; CYS-66; MET-138; GLU-143 AND GLN-227.
 RX MEDLINE: 95243222.
 RA CHOU Y.-H.W., POLAK M.R., BRANDI M.L., TOSS G., ARNOVIST H.,
 RA ATKINSON A.B., PAPADOPOULOS S.E., MARX S., BROWN E.M., SEIDMAN J.G.,
 RA SEIDMAN C.E.;
 RT "Mutations in the human Ca(2+)-sensing-receptor gene that cause
 RL familial hypocalcemic hypercalcemia.";
 Am. J. Hum. Genet. 56:1075-1079(1995).
 [8]
 RP SEQUENCE OF 1-61 FROM N.A., AND VARIANT FHH ALA-39.
 RX MEDLINE: 95403641.
 RA AIDA K., KOISHI S., INOUE M., NAKAZATO M., TAMATA M., ONAYA T.;
 RT "Familial hypocalcemic hypercalcemia associated with mutation in the
 RL human Ca(2+)-sensing receptor gene.";
 J. Clin. Endocrinol. Metab. 80:2594-2598(1995).
 [9]
 RP VARIANTS NSHPT LEU-227 AND TYR-598.
 RX MEDLINE: 96292293.
 RA PEARCE S.H.S., TRUMP D., WOODING C., BESSER G.M., CHEW S.L.,
 RA GRANT D.B., HEATH D.A., HUGHES I.A., PATERSON C.R., WHITE M.P.,
 RA THAKKER R.V.;
 RT "Calcium-sensing receptor mutations in familial benign hypercalcemia
 RL and neonatal hyperparathyroidism.";
 J. Clin. Invest. 96:2683-2692(1995).
 [10]
 RP VARIANTS ADHP THR-116; HIS-681 AND SER-806, AND VARIANT SER-851.
 RX MEDLINE: 96311554.
 RA BARON J., WINER K.K., YANOVSKI J.A., CUNNINGHAM A.W., LAUE L.,
 RA ZIMMERMAN D., CUTLER G.B. JR.;
 RT "Mutations in the Ca(2+)-sensing receptor gene cause autosomal
 RL dominant and sporadic hypoparathyroidism.";
 Hum. Mol. Genet. 5:601-606(1996).
 [11]
 RP VARIANT FHH ARG-174.
 RX MEDLINE: 97442275.
 RA WARD B.K., STUCKEY B.G.A., CUTTERIDGE D.H., LAING N.G., PULLAN P.T.,
 RA RATAJCZAK T.;
 RT "A novel mutation (L174R) in the Ca2+-sensing receptor gene
 RL associated with familial hypocalcemic hypercalcemia.";
 Hum. Mutat. 10:233-235(1997).
 [12]
 RP FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF
 CC CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A
 CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM.
 CC
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS SEEM TO BE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC
 CC -1- TISSUE SPECIFICITY: FOUND IN KIDNEY, BUT NOT IN BRAIN, LUNG,
 CC LIVER, HEART, SKELETAL MUSCLE, OR PLACENTA.
 CC
 CC -1- DISEASE: DEFECTS IN CASR ARE A CAUSE OF FAMILIAL HYPOCALCAEMIC
 CC HYPERCALCAEMIA (FHH) AND NEONATAL SEVERE HYPERPARATHYROIDISM
 CC (NSHPT). TWO INHERITED CONDITIONS CHARACTERIZED BY ALTERED CALCIUM
 CC HOMEOSTASIS. THE MUTATIONS REDUCE THE ACTIVITY OF THE RECEPTOR.
 CC FHH AFFECTED INDIVIDUALS EXHIBIT MILD OR MODERATE HYPERCALCAEMIA.
 CC RELATIVE HYPOCALCAEMIA, AND INAPPROPRIATELY NORMAL PTH LEVELS. IN
 CC CONTRAST, NSHPT IS A RARE AUTOSOMAL RECESSIVE LIFE-THREATENING
 CC DISORDER CHARACTERIZED BY VERY HIGH SERUM CALCIUM CONCENTRATIONS,
 CC SKELETAL DEMINERALIZATION, AND PARATHYROID HYPERTROPHY. IN SOME
 CC INSTANCES NSHPT HAS BEEN DEMONSTRATED TO BE THE HOMOZYGOUS FORM OF
 CC FHH.
 CC
 CC -1- DISEASE: DEFECTS IN CASR ARE ALSO THE CAUSE OF AUTOSOMAL DOMINANT
 CC HYPOCALCAEMIA (ADH) IN WHICH THE RECEPTOR IS ACTIVATED AT SUBNORMAL
 CC CA(2+) LEVELS.
 CC
 CC -1- DISEASE: DEFECTS IN PCAR1 ARE ALSO THE CAUSE OF AUTOSOMAL DOMINANT
 CC HYPOPARATHYROIDISM (ADHP). ADHP IS CHARACTERIZED BY HYPOCALCAEMIA
 CC AND HYPERPHOSPHATEMIA DUE TO INADEQUATE SECRETION OF PARATHYROID
 CC HORMONE. SYMPTOMS ARE SEIZURES, TETANY AND CAMPS.
 CC
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC or send an email to license@sib.ch).
 CC
 CC -----
 CC EMBL: X81086; CAA56990.1; -
 CC DR EMBL: U20759; AAA86503.1; -
 CC DR EMBL: U20760; AAA86504.1; -
 CC DR EMBL: D50855; BAA09453.1; -
 CC DR EMBL: S83176; AAB66873.1; -
 CC DR EMBL: S79217; AAB35262.1; -
 CC DR EMBL: S68032; AAB29413.1; -
 CC DR EMBL: S68033; AAB29414.1; -
 CC DR EMBL: S68036; AAB29415.1; -
 CC DR GCRDB; GCR_1337; -
 CC DR GCRDB; GCR_1874; -
 CC DR GCRDB; GCR_2012; -
 CC DR GCRDB; GCR_2013; -
 CC DR GCRDB; GCR_2696; -
 CC DR GCRDB; GCR_2697; -
 CC DR MIM; 601199; -
 CC DR MIM; 145980; -
 CC DR MIM; 601198; -
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 CC DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
 CC DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
 CC DR PFAM; PF00003; 7tm_3; 1.
 CC DR PFAM; PF01094; ANF_receptor; 1.
 CC DR G-protein coupled receptor; Transmembrane; glycoprotein; signal;
 CC Disease mutation; Alternative splicing; Polymorphism.
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 CC FT DOMAIN 638 649
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 CC FT TRANSMEM 725 745
 CC FT DOMAIN 746 769
 CC FT TRANSMEM 770 792
 CC FT DOMAIN 793 805
 CC FT TRANSMEM 806 828
 CC FT DOMAIN 829 836
 CC FT TRANSMEM 837 862
 CC FT DOMAIN 863 1078
 CC FT CARBOHYD 90 90
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 CC FT CARBOHYD 400 400
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 CC FT CARBOHYD 468 468
 CC FT CARBOHYD 488 488
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 CC FT CARBOHYD 594 594
 CC FT CARBOHYD 536 536
 CC FT VARSPLIC 39 39
 CC FT VARIANT 62 62
 CC FT VARIANT 66 66
 CC FT VARIANT 116 116
 CC FT VARIANT 127 127
 CC FT VARIANT 127 127
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 CC R -> M (IN WILD FHH AND NSHPT).
 CC /FTId=VAR_003586.
 CC R -> C (IN FHH).
 CC /FTId=VAR_003587.
 CC A -> T (IN ADHP).
 CC /FTId=VAR_003588.
 CC E -> A (IN ADH).
 CC /FTId=VAR_003589.
 CC
 CC Note: remainder of annotations omitted.

Query Match 19.9%; Score 1160; DB 1; Length 1078;
 Best Local Similarity 31.9%; Pred. No. 2,67e-235;
 Matches 263; Conservative 232; Mismatches 250; Indels 80; Gaps 57;

DB 60 C19NFGEFWMQAMTAIEEINSPLLNLTGRIPTCTVSKALEA--TLSEVAQ 117
 C-SENEGYHLPQAMRIGVEINNSTLPLNTLGYDVCSDSNAVYTLRLSLPGQ 61
 DB 118 NKIDSLNDEFCNCEHPIPTIAVVGATGSVSTAVANLGLFIPVSVASSRLSNK 177
 HHE-LO-GDLHRS---PYLAVIGDSTRRAITALLSPFLV-HISAASETLSVK 115
 DB 178 NOEKFRLTIPNDEHOATAMADIEFRMNVGTIADDYGRPGIKFEFEAEEDICI 237
 ROYPSFLRTIPNDKYQETVWLLQKRGWMLSVGSSDDYGGQVQALEMQLVRIICI 175
 DB 238 DESELSIQYDE--EE-IGHVEYIIONSTAKVYVESGGDLEPLKE-IVRRNITGKIW 293
 AFQDIMP-FSAQVODERMOCLMRHLAGATVYVVFES--ROLARVPESEVLTTLTGKW 233
 DB 294 LASEANSSSLIAMPQYFHVVGITGFALAGDIPGREFLKVKHPRKSVHNGPAKEME 353
 VASEANA--L-S--R--HITVP-GIQ-RIGMYLV-A-IQK--R-APV-GI-KAF-E 274
 DB 354 ETENCLQEGAKGPLPYDTFLRGHEESGDRFSNSTAFRLCTGDENISSVEPYDYTH 413
 EAVA-R-ADKE-APRCH---KSGMCSNQLCRECAAF--M-A--HTMPLKA---FS- 318
 DB 414 LRISYNYLAVYSTAHMLDQIYICLPGRGFTNSCADIKVEMOVLKHLRHLNFNNM 473
 MSAYNAYRVYVAVHGLHDLGC-AS-EL---CS-RGRVYFMWLEIDHVKHFLHK 370
 DB 474 GEOVTEDECGLVGNYSIIMMHLSPEDGSIVFKEVGYNYAKGEBLFINKEILMSGF 533
 DVAIFNDNDPLSSYIIMDMNGR-WI-FYVLGS-SWSP-VQ-LINNETKIOMHGK 424
 DB 534 SREVPSSNCRDCLAGTRKIIIGSEPTCECEVCPGDEYSDETASACNKPDPDFMSNE 593
 NHQVPSKVCSSDLEGHOR-VVTGFHHCCEFCVCGAGTFLNKSELYRCQPCGTEWAPE 483
 DB 594 NHNSCIKAELEFISWTEPFG-IALTFLAVIGIFLAVLVFIFKRTPIYKATNRELSY 652
 GSOTCEPRIVFALRHTSWLLANTLILLGLG-TAGLFAHMLDTPVARSAGRLCF 542
 DB 653 LILFSLCCSSSLF-FIGEPDWTCLROPARISFVLCISCLITVNTNVLVE--AK 709
 LMGSLAAG-SGSLXGFGEPTRACILRLRALGTTITLSCLTYSFOLIIIFKSTK 601
 DB 710 IPTSPHRKMWGLMLQFLVLELCTFMQIVICVILYTAPESSSYNOLEDEIIFITCHE-G 768
 VPI-FYHAWQNHGAGLFVMISSAQLICTLMLVWTPPLPAREYQRPPLVMECTETN 660
 DB 769 SL-MALGELIGYCLALAIFFFAFRKRPENNEKFTFSLIFFIYIWIPIYAS 827
 SLGFIILAFI--YNGLLISAFACSYLGKIDLPENNEKACTFSLIFVSWIAFFT-AS 717
 DB 828 TY-GKEVSAVEVAILAA-SFGLLACIFFKIYIILFKPSRNTIE 870
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 QY 718

RESULT 3
 ID CASR RAT STANDARD; PRT; 1079 AA.
 AC P48442;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 33, Last annotation update)
 DE EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID
 CELL CALCIUM-SENSING RECEPTOR).
 GN CASR OR PCARL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-KIDNEY OUTER MEDULLA;
 RX MEDLINE; 9516508.
 RA RICCARDI D., PARK J., LEE W., GAMBA G., BROWN E.M., HERBERT S.C.;
 RT "Cloning and functional expression of a rat kidney extracellular
 RL "calcium/polyvalent cation-sensing receptor".
 RN Proc. Natl. Acad. Sci. U.S.A. 92:131-135(1995).
 RP [2]
 RP SEQUENCE OF 1-294 FROM N.A.
 RC STRAIN-MISTAR;
 RX MEDLINE; 95241465.
 RA RUAT M., SNOWMAN A.M., SNYDER S.H.;
 RT "Calcium sensing receptor: molecular cloning in rat and localization
 RT to nerve terminals".
 RL Proc. Natl. Acad. Sci. U.S.A. 92:3161-3165(1995).
 CC -I- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF
 CC CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A
 CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM.
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -I- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC CC
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 CC
 CC DR EMBL; U10354; AAC52149.1; .
 CC DR EMBL; U20289; AAC52195.1; .
 CC DR GCRDB; GCR.1449; .
 CC DR PROSITE; PS00979; G-PROTEIN_RECEP_F3_1; 1.
 CC DR PROSITE; PS00980; G-PROTEIN_RECEP_F3_2; 1.
 CC DR PROSITE; PS00981; G-PROTEIN_RECEP_F3_3; 1.
 CC DR PFAM; PF00003; 7tm_3; 1.
 CC DR PFAM; PF01094; ANF_receptor; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 CC FT SIGNAL 1 19
 CC FT CHAIN 20 1079
 CC FT DOMAIN 20 612
 CC FT TRANSMEM 613 635
 CC FT DOMAIN 638 649
 CC FT TRANSMEM 650 670
 CC FT DOMAIN 671 681
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 CC FT TRANSMEM 725 745
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 CC FT TRANSMEM 770 792
 CC FT DOMAIN 793 805
 CC FT TRANSMEM 806 828
 CC FT DOMAIN 829 836
 CC FT TRANSMEM 837 862
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 CC FT CARBOHYD 90 90
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 CC FT CARBOHYD 261 261
 CC FT CARBOHYD 287 287
 CC FT CARBOHYD 386 386
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 CC FT CARBOHYD 468 468
 CC FT CARBOHYD 488 488
 CC FT CARBOHYD 541 541
 CC FT CARBOHYD 594 594
 CC SQ SEQUENCE 1079 AA; 120867 MW; 34118BE9 CRC32;

Query Match 19.8%; Score 1158; DB 1; Length 1079;
 Best Local Similarity 31.4%; Pred. No. 8,09e-235;
 Matches 262; Conservative 233; Mismatches 261; Indels 78; Gaps 55;

Best Local Similarity 27.0%; Pred. No. 2,132-160;
Matches 216; Conservative 220; Mismatches 298; Indels 66; Gaps 53;

Db 72 KKKGHRLEALNLFADLRINNDPILPNTLLARILDTOSRTHALDQGLTVQALIKNDG 131
QY 6 NEHGHLFQARLRGEEINNSTALLPNTLLGQLDVDS--DSANYATLR-VLSLPGQH 63
Db 132 TEVRGSGGPPIITKPEHVGVIGASGVSSIMVANIILRKIPQIPIASTAPDLSMSR 191
QY 64 IELQ---GDL-LHYSPT-VLAVIGDSTNRATATALLSPFLV-HISTAASETISVQRQ 117
Db 192 YDFSSRVVSPDTYQAQAAVDIVALKMYSTVASSEGSYGAEAFIQKREDGVCIA 251
QY 118 YPSFLRTIPNDKYQVETVALLQKFGWIMISVSGSSDYQGLQVQALBNQALVRG-ICIA 176
Db 252 QSVVPIPRPKAGFEDI--IRLLETSNARAVIIFANDDIRVLEAKRANQCHFFWM 309
QY 177 FKDIIMPESAQVGD-ERMOCMLRHQAQATVAVVSSQLARVEESVVLNTLGKV-WV 234
Db 310 GSDSMG-SK-IAPYLHLEVAEG-AVITLPRKMS-VRGDFRFSRTIDNNRRNIMFAEF 365
QY 235 ASEMALSRHTIGVPGIORIGMWLVQAKRAVPGKAFEEAYR-RALKKAPRRC-HKGS 292
Db 366 W-EDNFHCKLSRAHLKKGSHVKKCTNRERIGDSAYEGEGVQVYDAVYAGHALAMH 424
QY 293 WCSSNQLCRG-QAFM-AHTMP-KLKA-FSMSAYN--A--Y-R-AVVAHAGHLQLL 340
Db 425 RDLGPRGRLGPRMDPVDTGLTKIRVNVNSGIANPVYTNENGDAGRDIDYQYLRN 484
QY 341 -G-CAS--ELCSR-GRVYPMQLQDIAHKVHL-LHKDVAANDNDPSSNIILAMDNQ 394
Db 485 DSAEYVIGS--WTD-HLHRIERHMHGSGOOLPRISICSLPCPGGERKTYVGMW-CGW 540
QY 395 PKMFTYVIGSSITSPVOININETKIQWGHKNQVPSKYSDDCEG-HQRYVTGFHCCF 453
Db 541 HCEPC-TG-YOYQVDRYCTKCPYDMRPTENRTGCRPIIKLE-WG-SPMAVLPFLAV 596
QY 454 ECVPGAGTFINKSELYRCQPCGTEEMAPEGSQTCFPTVYFLALREHTSW-VL-LAANT 511
Db 597 VGIAATLVVITFYRYNDPTVYKASGRSLSVLLAGIFLCATITFLMAEDLGICSLR 656
QY 512 LLLLLLGTAGLFAMHDTPTVARSAGRLCLFGLMGLSLAGSGSLGFGFETPRACPL 571
Db 657 IFLGMSISYAALTKINRIYRIFE--GKRVSAPRPI-SPASOLATITFLISHLGLI 714
QY 572 ALFALGTITFLISCLTVRSFOLIIIFKSTKVPFYHANVQHGAGLFWMISSAA-QLL-I 629
Db 715 CV-WFVVDPSHVVDFOODRTLDPRFARGVKC-DISPLDILLGYSMLMVTCTVYAI 772
QY 630 CLTLLVMTPLPAREYQ--R-F-PHLV--MLECTETNSLGLIFLAFVLYGLLSIFACSY 683
Db 773 KTRVPEFENFAKPIGFMITTCIWMIAFIPIFGTSSAKKLIQTITLLVSLSLSV 832
QY 684 LKGLDPENYNNAKCVTSLFLENVSWIAF---FTTASYDGK-YLPANMMAGLS-SLS 738
Db 833 SIGMLYMPKVIILFHEPON 852
QY 739 GFGGYFLPKCVIILCRPDLN 758

RESULT 6
ID MGRS-RAT STANDARD: PRT: 1203 AA.
AC P31424;
DT 01-JUN-1993 (Rel. 26, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.
GN GRM5 OR MGUR5.
OS Rattus norvegicus (Rat).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:
OC Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Rattus.
RN (1)
RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;
RX MEDLINE; 92317054.
RA ABE T., SUGIHARA H., NAMA H., SHIGEMOTO R., MIZUO N., NAKANISHI S.;
RT "Molecular characterization of a novel metabotropic glutamate
RT receptor mgur5 coupled to inositol phosphate/Ca2+ signal
RT transduction.";
RL J. Biol. Chem. 267:13361-13368(1992).
RN [2]
RP SEQUENCE OF 859-923 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE-BRAIN;
RX MEDLINE; 93343913.
RA MINAKAMI R., KATSUKI F., SUGIYAMA H.;
RT "A variant of metabotropic glutamate receptor subtype 5: an
RT evolutionally conserved insertion with no termination codon.";
RL Biochem. Biophys. Res. Commun. 194:622-627(1993).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
CC CHLORIDE CURRENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF
CC 32 RESIDUES.
CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN NEURONAL CELLS OF THE
CC CENTRAL NERVOUS SYSTEM.
CC -1- MISCELLANEOUS: ACTIVATED BY OUTSOULATE > GLUTAMATE > IBOTENATE >
CC TRANS-1- AMINOCYCLOPENTYL-1,3-DICARBOXYLATE.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGUR1.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb.ch/announce/>
CC or send an email to license@isb.ch).
CC -----
DR EMBL; D10893; -. NOT_ANNOTATED_CDS.
DR EMBL; S64315; AB27666.1; -.
DR PIR; A42916; A42916.
DR GCRDB; GCR_0444; -.
DR GCRDB; GCR_0760; -.
DR PROSITE; PS00979; G-PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G-PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G-PROTEIN_RECEP_F3_3; 1.
DR PFAM; PF00003; 7tm_3; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 1203
FT DOMAIN 22 578
FT TRANSSEM 579 601
FT DOMAIN 602 615
FT TRANSSEM 616 635
FT DOMAIN 637 647
FT TRANSSEM 648 666
FT DOMAIN 667 692
FT TRANSSEM 693 713
FT DOMAIN 714 736
FT TRANSSEM 737 758
FT DOMAIN 759 771
FT TRANSSEM 772 794
FT DOMAIN 795 806
FT TRANSSEM 801 826
FT DOMAIN 827 1203
FT CARBOHYD 88
FT CARBOHYD 209
FT CARBOHYD 377
FT CARBOHYD 381
FT CARBOHYD 444
FT CARBOHYD 733
FT POTENTIAL.
FT METABOTROPIC GLUTAMATE RECEPTOR 5.
FT I (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT II (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT III (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT IV (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT V (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT VI (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT VII (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT POTENTIAL.
FT POTENTIAL.
FT POTENTIAL.
FT POTENTIAL.
FT POTENTIAL.

FT VARSPLIC 876 907 MISSING (IN ISOFORM 5A).
 SQ SEQUENCE 1203 AA; 131885 MW; 2955EA33 CRC32;

Query Match 13.7% Score 798; DB 1; Length 1203;
 Best Local Similarity 26.4%; Pred. No. 4,44e-149;
 Matches 212; Conservative 207; Mismatches 329; Indels 55; Gaps 51;

Db 55 KRCGAVERQGIQRYEAMLTLEIRINSDPTLPLNTLCEIISDCMWSNAVALEOSIEFIR 114
 1 RSC-SFNH-GVHLFOARLGYEELNNSTALLPNTLITGLDVCSDSANYA-TLR-VL 56
 Db 115 DLSISEEEGLVRCVDSRSSRKKPIYGVIGPSSSAIDVONLQLENIPOIAYSAT 174
 57 -SL-PGOHHEIL-Q-GD-LLHY-SPT-VLAVIGPSTNAAATALLSPFLY-HISYAS 108
 Db 175 SMDSDKTLFKFMRYVSDAQAARAMDIVRYKMTVYSAVHTEGANGESMEAFKMS 234
 109 SETLSVKQYPSFLRTIPDKYQVETWVLLQKFMFTWISLSSGDDYGOGLVQALEMFA 168
 Db 235 AKEGICIA-HSYKIXSN-AGESEFDLKLKLRSHLPKARVAVACEGEMTVRGLAMRRL 292
 169 LVRGICIAFKDIMPFSAGVDERMOCILMRHL-AQ-AGATVVVVFSSRLARVFEFSVLT 226
 Db 293 GLAGEFLLGSDGMA-DRYDV-TDGYOREA-VGITT-KLQSPDYKWDYLYLRPETN 348
 227 NLTKR-VWVASEAMALSHRITGVPGIORIGVYLAIOKRAVPGILKAFEEAFA--RADKE 283
 Db 349 LRNPFGQFQWQRFQ-CRLEGAQNSKYNKNCSSLLRTHVQDSKMGFINAYGMA 407
 284 APRPHKSSWCSSNOLCR-E--CQ--A-F-MA-HTMPKIKASMSASINAY--RAVITVA 333
 Db 408 YGLHNMQSLCPGYAGLDDAMKPIDGRKLLDSIMKTNFTVSGMDILPDENGDSRGREI 467
 334 HGLHQL-LG-CAS-E-LCSRGR-VYPMQLEQIHVHFL-LHKDVAFANDNDPLSYNI 387
 Db 468 MFKEMGADY-FDIYNGSVNGELKADDEY-W-SKNNITRYSCEPECEGQITVIRK 524
 388 IAMDNGKMTFTVYLGSSVSWSPVQOLINETKIQMHGKNHVPKSVCSXCLEGHORVY-T 446
 Db 525 GEVSCWMTCPCKENEYAF-DE-YTCRACQQLGSWPTDLDLPGYLRMGDEPIAA 582
 447 GFHCCFECVPGAGTFLKSELKQCPGTEEMAPESQCTFPRTVFLARETTSWL 506
 Db 583 VYFACIGLATLFTVVIPIYRDPVYVSSSRELCYIILAGICGLYCFCLIAKPKOY 642
 507 LAANTLTLTLGLTAGLFAMHLDPTVVSAGRGCLFMGLSIAAGSGLYGFEGETRA 566
 Db 643 CYLQRIIGLSFAMYSALVTKTNRIARILLAGSKKICTKKRFMSACAQIVIAFILCI 702
 567 CLLRQALALGFTIPLSCILTVASFOLIIIFKFSR-VPTFYHAMVONHGAFLFVMISSA 625
 Db 703 OGLIIVAFIEMPPDLMHDYSIRE-VYLICNTN-LGVVPLAGYNGLLISCFE-YAFK 759
 636 OLLILTLVWVTPLPAREYORFPLVMECTETSLSGLITLAFYNGLLIS-ARACSTL 684
 Db 760 TRNVPANFENAKYIAFTYTTCTIIMLA-FVPIY-FGSNYKIITMCFVSLSA-TVALGCM 816
 685 GKDPENENAKCVTFSLFLNFVSMIAFTTASVYDGR-LPAAMMAGLSLSSGFGY 743
 Db 817 FVPKYIITLAKERNVRSATTS 839
 744 FLPKCYVILCRDLNSTEFOAS 766
 RESULT 7
 ID MGR1-RAT STANDARD: PRT: 1199 AA.
 AC P23385:
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 1 PRECURSOR.
 GN GRM1 OR MGLUR1.
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
 RX MEDLINE; 91156047.
 RA MASU M., TANABE Y., TSUCHIDA K., SHIGEMOTO R., NAKANISHI S.;
 RT "Sequence and expression of a metabotropic glutamate receptor.";
 RL Nature 349:760-765(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 92022526.
 RA HOUAMAD K.M., KUIJPER J.L., GILBERT T.L., HALDEMAN B.A., O'HARA P.J.,
 RT MOUTRIHILL E.R., ALMERS W., HAGEN F.S.;
 RT "Cloning, expression, and gene structure of a G protein-coupled
 glutamate receptor from rat brain.";
 RL Science 252:1318-1321(1991).
 RN [3]
 RP ALTERNATIVE SPLICING (1B).
 RC TISSUE-BRAIN;
 RX MEDLINE; 92110002.
 RA TANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;
 RT "A family of metabotropic glutamate receptors.";
 RL Neuron 8:169-179(1992).
 RN [4]
 RP ALTERNATIVE SPLICING (1C).
 RC TISSUE-BRAIN;
 RX MEDLINE; 93066232.
 RA PIN J.-P., WAEBSER C., PREZEAU L., BOCKAERT J., HEINEMANN S.F.;
 RT "Alternative splicing generates metabotropic glutamate receptors
 inducing different patterns of calcium release in Xenopus oocytes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10331-10335(1992).
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
 MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
 CALCINUM SECOND MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL
 ACTION OF GLUTAMATE IN THE CNS, SUCH AS LONG-TERM DEPRESSION IN
 THE HIPPOCAMPUS AND LONG-TERM DEPRESSION IN THE CEREBELLUM.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: THREE ISOFORMS: 1A (SHOWN HERE), 1B AND 1C;
 ARE PRODUCED BY ALTERNATIVE SPLICING. 1B AND 1C ARE C-TERMINALLY
 TRUNCATED FORMS OF 1A.
 CC -1- TISSUE SPECIFICITY: IS PREDOMINANTLY EXPRESSED IN CEREBELLAR
 PURKINJE CELLS, CA2-CA3 PYRAMIDAL CELLS OF THE HIPPOCAMPUS, AND
 MITRAL AND TUFTED CELLS OF THE OLFACTORY BULB.
 CC -1- MISCELLANEOUS: ACTIVATED BY OUTSIDE GLUTAMATE > IBOTENATE >
 TRANS-1'-AMINOCYCLOPENTYL-1,3-DICARBOXYLATE; INHIBITED BY
 2-AMINO-3-PHOSPHONOPROPIONATE.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST, TO MGLURS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X57569; CAA40799.1; -;
 DR EMBL; M61099; AAI19497.1; -;
 DR EMBL; S48085; AAB24138.1; -;
 DR PIR; S15362; S15362.
 DR PIR; A41939; A41939.
 DR GCRDB; GCR_0216; -;
 DR PROSITE; PS00979; G_PROTEIN_RECEPTOR_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECEPTOR_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECEPTOR_F3_3; 1.
 DR PFAM; PF00003; 7tm_3; 1.
 DR PFAM; PF01094; ANF_receptor; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Multigene family; Alternative splicing.
 FT SIGNAL
 1
 18

[illegible]

Dd	592	EPIINAAESCGIVLTLEVTILFLYRNEPVRKSSRELCTIIAGIFLGVCPTIIAK	651
Oy	502	TSWILLANTLILLILLBLITACLFAMHNDTPVVRBAGGCLCTMLGSIAAAGSGSLXPFGE	561
Dd	652	PRTSCYLQRLVLVGISSAACMSALVTKTNRIARILAGSKKICTRKPFRFSMAQVIITAS	711
Oy	562	PTRPACILIRQALFALGFETPLFSCLTVRSFOLIIIFKESTK-VPTFYHAMVNHGAEFLVM	620
Dd	712	ILISVOLTLVTLIMEPPMPLISPSIKE-VYLIC-NTSNLGVAPLGYNGLLMGSTY	769
Oy	621	ISSAQQLLICLTWLVWPVPPLAREYORPHLMLECTENSLGLFIPLFNGLGIS-AF	679
Dd	770	-YAFTNRVPANPENAKAIATMTTCITIMAF-VPIY-FGSNKKITTCVAISLS-VTV	825
Oy	660	ACSIGNKLPEKNYEAKCVTSLFNFYSWAIFTIASVYGKI-LPRANNAGLSLSLS	738
Dd	826	ALGCFTPKMYIIIAKPERNVRSAPTS	853
Oy	739	GFGGYFLPKCYVILCRPDLNSTEHFQAS	766
RESULT	11	STANDARD;	PRT; 908 AA.
ID	MGR8_MOUSE	P47743;	
AC	01-FEB-1996	(Rel. 33, Created)	
DT	01-FEB-1996	(Rel. 33, last sequence update)	
DT	15-JUL-1998	(Rel. 36, last annotation update)	
DE	METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.		
GN	GRM8 OR MGLUR8.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
CC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
RN	[1]		
RZ	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6; TISSUE=RETINA;		
RX	MEDLINE; 952939344.		
RA	DIVOISIN R.M., ZHANG C., RAMONELL K.;		
RT	"A novel metabotropic glutamate receptor expressed in the retina and olfactory bulb".		
RL	J. Neurosci. 15:3075-3083(1995).		
CC	-1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.		
CC	-1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN OLFACTORY BULB, ACCESSORY OLFACTOR BULB, AND NASALLARY BODY. WEAKER EXPRESSION IN THE RETINA, AND IN SCATTERED CELLS IN THE CORTEX AND HINDRAIN.		
CC	-1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.		
CC	-----		
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CC	-----		
DR	EMBL: U17252; AAA68149.1; .		
DR	GCDB: GCR_1712; .		
DR	MGD; MG1:109600; GRM8.		
DR	PROSITE; PS00979; G-PROTEIN_RECEP_F3_1; 1.		
DR	PROSITE; PS00980; G-PROTEIN_RECEP_F3_2; 1.		
DR	PROSITE; PS00981; G-PROTEIN_RECEP_F3_3; 1.		
DR	PFAM; PF00003; 7tm_3; 1.		
DR	PFAM; PF01094; ANF_receptor; 1.		
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; signal;		
FT	MultiGene family; Olfaction.		
FT	SIGNAL	1	33
FT	CHAIN	34	908
FT	DOMAIN	34	583
FT	TRANSMEM	584	608
FT	DOMAIN	609	620
FT	DOMAIN	609	620
FT	CYTOSOLSMC (POTENTIAL);		
FT	POTENTIAL.		
FT	METABOTROPIC GLUTAMATE RECEPTOR 8.		
FT	EXTRACELLULAR (POTENTIAL).		
FT	I (POTENTIAL).		
FT	CYTOSOLSMC (POTENTIAL).		
FT	POTENTIAL.		


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FT TRANSMEM 621 641 II (POTENTIAL).
FT DOMAIN 642 647 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 648 658 III (POTENTIAL).
FT DOMAIN 659 665 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 666 695 IV (POTENTIAL).
FT DOMAIN 696 716 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 717 746 V (POTENTIAL).
FT DOMAIN 747 768 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 769 781 VI (POTENTIAL).
FT DOMAIN 782 803 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 804 818 VII (POTENTIAL).
FT DOMAIN 819 843 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 844 908 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 95 95 POTENTIAL.
FT CARBOHYD 298 298 POTENTIAL.
FT CARBOHYD 452 452 POTENTIAL.
FT CARBOHYD 480 480 POTENTIAL.
FT CARBOHYD 565 565 POTENTIAL.
SQ SEQUENCE 908 AA: 101413 MW: 255810FF CRC32:

Query Match 13.2% Score 772; DB 1; Length 908;
Best Local Similarity 25.8%; Pred No. 5,74e-143;
Matches 205; Conservative 221; Mismatches 311; Indels 59; Gaps 51;

Db 69 KEGG1HRLAMLYAID0TKDPLDLSNITLGYRIUDTGSRDYALQSLTEVOALIERDA 128
6 NEHGHLFOARLGYEEINNSTALLPITLGYQYDVCSSDANYATLRL-VLSLPGQH- 62
129 SDVKANDDPPIFTKPKDISGYTGAASSVSIMVANIIRLFRIPDISASTAPELSDNTR 188
63 -HIE-LOGDLHYS-P-TLVAVIGDSTNRATTAALLSPFLV-HISYASSETLSVRSQ 117
189 YDFSRVPPDSYQAOAWDVTALGMVYSTSLASEGNGEGGAFAFOISREIGVCIA 248
118 YPSFLRTIPNDKYQVETWLLQKGTWISLVGSSDDYQGLQVLAENQAL-VGICIA 176
249 QSQIKIPREPRGEEFKI--IKRLLEPNARAVIMEFANEDINGLIEAAKKNQSGHFLMI 306
177 FKDIWPFSAQVGD-ERMQCLMRHLAAGATVYVSSRQLAVFESVLTNLTKG-VWV 234
307 GSDSNG-SK-TAPVYQOEIEAGANTIPKRASTIDGFDRYFSRLANRRVWFAEISE 364
235 ASEAAALRHRTITGVGIRIGVLAVALQKRA-VPGL-KAEFEAVARADKEAPR-P-CHK 290
365 GNFQKSSGSHCKRNSHIKCTGLERIARDSYEGKVQVDAVYSAVYALHNHKELC 424
291 GSW-C-SSNOLCREQOAMAHMFKL-K-AFSSMSAATN-ATRAYAVAHGHOLL-G-C 342
425 PGYIGLCPRMYTIDCKELLGYIRAVNFNGSAGTPYTFENGDPARGYDIFQYQINN-KST 483
343 AS-ELCSR-GRVYRWQWLEQIHKVFLLHKDT-VAFNDNRPLSSSYNIAMDMNGPKWT 398
484 EYKIIIGH-WTN-QLHLKVEDMOMANREHTHDASVCSLPCKRGEEKKTVKVP-CCHMG 539
399 -FTVVGSTWSPVOLINNETKIQWNGKNHOVKSVCSSDCLLEG-HQRYVTGHNHCCECV 456
540 RCEGNYN-OVDEL-SCELCPIDQRPINRITGC-QR-IPILIKEMSPPAVYVLLAIIIGI 595
457 PCGAGTFLNKSELYRCQCGTEEMWAPBSQCPRVTVFLARETSVWLAANTLLLL 516
596 IATFVITFEVRYNDPIVRASGRELIVLLGLIFLCISITFLMAADTIICSEFRIL 655
517 LLGT-AGL-FAMHLDTPVVRASGRLCLMLGSLAAGSGSLGFGFETPRACLLRQALF 574
575 ALGFTIIFSLCTLVSEFOIIFKFSTKYVTFEYHAWONHAGLFWMIS-SAOOLICLTM 633
656 GLGMCFSIAALLTKTNRIHRIFEQKGSVTA-PKEI-SPASOLVITFSLISVOLIGVFW 713
714 FVVDPRHIIIDYGEORITDPENARGVLC-DISDLSLCSLSGYSLLVAVTCVYAKIRG 772
634 LVVWTPLPAREY--OR-F-P-HL-VMLECTETNSLGFILAFYNGLLISAFACGYLKD 687
773 VPETFNKAPRIGFTWYITCIIMLAFIPFFGTAQGAEMKIQTTLTYSMSLSASVSLGM 832

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QY 688 LPENINAKCVTFSLLENFVSW---IA-FTTASYDGKULPAANMAGLS-SLSGFGG 742
Db 833 LYMPKYVIIIIHPEN 848
QY 743 YELPRCVILCRPDLN 758

RESULT 12
ID MGR8_RAT STANDARD; PRT; 908 AA.
AC P70579;
DI 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DI 15-JUL-1998 (Rel. 36, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
GN GRM8 OR MGLUR8.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE; 97166750.
RX SAUGSTAD J.A., KINZIE J.K., SHINOHARA M.M., SEGGERSON T.P.,
RA WESTBROOK G.L.;
RT "Cloning and expression of rat metabotropic glutamate receptor 8
RT reveals a distinct pharmacological profile."
RL Mol. Pharmacol. 51:119-125(1997)
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: PROMINENT EXPRESSION IN OLFACTORY BULB,
CC PONTINE GRAY, LATERAL RETICULAR NUCLEUS OF THE THALAMUS, AND
CC PIRIFORM CORTEX. LESS ABUNDANT EXPRESSION IN CEREBRAL CORTEX,
CC HIPPOCAMPUS, CEREBELLUM, AND MAMMARY GLAND.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U63288; AAB09537.1; -.
DR GCRDB; GCR1411; -.
DR PROSITE; PS00979; G-PROTEIN_RECP_F3_1; 1.
DR PROSITE; PS00980; G-PROTEIN_RECP_F3_2; 1.
DR PROSITE; PS00981; G-PROTEIN_RECP_F3_3; 1.
DR PFAM; PF00003; 7tm_3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Olfaction.
FT SIGNAL 1 33
FT CHAIN 34 908 METABOTROPIC GLUTAMATE RECEPTOR 8.
FT DOMAIN 34 583
FT TRANSMEM 584 608
FT TRANSMEM 609 620
FT TRANSMEM 621 641
FT TRANSMEM 642 647
FT TRANSMEM 648 668
FT TRANSMEM 669 695
FT TRANSMEM 696 716
FT TRANSMEM 717 746
FT TRANSMEM 747 768
FT TRANSMEM 769 781
FT TRANSMEM 782 803
FT TRANSMEM 804 818
FT TRANSMEM 819 843
FT TRANSMEM 844 908
FT CARBOHYD 95 95
FT CARBOHYD 298 298
FT CARBOHYD 452 452

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[illegible]

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RX SEQUENC FROM N.A.
RA MEDLINE: 97446143.
RA SCHERRER S.W., SODER S., DUVOISIN R.W., HUIZENGA J.D., TSUI L.C.:
RT "The human metabotropic glutamate receptor 8 (GMR8) gene: a
RL disproportionately large gene located at 7q31.3-q32.1.";
CC Genomics 44:232-236(1997).
CC
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL: U92459; AAB51764.1; -.
DR EMBL: U95025; AAB72040.1; -.
DR GCDDB: GCR_1889; -.
DR GCDDB: GCR_2604; -.
DR MIM: 601116; -.
DR PROSITE: PS00979; G-PROTEIN_RECP_F3_1; 1.
DR PROSITE: PS00980; G-PROTEIN_RECP_F3_2; 1.
DR PROSITE: PS00981; G-PROTEIN_RECP_F3_3; 1.
DR PFAM: PF00003; 7tm_3; 1.
DR PFAM: PF01094; ANF_receptor; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Olfaction.
FT SIGNAL 1 33
FT CHAIN 34 908
FT DOMAIN 34 583
FT TRANSSEM 584 608
FT DOMAIN 609 620
FT TRANSSEM 621 641
FT DOMAIN 642 647
FT TRANSSEM 648 668
FT DOMAIN 669 695
FT TRANSSEM 696 716
FT DOMAIN 717 746
FT TRANSSEM 747 768
FT DOMAIN 769 781
FT TRANSSEM 782 803
FT DOMAIN 804 818
FT TRANSSEM 819 843
FT DOMAIN 844 908
FT CARBOHYD 95 95
FT CARBOHYD 298 298
FT CARBOHYD 452 452
FT CARBOHYD 480 480
FT CARBOHYD 565 565
FT CARBOHYD 194 194
FT CONFLICT 194 194
FT CONFLICT 460 460
FT CONFLICT 642 642
FT CONFLICT 768 768
FT CONFLICT 904 904
SQ SEQUENCE 908 AA; 101741 MW; 18865C0F CRC32;
Query Match 13.0%; Score 757; DB 1; Length 908;
Best Local Similarity 26.2%; Pred. No. 1,90e-139;
Matches 209; Conservative 218; Mismatches 307; Indels 65; Gaps 53;
Ddb 69 KEGG:HLRLEAMLAIVADINKDPDLLSITLGVRIIDTCSGSDIYALFEOSLTFVQALIEKDA 128
QY 6 NENHYHFLFOARLGEVEINNSTALPNITGYOLYDVC-DSANVYATLR-VLSPGOH- 62
Ddb 129 SDVCAANDPPIETFKPKXIGSIGVGAASISIVANVLRFLKPIQDSVASTAPELSDNTR 188
QY 63 -HIE-LOGDLHYS-P-TVLAVIGPDSINRAATFALSLPFLV-HISVYASSETLSVKRO 117

```


Db 189 YDFSRVVPDPSYQAQAVDITVATGAMNYVSTLASEGNYGSGVEATQISREIGVCIA 248
 QY 118 YPSFRTIPNDKYQVETWVLLQKFGMTWISLVGSSDYQGVQALVNOAL-VGICIA 176
 Db 249 OSQKIPRPRPREFEKI--IKRLTTPNARAVIMANEDDRIILEAKKLINOSHEPLMI 306
 QY 177 FKDIPEFAQVGD-ERMOCIMHRLAQAATVAVVSSRQLAVFESVYVLTNLTK-VWV 234
 Db 307 GSDSWG-SK-LAPVYQOEIAGAVTILPKRA--SIDGDFRFRRTIANNRNWFAEF 362
 QY 235 ASEMALRHITGVPCIGRIGVAVGLAOKRAVPLKAFEEY-ARAKREAPRC-HKGS 292
 Db 363 W-EENFGCKLGSGRNSHIKKCTGLERLARDSSYDEGKVOYIDAVYSMAVALHNHK 421
 QY 293 WCSSNQLCR-EOQAFM-AHTMP-K-LKAFFSSAYN-A--Y-R-AVYAVAHGLHQL- 340
 Db 422 DLCPGICLCPMSITDKELLGYIRAVNPNSSACTPTFNNGAPRDIPOVQ-ITN 480
 QY 341 G-CAS-ELCSR-GVNYWQLEQIHKVFLHKDT-VAFNDRDPLSSYNLIAMDMNGP 395
 Db 481 KSTERKIGH-WTN-QLHLKVEDQMAHREHTHPASVCSLPCKGERRKTVKVP-CCW 536
 QY 396 KWT-FTVVGSSVSPVQVQINNETKIQWGNKNQVKSVCSDCLG-HQVYVTFHCCF 453
 Db 537 HCEGCEGYNY-QVDEL-SCELCPIDQRPNNMTGCOLIPIKLE-W-HSPAAVPEVAI 592
 QY 454 ECVPGAGCTFLNKSRLKRCQPCGTENAPESQOTCFPRIVYALREHTSWVLIANTIL 513
 Db 593 LGIATTVIYTVFVRYNDPTVYRAGRELSYLLGIFLCSITPLMAADPTICRR 652
 QY 514 LLLLTGT-AGL-FAMHLDTPVRSAGRCFLMGLSLAGSSILGFGEPTRACLRQ 571
 Db 653 VFLGCMCFSAALTKTNRIHRIFEQCKSVTA-PKEI-SPASQVTFSTLISVQLGV 710
 QY 572 ALFALGFIPLSCLVRSFQILIIKFTKVPYTFHANVONHAGLFWMIS-SAQQLIC 630
 Db 711 FVWVYVDPHIIIDYGEORTLDPERAGVLC-DISDISLCSLGSITLWVTCVYANK 769
 QY 631 LTMVYVMTPLPAREX--OR-F-PHYV--MLECTENSLGFIILAFYINGLISAFACSYL 684
 Db 770 TRGVETFEKAPRIGFTWYTCITWLAIFIPFGTAQSAEKYIOTITLLYMSLSASVS 829
 QY 685 GKIDPEENTENAKCVTFSLTFNVSW--TA-FTTASVYDGKYLPAANMAGLS-SLSSG 739
 Db 830 LGMLYPRVYIIIFHEON 848
 QY 740 FGYYFLPKCYVILCRDLN 758

RESULT 15
 ID MGR6_RAT STANDARD; PRT; 871 AA.
 AC P35349;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.
 GN GRM6 OR MGLUR6.
 OS Rattus norvegicus (Rat).
 CC Eutheria: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:
 CC Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Rattus.
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-RETINA;
 RX MEDLINE: 93280152.
 RA NAKAJIMA Y., IMAKABE H., AKAZAWA C., NAWA H., SHIGEMOTO R.,
 "Molecular characterization of a novel retinal metabotropic glutamate
 RT receptor mglur6 with a high agonist selectivity for L-2-amino-4-
 RL J. Biol. Chem. 268:11868-11873(1993).
 CC -I- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
 CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
 CC ACTIVITY.

CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -I- TISSUE SPECIFICITY: RESTRICTEDLY EXPRESSED IN THE INNER NUCLEAR
 CC LAYER OF THE RETINA.
 CC -I- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST, TO MGLUR4.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL: D13963; BAA03066.1; -
 DR PIR: A46742; A46742.
 DR GCRDB: GCR_0623; -
 DR PROSITE: PS00979; G_PROTEIN_RECP_F3_1; 1.
 DR PROSITE: PS00980; G_PROTEIN_RECP_F3_2; 1.
 DR PROSITE: PS00981; G_PROTEIN_RECP_F3_3; 1.
 DR PFAM: PF00003; Tlm_3; 1.
 DR PFAM: PF01094; ANF_receptor; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Multigene family; Vision.
 FT SIGNAL 1 18
 FT CHAIN 19 871
 FT DOMAIN 19 579
 FT TRANSSEM 580 602
 FT TRANSSEM 603 616
 FT TRANSSEM 617 637
 FT TRANSSEM 638 648
 FT TRANSSEM 649 667
 FT TRANSSEM 668 691
 FT TRANSSEM 692 712
 FT TRANSSEM 713 742
 FT TRANSSEM 743 764
 FT TRANSSEM 765 777
 FT TRANSSEM 778 800
 FT TRANSSEM 801 813
 FT TRANSSEM 814 839
 FT TRANSSEM 840 871
 FT CARBOHYD 290 290
 FT CARBOHYD 445 445
 FT CARBOHYD 473 473
 FT CARBOHYD 561 561
 SQ SEQUENCE 871 AA; 95089 MW; 81A229E4 CRC32;

Query Match 12.5%; Score 729; DB 1; Length 871;
 Best Local Similarity 26.5%; Pred. No. 6.82e-133;
 Matches 215; Conservative 219; Mismatches 308; Indels 70; Gaps 56;

Db 49 RACGLKKEGVHRLMELVADLVNADPELPGVRLGARLDTCSRDYALBOALSFYQ 108
 QY 1 RSC-SFN-EHYHLPQMRIGVEINNSTALLPRITIGYLDVCS-DSANVATILR-VL 56
 Db 109 ALIRGRDGDGEAYRCBPVPLRSAPPERVAVVGSASVSIMAVNLRLPAIDISY 168
 QY 57 SL--PqG-HHIEQ--GDL--LHYSPT--VIAVIGDSINRAATFALLSPFLV-HISY 105
 Db 169 ASTPELSDSTRIDFESRVVPPDSYQAQAVDITVATGAMNYVSTLASEGNYGSGVEAFY 228
 QY 106 AASETSLSVKQYPSFLRTPINDKYQVETWVLLQKFGMTWISLVGSSDYQGVQALV 165
 Db 229 QISREAGVCIAGIKIPREKPEFEKI-VIRRLMTPNARAGIIFANEDDIRVLEATR 267
 QY 166 NQAL-VGICIAFKDIPEFAQVGDERMOCIMHRLAQAATVAVVSSRQLARVFESVY 224
 Db 288 QANLTGFHLWSDSWG-SK-ISPLNLEEEA-VGATILPKRA--SIDGDFQYFMTSL 342
 QY 225 LTNLTGR-VWVASAWMLSHITGVPCIGRIGVAVGLAOKRAVPLKAFEEY-ARAD 281
 Db 343 ENNRNWFADFW-EENFNCKLTSSGGQSDSTRCKTGEEIRIGQDSAYDEGKVOYIDA 401

MUSEE (TM)

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Msarch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Mar 17 13:28:14 2000; MasPar time 32.72 Seconds
Tabular output not generated. 951.456 Million cell updates/sec

Title: >US-09-361-652-3
Description: (1-777) from US09361652.pep
Perfect Score: 5838
Sequence: 1 RSCSFNENGYHLFOAMRLGV.....NSTEFQASIDYTRCGST 777

Scoring table: PAM 150
Gap 11

Searched: 122810 segs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r62
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 52.083; Variance 105.499; scale 0.494

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1170	20.0	1085	2	S40476	Ca(2+)-sensing recept	5.20e-203
2	1163	19.9	1078	2	S49341	calcium-sensing recep	1.42e-201
3	1160	19.9	1078	2	A56715	calcium receptor (clo	5.86e-201
4	1158	19.8	1079	2	I59382	calcium/polyvalent ca	1.51e-200
5	1063	18.2	1088	2	B56715	calcium receptor (clo	4.26e-181
6	856	14.7	912	2	JH0563	metabotropic glutamat	4.92e-139
7	854	14.6	912	2	I58149	metabotropic glutamat	1.25e-138
8	798	13.7	1171	2	A42916	metabotropic glutamat	2.38e-127
9	796	13.6	1180	2	JC2132	metabotropic glutamat	6.00e-127
10	796	13.6	1199	2	A41939	G protein-coupled glu	6.00e-127
11	796	13.6	1212	2	JC2131	metabotropic glutamat	6.00e-127
12	789	13.5	872	2	JH0561	metabotropic glutamat	1.53e-125
13	772	13.2	908	2	I49142	metabotropic glutamat	3.95e-122
14	755	12.9	1218	2	S71376	glutamate receptor ho	1.01e-118
15	729	12.5	871	2	A46742	metabotropic glutamat	1.59e-113
16	718	12.3	879	2	JH0562	metabotropic glutamat	2.50e-111
17	674	11.5	915	2	A49874	metabotropic glutamat	1.43e-102
18	228	3.9	958	2	T02741	probable ligand-gated	1.66e-18
19	196	3.4	940	2	T02740	probable ligand-gated	3.00e-13
20	185	3.2	960	2	JE0356	gamma-aminobutyric ac	1.68e-11
21	165	2.8	938	2	T01809	hypothetical protein	2.01e-08
22	150	2.6	986	1	CYURCA	speract receptor prec	3.27e-06
23	147	2.5	934	2	T02742	probable ligand-gated	8.82e-06

24	126	2.2	965	2	I51244	N-methyl-D-aspartate	6.76e-03
25	128	2.2	1125	1	CYURCP	speract receptor prec	3.68e-03
26	123	2.1	1203	2	I55466	N-methyl-D-aspartate	1.66e-02
27	123	2.1	1229	2	I49705	glutamate receptor ch	1.66e-02
28	122	2.1	1250	2	B45219	N-methyl-D-aspartate	2.24e-02
29	116	2.0	532	2	D71676	bicyclomycin resistan	1.29e-01
30	117	2.0	532	2	S46831	probable membrane pro	9.66e-02
31	117	2.0	962	2	C43274	N-methyl-D-aspartate	1.29e-01
32	116	2.0	2695	2	SS4974	type 1 inositol 1,4,5	1.29e-01
33	116	2.0	2713	2	AS5713	inositol 1,4,5-trispho	1.29e-01
34	116	2.0	2749	1	ACX517	inositol 1,4,5-trispho	1.29e-01
35	109	1.9	360	2	JC4587	chemokine (C-C) recep	9.17e-01
36	109	1.9	368	2	G65119	hypothetical 40.4 kD	9.17e-01
37	111	1.9	491	2	B70414	NADH dehydrogenase I	5.28e-01
38	111	1.9	1131	2	A23944	chitin synthase (EC 2	5.28e-01
39	109	1.9	2670	2	A46719	inositol 1,4,5-trisph	9.17e-01
40	109	1.9	2671	2	A49873	inositol 1,4,5-trispho	9.17e-01
41	113	1.9	2693	2	A40743	IP3 receptor, XIP3R -	3.02e-01
42	107	1.8	275	2	S74417	hypothetical protein	1.58e+00
43	108	1.8	429	1	B25937	arsenical pump membra	1.20e+00
44	108	1.8	931	2	E70140	hypothetical protein	1.20e+00
45	107	1.8	1005	2	S33525	guanylate cyclase (EC	1.58e+00

ALIGNMENTS

RESULT 1
ENTRY S40476 #type complete
TITLE Ca(2+)-sensing receptor - bovine
#formal_name Bos primigenius laurus #common_name cattle
ORGANISM 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
DATE 17-Mar-1999

ACCESSIONS S40476
REFERENCE S40476
#authors Brown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butters, R.; Kifor, O.; Sun, A.; Hediger, M.A.; Lytton, J.; Hebert, S.C.

#journal Nature (1993) 366:575-580
#title Cloning and characterization of an extracellular Ca
(2+)-sensing receptor from bovine parathyroid.
#cross-references M01D:94077182
#accession S40476

##status preliminary
##molecule_type mRNA
##residues 1-1085 ##label BRO

SUMMARY
#length 1085 #molecular-weight 121170 #checksum 5738

Query Match 20.0%; Score 1170; DB 2; Length 1085;
Best Local Similarity 31.9%; Pred. No. 5.20e-203;
Matches 263; Conservative 227; Mismatches 256; Indels 78; Gaps 56;

Db	61	CIRYNRGFRMLQAMFAEINSSPALLPNTIGYRIEDICNVKALEA--TISFVAQ 118	
QY	3	C-SFENEGYHLFOAMRLGVEINNSTALLPNTILGQYVDCSDSANVATRLVSLPGQ 51	
Db	119	NKIDSLNIDFCNCSEHIBSTIVAGTSGISTAAVNLGLTYITOVSAASSRLLSNK 178	
QY	62	HTE-LQ-GDLHYS--PVLAVIGPDSNRAATLALSPYL-HISVAASSETLSVK 115	
Db	179	NOKSFRLTIPNDHQAATAADIIIEFRMWGTIAADDGARGIEKEFESEEDIDCI 238	
QY	116	RQYPSFLRTIPNXYQVETVALLQKFGTWISLVSSDDYGLGQALENLVAGICIT 175	
QY	176	AFQDIMPESAQVODERMOCMRLHAQAGAVVVFSS-RQLAVPFESVLTMLTGKVV 234	
Db	239	DFSE-L-ISOYSDERIQOQVEVIONSTAKVIVFSSGPDLEPLIKE-IVRNITGRIML 295	
QY	176	AFQDIMPESAQVODERMOCMRLHAQAGAVVVFSS-RQLAVPFESVLTMLTGKVV 234	
Db	296	ASDAMSSSLIAMPETFYVGGTIGGLAAGQIPGRFPLQKHHPKSYNGAKKEFME 355	
QY	235	ASDAMA--L-SR---HITGVP-GIO-RIGVNLGV-A-IQK--R-AVP-GK-KAF-DE 275	
Db	356	TFNCHLOEGAKGPLPDTFLRGHEBGARLSNPTRFPLCSEENISSVETPYMDYTHL 415	

Qy	276	AYA-R-AD-KEA-P-----RPHCHG-SWCSNOLC-RE-C--QAFAHATMPKLAFS-M	319
Db	416	RISYVAVYAVSIAMHALODITYCIPGRCLFNFNGSCADIKRYEAOUYKXHLRLNFTSNMG	475
Qy	320	SSAHNAAYAVAVAGHLQOLGCG-AS-EL-----CS-GRGYPMQOLQIHKYHFLLHK-	370
Db	476	EQYFDECGDLAGNYSIINMHLSPEDSIVKEGYVYVYAKKGBERLFINDEKILMGFS	535
Qy	371	DYVANDNRDPLSSYNITIAMONGPK-WT-PTVAGS-STWSP-VQ-LNINETRIOMGKN	425
Db	536	REVPYNSNRCLAGTRKGIIEGEPTCCFEVECPDGEYSDEITDASACDKCPDDFMSNEN	555
Qy	426	HOVPYSVSSCSLCGHOR-VYTGHHCCFEVCPGAGTFLKRSLSYKQCPGTEVMAPEG	484
Db	596	HTSCIAKEIFLSTWTEPG-IATLFLVAFGLTFAVLGYIKFRNPYKATNRELSY	654
Qy	485	SQTCPPRYVFLALREHISWLLANLITLILLLLG-INGLEFAMHLDTPVRSAGRCLFL	543
Db	655	LLFSLCCFSSSLF-ETGEPODMTCRLROPAGISFVLCISCIIVKTNRVLVEE-AKT	711
Qy	544	MIGSLAAG-SGSLISGFEPEYPRPACLLRQALFALGFIITLCLVRSFOLITIFKESTKY	602
Db	712	PTSFHRKMWGLNGLFLVFLCTPMOYICAIWMTAPPSVRNHLEDELFIITCHP-GS	770
Qy	603	PT-FYHANVQHGGGLFPMISSAAQOLCLTLWLVMTPLPAREQRPHPLVMECTETNS	661
Db	771	L-MALGELIGYCLLAAICFFFAKRSKRLEPENNENAKETIFSMILFIYVISEIPAYAST	829
Qy	662	LGLFIILAFU-YNGLLISAFACSYLKGDLPENYNEACVTFSLFNFVSIATPEFTT-ASV	718
Db	830	Y-KGVFSAVEYIATLAA-SFGLLACIFENKYYILITFKPSRNTIE	871
Qy	719	YDGKTLPLANNAAGLSSLSSEGGG-FLPKCYVLLCRDLNSTE	761

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RESULT      2
ENTRY       S49341          #type complete
TITLE       Calcium-sensing receptor - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE         16-Feb-1995 #sequence_revision 12-May-1995 #text-change
              03-Aug-1995
ACCESSIONS  S49341; A49419; B49419; C49419
REFERENCE    S49341
#authors     Pearce, S.H.S.; Thakker, R.V.
#submission  submitted to the EMBL Data Library, August 1994
#accession   S49341
#status      preliminary
#molecule_type DNA
##residues   1-1078 ##label PEA
##cross-references EMBL:X81086
REFERENCE    A49419
#authors     Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx,
              S.J.; Steinmann, B.; Levi, T.; Seidman, C.E.; Seidman, J.G.
#journal     Cell (1993) 75:1297-1303
#title       Mutations in the human Ca(2+)-sensing receptor gene cause
              familial hypocalcemic hypercalcaemia and neonatal severe
              hyperparathyroidism.
#cross-references NUTD:94094324
#accession   A49419
#status      preliminary
#molecule_type DNA
##residues   178-180,'K','I',182-192 ##label POL
#experimental_source family N
#note        sequence inconsistent with nucleotide translation
#note        sequence modified after extraction from NCBI Backbone
#note        186-arg mutation is associated with familial
              hypocalcemic hypercalcaemia and neonatal severe
              hyperparathyroidism
#note        sequence extracted from NCBI Backbone (NCBIN:142453)
#accession   B49419
#status      preliminary
#molecule_type DNA
##residues   289-303 ##label PO2

```

```

##experimental_source family E
##note sequence modified after extraction from NCBI backbone
##note 298-Tys mutation is associated with familial
##note hypocalcemic hypocalcemia and neonatal severe
##note hyperparathyroidism
#accession C49419
#note sequence extracted from NCBI backbone (NCBIN:142455)
#status preliminary
#molecule_type DNA
#residues 788-802 #label p03
##experimental_source family f
##note sequence modified after extraction from NCBI backbone
##note 796-Tyr mutation is associated with familial
##note hypocalcemic hypocalcemia and neonatal severe
##note hyperparathyroidism
#note sequence extracted from NCBI backbone (NCBIN:142457)
#length 1078 #molecular_weight 120672 #checksum 8159

SUMMARY
Query Match 19.9% Score 1163; DB 2; Length 1078;
Best Local Similarity 31.9%; Pred. No 1 42e-701;
Matches 253; Conservative 232; Mismatches 250; Indels 80; Gaps 57

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[illegible]

RESULT	3
ENTRY	A56715 #type complete
TITLE	calcium receptor (clone pHPcAR-4.0) - human
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-1999
ACCESSIONS	A56715
REFERENCES	A56715
authors	Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P., Brown, E.M.; Hebert, S.C.; Nemeth, E.F.; Fuller, F. J. Biol. Chem. (1995) 270:12919-12925
#journal	Molecular cloning and functional expression of human parathyroid calcium receptor cDNAs.
#title	parathyroid calcium receptor cDNAs.
#cross-references	MUID:95279439
#accession	A56715
##status	preliminary
##molecule_type	mRNA
##residues	1-1078 ##label GAR
##cross-references	GB:U0759; NID:9683744; PID:9683745
KEYWORDS	glycoprotein; receptor; transmembrane protein
SUMMARY	#length 1078 #molecular_weight 120573 #checksum 7868
Query Match	19.9%; Score 1160; DB 2; Length 1078;
Best Local Similarity	31.9%; Pred. No. 5.86e-701;
Matches	263; Conservative 232; Mismatches 250; Indels 80; Gaps 57;
Db	60 CIRNFRGEFRLQAMFAIFEINSPALLPLNLGLYRIPTQMTVSKALEA--TLSEFAO 117
Oy	3 C-SFENEHYHLPQMRIGVEINNSTALLNITLGIQIDVDCDSANVATRLVSLPeQ 61
Db	118 NKIDSLNDFEPCNCEHLPSTIAVAGTSGVSTAVANLLGLFPIPOVSASSRLLSNK 177
Oy	62 HHIE-LQ-GDLHYS---PTVLAVIGDSTNRATTAALLSPVLV-HISYAASSETLSVK 115
Db	178 NQFSEFLRTINDEHQATAMADIEFRKRWVGTIAADDYGGPGLIEKREAEEDIDCI 237
Oy	116 RQYFELRTINDKYQVETWLLQKRGKWMISLVGSSDDYGGQVQALENQALVNGI 175
Db	238 DFSELISQSPD--EE-IQHVVEIQNSTAKVIVSSGGDDEPLIKE-IVRNINIGKI 293
Oy	176 AFKQDMP-FSAQVDEDERKQCLMRILAQAQITVVYVSS-RQLRVFFESVLTNLGKYM 233
Db	294 LASEAMASSSLIAMPQYFHHVGGTIGFALKAQGIPEGREFLKRVPRKSYHNGFAKEWE 353
Oy	234 VASEAMA--L-S--R--R-HITGVF-GIQ-RIGWLVG-A-IQK--R-AVP-GL-KAF-E 274
Db	354 ETPFNCHLOEGAKGLPVDPTFLRGHEBSGCDPFSNSTAFRLCTGDENISSVEFPIDYH 413
Oy	275 EAYFA-R-ADKE-APRPH--KGSWCSSNDLCRECAF-M-A--RTMKRLXN---FS- 318
Db	414 LRISYNYLVYLAJAHLODIYTCLPGRGFTNGSCADIKKYAAQOVLLKHLRLNTNNK 473
Oy	319 MSSAYNAKRAYVAHAHGHLQILGC-AS-EL-----CS-RGRVYPMQLLEQIKHVFHLHK 370
Db	474 GEQYTFDECGDVLGNYGILNMHLSPEDGSIYFEVEGYNYNAAKGRFLFINEKILMSGF 533
Oy	371 -DTVAENNDNRPLSSSYNIAMDMNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQMHGK 424
Db	534 SREVPFNSGSDCLAGRKGIIEBEPICCECEVCECPRGESDDETDASACNKGCDPWSNE 593
Oy	425 NHOVPKSYCVSSDDCLEGHQR-VVTGFHHGCEQVPCGAGITLNSSELYRKQPCOTEMAE 483
Db	594 NHTSIAKEIEFLSMTEPG-IALTFAVIGIFATVAVLVFKFNTPIVAKTNTNELSY 652
Oy	484 GSGQTFPRITVFLALREHITSVYLLAANTLLLLLLLG-TALFLAMHMDITPVYRAGRGLOCF 542
Db	653 LLFSLLOCSSSLF-FIGEPDMTCFLRQPAIGISVILCISILVKNRVLLVEF--AK 709

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OY      543  LMTGSLAAG--SGSLYGFGEPTBRALQALPALTSTIITLSCITVRSPLIITIFNPSIK 601
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      710  IPTSFHRKMGWGLNIQFLVYFCITMQIVICWLYTAPSSYNOEJDEIIFITCHE-G 768
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY      602  VPT--FYHAWYONHGAGFGFVMAISSAQLIIDLTLTWVTPLPAREYORFPLTWLECTEIN 660
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      769  SL-MALGFLIQCITLALICFFFAFKSRKILPENNEKFTTEMLFFIIFYISFIAYAS 827
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY      661  SLGFLIABL--YNGLLTSAPACYSGLDKDPENINNEKCVTISLLEFVSWIAFFET--AS 717
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      828  TY-GKEVASVEVIAIILAA-SFGLLACIFFEFKYIITLEKPSRNITE 870
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY      718  VYDKYILPAAVMAGISLSISGFGCY-FLKCYVIILCRPLDNSTE 761
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT      4
ENTRY      159362      #type complete
TITLE      calcium/polyvalent cation-sensing receptor precursor - rat
ORGANISM   #formal_name Rattus norvegicus #common_name Norway rat
DATE       02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
          01-May-1998
ACCESSIONS 159362; A55594
REFERENCE   159362
#authors    Ruat, M.; Molliver, M.E.; Snowman, A.M.; Snyder, S.H.
#journal    Proc. Natl. Acad. Sci. U.S.A. (1995) 92:3161-3165
#title      Calcium sensing receptor: molecular cloning in rat and
            localization to nerve terminals.
#cross-references MIMD:95241465
#accession   M59362
#status      translated from GB/EMBL/DBJ
#molecule-type mRNA
#residues    1-1079 ##label RES
#cross-references EMBL:U02089; NID:q790578; PID:q790579
REFERENCE   A55594
#authors     Riccardi, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.;
            Hebert, S.C.
#journal     Proc. Natl. Acad. Sci. U.S.A. (1995) 92:131-135
#title      Cloning and functional expression of a rat kidney
            extracellular calcium/polyvalent cation-sensing receptor.
#cross-references MIMD:95116508
#accession   A55594
#molecule-type mRNA
#residues    1-133,'X',135-1079 ##label RIC
#cross-references GB:U10354
#experimental_source kidney
KEYWORDS     calcium; glycoprotein; phosphoprotein; transmembrane protein
FEATURE
1-20        #domain signal sequence #status predicted #label SIG\
187-212     #region hydrophobic\
613-635     #domain transmembrane #status predicted #label TM1\
650-670     #domain transmembrane #status predicted #label TM2\
683-700     #domain transmembrane #status predicted #label TM3\
725-744     #domain transmembrane #status predicted #label TM4\
770-790     #domain transmembrane #status predicted #label TM5\
806-828     #domain transmembrane #status predicted #label TM6\
841-860     #domain transmembrane #status predicted #label TM7\
90,261,287,386,468,
468,594,893,1005
#binding_site carbohydrate (Asn) (covalent) #status
predicted\
#binding_site phosphate (Ser) (covalent) (by protein
kinase C) #status predicted\
#binding_site phosphate (Ser) (covalent) (by protein
kinase A) #status predicted
899,901     #length 1079 #molecular_weight 120867 #checksum 8153
SUMMARY
Query Match      19.8%; Score 1158; DB 2; Length 1079;
Best Local Similarity 31.4%; Pred. No. 1,51e-200;
Matches 265; Conservative 233; Mismatches 261; Indels 78; Gaps 55;
Db      60  CIRVHGFRLQAMIRAFIEINSSPLLNNMIGYIFDTCNTVSKALEA--TISFVAQ 117
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY      3 C-SFNEHGYHLFOAMRLGVEEINNSTALPNTLIGYQLDYVDCSDSANVATLRYLSLPGQ 61
Db      118 NKIDSLNLEDFNCSEHIFSTIAVVGATGSGVSTAVANLGLFIYPOVYASSSRLLSNK 177
QY      62 HHLE-LQ-GDLHYS---PTVLAVIGPDSINRAITTAALSPFLY-HISTAASSETLSVK 115
Db      178 NOYKSLRTIPNDEHOATAMADIEFRNMVGTIAADDYGRPGIEKREAEEDIC 237
QY      116 ROYPSFLRTIPNDKYQVETWVLLQKFGMTWISLVGSSDDYQGLQVQALENLAVRGICI 175
Db      238 DFEELISOYDE--EEIQQ-VVEYIIONSTAKYIVVSSGDLPLELKE-IVRRNITGRIM 293
QY      176 AFQDIMP-FSAQYGDERRMOCIMRLAQAGATVYVFS--ROLARVFESVYLTNLGKVM 233
Db      294 LASEAMASSSLIAMPYEFHYVGGTIGFALKAQIPGPREFLKVPHPKSVHNGFAKEWE 353
QY      234 VASEAMA---L-SR---HITGVP-GIQ-RIGWLVG-A-IQK---R-AVP-GL-KAF-E 274
Db      354 ETNCHLQEGAKGPLVDFTLGHESGDRFSSNSTAFRPLCTGDNISVETPIYDIYH 413
QY      275 EAVA-R-AD--KEA-P-----RPHKGS-W---CSSN-Q-LCRECAFMATMPKLAFS 318
Db      413 HLISVNVYIAVYSIALADIDITCLPGRGLFTNGSCADIKKYEAMOVHLRLHNTNN 472
QY      319 -MSATNAAYAVAVAGLHQLLGC-AS-EL-----CS-RGRYIPMQLQIKHVKHLLH 369
Db      473 MGEQVTEDECGDLVGNYSIINWHLSPEDGSIVKEVGYNVYAKKGERLPIINEKILMSG 532
QY      370 K-DTVAFNDRDPLSSNIITAMDMNGPK-WT-FTVLGS-STWSP-VQ-LNINEKTIQWNG 423
Db      533 FSEVFPNSNSRCCQAGTRKGIIEGPTCFCEVECEPDGEYSGEYSDTASACDKCPDEWSN 552
QY      424 KNOQVPRSVSSDCLBHQH-VYGFHHCCEVCPCAGCFINKSELRYRQCPGTEEMAP 482
Db      593 ENHTSCAKIEFLWTEPRG-IALTFLAVIGFLTFVGLFKENETIVAKTINELS 651
QY      483 EGSQTCPRIVLALREHTSWVLANLTLILLIG-TAGLFRMHLDTVVSAGGRIC 541
Db      652 YLLLFSLICFSSSLF-FIGEPDWTCLRQPAFGISFVLICISCIIVKTRVLVEE--A 708
QY      542 FLMLGSLAAG-SSLYGFEGEPTRPACLLRQALFALGFTIFLSGLIYRSQLIIFEFST 600
Db      709 KIPTSFHRKMGWGLNLOFLVFLCTFMQILCIITWLYTAPSSYRNHELEDEIIFITCHEG 768
QY      601 KVPY-FYHAWQNHGAGLFWISSAQLLICTLWLVWTPLPAREYORFPHLVLECTET 659
Db      769 SLAAGSLIGYTLAALICFFAFKSRKLPEINNEAKETIFSMILFIYVISPAAST 828
QY      660 NSLGFILAFIYNGULISAFACSLGKDPENINEAKCVTFSLFNFSWIAFFTT-ASV 718
Db      829 Y-GKFVSAVEVIAIIAA-SFGLIACIFFNKYIILFKPSRNTIEEVSSTAHA 880
QY      719 YDKYIPLAANMAGLSLSSGFGY-FLPKCYVILCRDNLNTEHQAISQIDYT 771

RESULT      5
ENTRY      B56715 #type complete
TITLE      calcium receptor (clone pnpCar-5.2) - human
ORGANISM   #formal name Homo sapiens #common name man
DATE      19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change
17-Mar-1999

ACCESSIONS
REFERENCE   B56715
#authors   Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.;
#journal   J. Biol. Chem. (1995) 270:12919-12925
#title     Molecular cloning and functional expression of human
#          parathyroid calcium receptor cDNAs.
#cross-references M0ID:95279439
#accession B56715
#status    preliminary
#molecule_type mRNA
#residues  1-1088 ##label GAR

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#cross-references GB:U20760; NID:g683746; PID:g683747
KEYWORDS   glycoprotein; receptor; transmembrane protein
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Query Match      18.2%; Score 1063; DB 2; Length 1088;
Best Local Similarity 31.6%; Pred. No. 4, 26e-181;
Matches 264; Conservative 231; Mismatches 250; Indels 90; Gaps 59;

Db      60 CYYNRGRFRWLOAMFALFEINSSPALLPNTLIGRIDTCTVKALEA--TISFVAO 117
QY      3 C-SFNEHGYHLFOAMRLGVEEINNSTALPNTLIGYQLDYVDCSDSANVATLRYLSLPGQ 61
Db      118 NKIDSLNLEDFNCSEHIFSTIAVVGATGSGVSTAVANLGLFIYPOVYASSSRLLSNK 177
QY      62 HHLE-LQ-GDLHYS---PTVLAVIGPDSINRAITTAALSPFLY-HISTAASSETLSVK 115
Db      178 NOYKSLRTIPNDEHOATAMADIEFRNMVGTIAADDYGRPGIEKREAEEDIC 237
QY      116 ROYPSFLRTIPNDKYQVETWVLLQKFGMTWISLVGSSDDYQGLQVQALENLAVRGICI 175
Db      238 DFEELISOYDE--EEIQQ-VVEYIIONSTAKYIVVSSGDLPLELKE-IVRRNITGRIM 293
QY      176 AFQDIMP-FSAQYGDERRMOCIMRLAQAGATVYVFS--ROLARVFESVYLTNLGKVM 233
Db      294 LASEAMASSSLIAMPYEFHYVGGTIGFALKAQIPGPREFLKVPHPKSVHNGFAKEWE 353
QY      234 VASEAMA---L-S--R--HITGVP-GIQ-RIGWLVG-A-IQK---R-AVP-GL-KAF-E 274
Db      354 ETNCHLQEGAKGPLVDFTLGHESGDRFSSNSTAFRPLCTGDNISVETPIYDIYH 413
QY      275 EAVA-R-ADKE-APRCH--RGSWCSNQLCRECAF--M-A--HTMKRLA---FS- 318
Db      414 LRISVNVYIAVYSIALADIDITCLPGRGLFTNGSCADIKKYEAMOVHLRLHNTNN 473
QY      319 -MSATNAAYAVAVAGLHQLLGC-AS-EL-----CS-RGRYIPMQLQIKHVKHLLH 369
Db      473 MGEQVTEDECGDLVGNYSIINWHLSPEDGSIVKEVGYNVYAKKGERLPIINEKILMSG 532
QY      371 -DTVAFNDRDPLSSNIITAMDMNGPK-WT-FTVLGS-STWSP-VQ-LNINEKTIQWNG 423
Db      533 FSEVFPNSNSRCCQAGTRKGIIEGPTCFCEVECEPDGEYSGEYSDTASACDKCPDEWSN 552
QY      424 -KNH-----QVPRSVSSDCLBHQH-VYGFHHCCEVCPCAGCFINKSELRYRQ 482
Db      594 KCPDDESMENHTSCAKIEFLWTEPRG-IALTFLAVIGFLTFVGLFKENETIVAKTINELS 651
QY      474 PCGTEEMAPBGSTCPRIVLALREHTSWVLANLTLILLIG-TAGLFRMHLDTV 532
Db      653 VKATNELSYLLFSLICFSSSLF-FIGEPDWTCLRQPAFGISFVLICISCIIVKTR 711
QY      533 VRSAGGRILCFIMGLAAG-SSLYGFEGEPTRPACLLRQALFALGFTIFLSGLIYRS 591
Db      712 VLVFE--AKIPTSFHRKMGWGLNLOFLVFLCTFMQIVICVIMLYTAPSSYRNQLEDE 769
QY      592 LIITFEFTSTKVP-FYHAWQNHGAGLFWISSAQLLICTLWLVWTPLPAREYORPH 650
Db      770 LIITFEH-GSL-MALGFIYGTCLLAALICFFAFKSRKLPEINNEAKETIFSMILFIY 827
QY      651 LVWLECTEINSLGFIALF--YNGULISAFACSYGRKLPENYNAKCVTSLEFNFS 708
Db      828 WISFIPAVASTY-GKFVSAVEVIAIIAA-SFGLIACIFFNKYIILFKPSRNTIE 880
QY      709 WIAFFTT-ASVYDGYLPLAANMAGLSLSSGFGY-FLPKCYVILCRDNLNTE 761

RESULT      6
ENTRY      JH0563 #type complete
TITLE      metabotropic glutamate receptor 4 precursor - rat
ORGANISM   #formal name Rattus norvegicus #common name Norway rat
DATE      30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
13-Sep-1998

ACCESSIONS
REFERENCE   JH0563
#authors   JH0561

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#authors Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
#journal Neuron (1992) 8:169-179
#title A family of metabotropic glutamate receptors.
#cross-references MUID:92110002
#accession JH0563
#molecule-type mRNA
#residues 1-912 #label TAN
#experimental-source brain
COMMENT This protein is coupled to a G protein and evokes a variety of
functions by mediating intracellular signal transduction.
CLASSIFICATION #superfamily metabotropic glutamate receptor 4
KEYWORDS G protein-coupled receptor; glycoprotein; phosphoprotein;
transmembrane protein
FEATURE
1-32 #domain signal sequence #status predicted #label S1C\
33-912 #product metabotropic glutamate receptor 4 #status
588-610 #domain transmembrane #status predicted #label TR1\
625-645 #domain transmembrane #status predicted #label TR1\
657-675 #domain transmembrane #status predicted #label TR1\
700-720 #domain transmembrane #status predicted #label TR1\
751-772 #domain transmembrane #status predicted #label TR1\
786-807 #domain transmembrane #status predicted #label TR1\
822-847 #domain transmembrane #status predicted #label TR1\
98,301,454,484, #domain transmembrane #status predicted #label TR1\
569 #binding-site carboxylate (Asn) (covalent) #status
621,689,695,859, #binding-site phosphate (Ser) (covalent) #status
870 #binding-site predicted
SUMMARY #length 912 #molecular-weight 101818 #checksum 808
Query Match 14.7%; Score 856; DB 2; Length 912;
Best Local Similarity 27.3%; Pred. No. 4,92e-139;
Matches 219; Conservative 225; Mismatches 289; Indels 68; Gaps 54;
Db 72 KEGGIRHLEAMFLADRIINDDPDLIPNITIGARLIDCSRDTHALEOSLFLVALIENKDG 131
6 NEHYHLFQAMRGLVEELNNSTALLPNTLIGLYDYCS-DSANVAVTLR-VLSLPQGH 63
132 TEVRGSGGPPITKPRVGVIGASSSVSIYANILRFKIPQISASTAPLSDNSR 191
64 IELD---GDL-LHYSPT-VLAVIGPDSINRAATLALSPFLV-HISYASSETLSVRQ 117
192 YDFSRVPSDTYQAOAMVDIVRAKWNVSTLASSEGSYGSEVATIQKRENGVCIA 251
118 YPSFLRTIPNDKYOVEITVLLQKFGMTWISLVSSDDYQGLQVQALENOALVRG-ICIA 176
252 QSVKIPREPRTGEFDKI--IKRLLETNAGIIIFANEDDIRVLEAARANOTGHEFFM 309
177 FKDIIMPSSAOGD-ERMOCMLRHLAGAGATVYVVFSSRLQARVFESVLTNLTKGV-WV 234
310 GSDSMG-SKS-APVLRLEEAAG-AVTILPKRMS-VGDFRYESSRILDNRRNIMFAEF 365
235 ASEAMALSRHTIGVPGIORIGMVGLVAIQKRAVPGKAKFEBAVA-RADKEAPRC-HKGS 292
366 W-EDNEFHCKLSRAHLKKGSHIKCTNERNRIGODSAVEQEGKVOFIDAVYAMGALHAMH 424
293 WCSSNQLCRRC-QAFM-AHTMP-KLKA-FSMSAYN-A---Y-R-AVAVAHGLHOLL 340
425 RDLCPGVGLCPMDPDVDTOLTKYIRNVNFSAGNPFVFNENGADAGRDIDYOYOLRN 484
341 -G-CAS--ELCSR-GRVYPMOLLEQIHKVHL-LHKDTVAANDNRDPLSINIITAMD-CN 393
485 GSA-EYVVGIS--WTD-HLHRIERKMPGSGGQOLPRSICGLPCOPGRRKTVKMA-CC 539
394 GPKMTFTVLGSGTSPVOLNINETKIQWGHKNHQPXSVCSDDLEG-HQHVIVGFFHCC 452
540 WHCPRC-TG-YOYOVDRYTKCTCYDMAPRTNRTSCOPIPYKLE-WD-SPMVLPFLA 595
453 FECPGCGAGITLNSKSEIRQCPCTEEHAPGDSOTCPRTIVFALRHISM-VL-LAAN 510
596 VVGIAATLVVVTVFVRVNDPIVRAKSGRELSYVLLAGIFLCYATTFIMIAEPDICTSLR 655

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511 TLLILLIGTAGLFAWHLDPVYRSAGRCFLMLGLSAGSLVGFGEPRRPACTLR 570
656 RIFPLGMSISYALALLTKRIRIRIFEOGKRSVAPRFISPAQALITFLIIS--LQLLG 713
571 QALFALGFTIFLSCLTVRSFOLLIRFISFK-VPIYHANVONHGAGLFWISSAQL- 628
714 ICV-MFVVDSSHVDPDODRTLDPRFARGLKC-DISDLSICLLGYSMLAVNCTVYA 771
629 ICLTWLVMTPLPAREQ--R-F-PHLY--MLECTERNISGIFLAFIYNGLSISAFCS 692
772 IKRGVPEIENKAPRIGFTYTCIWLAFIPFPGTSQSDADKLXIQTTLTVSVSLAS 831
683 YLGKDPENYENKACVTFSLFNFVSWIAF---FTIASYDGR-YLPANMAMAGLS-SLS 737
832 VSLGMLYKPVYITLHPEDN 852
738 SGEGYFLPKCYVILCRPDLN 758
RESULT 7
ENTRY 158149 #type complete
TITLE metabotropic glutamate receptor - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
13-Sep-1998
ACCESSIONS 158149
REFERENCE 158149
#authors O'Hara, P.J.; Sheppard, P.O.; Thøgersen, H.; Venezia, D.;
Haldeman, B.A.; McGrane, V.; Houamed, K.M.; Thomson, C.;
Gilbert, T.L.; Mulvihill, E.R.
#journal Neuron (1993) 11:41-52
#title The ligand-binding domain in metabotropic glutamate receptors
#cross-references MUID:93352699
#accession 158149
#status preliminary: translated from GB/EMBL/DBJ
#molecule-type mRNA
#residues 1-912 #label RES
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#gene GLUR4
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#keywords neurotransmitter receptor
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Best Local Similarity 27.3%; Pred. No. 1,25e-138;
Matches 219; Conservative 225; Mismatches 289; Indels 68; Gaps 54;
Db 72 KEGGIRHLEAMFLADRIINDDPDLIPNITIGARLIDCSRDTHALEOSLFLVALIENKDG 131
6 NEHYHLFQAMRGLVEELNNSTALLPNTLIGLYDYCS-DSANVAVTLR-VLSLPQGH 63
132 TEVRGSGGPPITKPRVGVIGASSSVSIYANILRFKIPQISASTAPLSDNSR 191
64 IELD---GDL-LHYSPT-VLAVIGPDSINRAATLALSPFLV-HISYASSETLSVRQ 117
192 YDFSRVPSDTYQAOAMVDIVRAKWNVSTLASSEGSYGSEVATIQKRENGVCIA 251
118 YPSFLRTIPNDKYOVEITVLLQKFGMTWISLVSSDDYQGLQVQALENOALVRG-ICIA 176
252 QSVKIPREPRTGEFDKI--IKRLLETNAGIIIFANEDDIRVLEAARANOTGHEFFM 309
177 FKDIIMPSSAOGD-ERMOCMLRHLAGAGATVYVVFSSRLQARVFESVLTNLTKGV-WV 234
310 GSDSMG-SKS-APVLRLEEAAG-AVTILPKRMS-VGDFRYESSRILDNRRNIMFAEF 365
235 ASEAMALSRHTIGVPGIORIGMVGLVAIQKRAVPGKAKFEBAVA-RADKEAPRC-HKGS 292
366 W-EDNEFHCKLSRAHLKKGSHIKCTNERNRIGODSAVEQEGKVOFIDAVYAMGALHAMH 424
293 WCSSNQLCRRC-QAFM-AHTMP-KLKA-FSMSAYN-A---Y-R-AVAVAHGLHOLL 340
425 RDLCPGVGLCPMDPDVDTOLTKYIRNVNFSAGNPFVFNENGADAGRDIDYOYOLRN 484
341 -G-CAS--ELCSR-GRVYPMOLLEQIHKVHL-LHKDTVAANDNRDPLSINIITAMD-CN 393
485 GSA-EYVVGIS--WTD-HLHRIERKMPGSGGQOLPRSICGLPCOPGRRKTVKMA-CC 539
394 GPKMTFTVLGSGTSPVOLNINETKIQWGHKNHQPXSVCSDDLEG-HQHVIVGFFHCC 452
540 WHCPRC-TG-YOYOVDRYTKCTCYDMAPRTNRTSCOPIPYKLE-WD-SPMVLPFLA 595
453 FECPGCGAGITLNSKSEIRQCPCTEEHAPGDSOTCPRTIVFALRHISM-VL-LAAN 510
293 WCSSNQLCRRC-QAFM-AHTMP-KLKA-FSMSAYN-A---Y-R-AVAVAHGLHOLL 340

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694-714 #domain transmembrane #status predicted #label TM4\
738-759 #domain transmembrane #status predicted #label TM5\
773-794 #domain transmembrane #status predicted #label TM6\
803-827 #domain transmembrane #status predicted #label TM7
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Matches 215; Conservative 204; Mismatches 329; Indels 56; Gaps 49;

Db 55 RKGCAVEQGIQVEMAFHLEKINSDPTLIPNITIGCELRDSCMSAVALEQSTEFIR 114
QY 1 RSC-SFNEH-GYHLFQAMRLGVEEINNSTALLPNTLGYQLYVCSDSANYA-TLR-VL 56
Db 115 DSLISSEEEGLVRCVGGSSSSFKKPIVGVIGPGSSSVAIQVONLQJFNQIAYSA 174
QY 57 -SL-POGHHIEL---QGDLHY-SPT-VLAVIGPDSNRATTAALLSPV-LV-HISYAA 107
Db 175 TSMDSLKTLFKYFMRVPSDAQARAMDIVKRYNNTYVSAVTEGNYGSGMEAEKDM 234
QY 108 SSEELSVKROQPSFLRTIPNDKYQVETMVLLOKFGMTWISLVGSSDDYQGLQVALENO 167
Db 235 SAKGGLTIA-HSKYIYN-AGEQSFDKLLKLTSHLPKARVACFCGEMTVRGLMARR 292
QY 168 ALVRGICIAKIDIPFSAQVDERMOCIMRHLA-Q-AGATVWVFSSROLARVFEESVVL 225
Db 293 LGLAGEFLLGSDGMA-DRYDV-TDGYOREA-VGGIT-KLOSPDYKMFDDYIKLREP 348
QY 226 TNLTKG-VWVASEAMALSRHTGTPGIGRIQGMVGLVAIORAVYGLAFEBAYV--RADK 282
Db 349 NHRNPFQEFQWHRFQ-CRLGEPQENSKYNTKCNSSLITKTHVQDSKMGFVINAIFY 407
QY 283 EAPRCHKSGWSSNQLCR-E--CQ--A-F-MA-HTMPKIKAFMSAYNAV--RAYVAV 332
Db 408 AYGHANQMSLCPEYALCDAMKPIDGRKLLSLMKTNFGVSGDTILFDENGSPGRYE 467
QY 333 AHGHOL-IG-CAS-E-LGSRGR-VYPMOLLEQIHKVHFL-LHKDTVAFDNRDPLSSYN 386
Db 468 IMNEKMGKDY-FDYINWGSMDNGELKMDDEV-W-SKSNIIKRSVCEPECKQIVIR 524
QY 387 IIAIDMNGPMTFTVLSSSTMSPVQLINETKIQMHGKNHOPKSVSSDCLBEGHORYV- 445
Db 525 KGEVSCMTGCPCKENEYV-DE-YTCKACQLGSMPTDGLDGLIFVQYLRMDDPPIA 582
QY 446 TGFHCCFECVPCGAGTFLNKSELRYRCQPGTEEMARPEGQTCPRVYVFLALNEHNSW 505
Db 583 AAVFACGLLATLFYVYVFIIRDPYVKKSSRELCTIILAGICGLTCTCLIAKQI 642
QY 506 LLAANTLLELLLTAGLTFAMHLDTPVRSAGRLCFMLGSLAAGSGSLYGFGEPTRP 565
Db 643 YCYLORIGIGSPAMYSALVTKNRIARLAGSKKICCTKPRFMSACQVLAFLILC 702
QY 566 ACLRLQALFLDGTIFLISCLTVRSFOLILFKESTK-VPIFYHAMVONHGGLVWISSA 624
Db 703 IOLGIIVALEIMEPDITMDHYSIRE-VYLICNTTN-LGVVTPLGYNGLILSCTF-YAF 759
QY 625 AOLLICLTWLVMPLPAREQRPHLYMELECTETNSLGLFATLRYNGLLIS-AFACSY 683
Db 760 KTRNVPANENAKYIAFTYTCIIMLAF-VPIY-FGSNKIITMCFVSLSA-TVALGC 816
QY 684 LGFDLPENYENAKCVTSLFENFVSMIAFFTASVYDGKY-LPAANMAGGLSSLSGFGG 742
Db 817 MFVPKVYIILAKPERNVSATFTS 840
QY 743 YFLPKCYVILCRPDLNSTEHQAS 766

RESULT 10 A41939 #type complete
ENTRY G protein-coupled glutamate receptor - rat
TITLE #formal_name Rattus norvegicus #common_name Norway rat
ORGANISM 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
DATE 20-Mar-1998

ACCESSIONS A41939; S15362
REFERENCE A41939
#authors Honnared, K.Y.; Kutter, J.L.; Gilbert, T.L.; Haldeman, B.A.;
O'Hara, P.T.; Mulvihill, E.R.; Almers, W.; Hagen, F.S.
#journal Science (1991) 252:1318-1321
#title Cloning, expression, and gene structure of a G
protein-coupled glutamate receptor from rat brain.
#cross-references MIMD:9202526
#accession A41939

##status preliminary; not compared with conceptual translation
##molecule_type nucleic acid
##residues 1-1199 ##label HOU
##cross-references G3:M61099; NID:9397806; PID:9204460
##experimental_source cerebellum
##note sequence extracted from NCBI backbone (NCBIP:60785)
REFERENCE S15362
#authors Masu, M.; Tanabe, Y.; Tsuchide, K.; Shigemoto, R.; Nakanishi, S.

##journal Nature (1991) 349:760-765
#title Sequence and expression of a metabotropic glutamate receptor.
#cross-references MIMD:91156047
#accession S15362
##status preliminary
##molecule_type mRNA
##residues 1-1199 ##label MAS
##cross-references EX31:X57559; NID:956645; PID:956647

KEYWORDS G protein-coupled receptor; transmembrane protein
SUMMARY #length 1199 #molecular-weight 133235 #checksum 5211

Query Match 13.6%; Score 796; DB 2; Length 1199;
Best Local Similarity 27.1%; Pred. No. 6,00e-127;
Matches 219; Conservative 210; Mismatches 318; Indels 61; Gaps 51;

Db 65 RKGCEIREQGIQVEMAFHLEKINADPVLLPNTIGSIRSCMHSSVALDOSIEFIR 124
QY 1 RSCS-FNEH-GYHLFQAMRLGVEEINNSTALLPNTLGYQLYVCSDSA-NVY-AT-LR 54
Db 125 DSLISIDEKDLNRCJLDPDQTLPPGRTKRPVIGVIGPGSSVAIQVONLQJFNQI 184
QY 55 -VL-SLFGQHH-IE-L-QGDLHYST---VLAVIGPDSNRATTAALLISF-LVHIS 104
Db 185 YSATSIDLSKTLKYKFLRVVPSDITQARAMDIVKRYNNTYVSAVTEGNYGSGMDAF 244
QY 105 YAASSETLSVYKROQPSFLRTIPNDKYQVETMVLLOKFGMTWISLVGSSDDYQGLQVAL 164
Db 245 KELAAQGLTIAHSDK-LYV-AGEKSFDLKRLRDLPRKARVYVCFGCMATVRLGLSA 302
QY 165 ENQALVNGICIAKIDIPFSAQVDERMOCIMRHL-AQ-AGATVWVFSSROLARVFEES 222
Db 303 MRLGVVGEFSLGSDGMA-DRDEV-IEGVE-VEANGGIT-KLOSPVRSFDYFLKLR 358
QY 223 VULTNLGKYW-VASEAMALSRHTGTPGIGRIQGMVGLVAIORAVYGLAFEBAYV--R 279
Db 359 LDTNRPWFPEFWHRFQ-CRLPGHLEPNFRKYCTGNSLEENYVDSKMGFVINAIFY 417
QY 280 ADKEAPRCHKSGWSSNQLCREQAFMAHT-MPKL-KAF-SMSAV--NA---Y-RAV 329
Db 418 YAAHAGLQNNHALLCPGHNGLCDAMKPIDGRKLLDLIKSSFYGVSGEYWFPEKGDAPG 477
QY 330 YAAVAGHQLL-G-CASE--LGSRGR-VYPMOLLEQIHKVHFL-LHKDTVAFDNRDPLS 383
Db 478 RYDMLNLOYTEAR-YDYVAVGTWHEGVLNIDYKITO-MKSGMV-RSVSEPCCLGOIK 534
QY 384 SYNIAMDNGPMTFTVLSSSTMSPVQLINETKIQMHGKNHOPKSVSSDCLBEGHORY 443
Db 535 VIRKGEVSCMTGCKENEYVQ-DE-FTCRACDLG-WPMNAELTGCEPIPRVYLEMSDI 591
QY 444 VV-TGFHCCFECVPCGAGTFLNKSELRYRCQPGTEEMARPEGQTCPRVYVFLALREH 501
Db 592 ESIIATFSCIGLIVLTVLFLVLRDTPYVKKSSRELCTIILAGIFLIGVYVFFLILAK 651
QY 502 TSWVLLAANTLLELLLTAGLTFAMHLDTPVRSAGRLCFMLGSLAAGSGSLYGFGE 561


```
832      predicted\
      #binding-site phosphate (Thr) (covalent) #status
SUMMARY      #length 872 #molecular-weight 95773 #checksum 5740

Query Match      13.5%; Score 789; DB 2; Length 872;
Best Local Similarity 27.8%; Pred. No. 1,53e-125;
Matches 221; Conservative 195; Mismatches 322; Indels 56; Gaps 51;

Db      54 NEHRGIORLEAMFALDRINRDEHLLPGVRLGAHILDSCKDTHALDQALDFVAKASISRG 113
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      6 NEH-GYHLFQAMRLGVEINNSTALLPNIITLGQYLDVCSDSANVYA-TL--RV-LSL- 58

Db      114 ADSRSRIICPGSATSHDAPTAATGAVIGSGVSDYSIOVANLLRFOIPOSYSTASKLS 173
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      59 P-GQHHELEOGDLL-HR-SPT-VLAVIGPDSINAAITALLSFTLV-HISYAASSSTLS 113

Db      174 DKSRVDYFAITVPDFDQAKAMAEILRFEMWYVSVASGSGYGETGEAFEELEARANI 233
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY      114 VKROYSEFLRTIPNDKYQVETWVLLQKFGMTWISLVGSSDDYQGLQVQALENQALVRGI 173

Db      234 CVATSEKVG-RA-MSRAAFEGVVRALLQKPSARAVLFTSEDAARELLATQRLN-ASFT 290
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY      174 CIAFKDIMPESAQVGERMOCLEKRLHQAQ-AGATVWVFSSRQLARVFEESVLTNLTKGV 232

Db      291 WVASDGMG-ALE-SVAGSERAEG-AITIELASYP-ISDFASYFQSLDPMNNSRNPFR 346
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      233 WVASAMALSRHITGVPGIDRIGVGLVAIQKRAVPGIAKAFEEYAAADR-EAPR-PCR 290

Db      347 EFWEERFH-CSFRORDCAHSLRAV-PFEQESKIMEVYNAVYAMAHLMHMRALCPNT 404
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      291 GSWCSSNQLORECO-AFMAHTMPKLFKAFSSMSAYN-AYRAVYVAHQLHQL-G-C--AS 344

Db      405 HLDAMRPVGRLLYKDFVNVNKFDAFRADDDDEFRPFGDGTIRYNIETFLRAGSG 464
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      345 ELCSRGH-VYPMQLLEHQ-IHKVHF-L-LHK-DT--VAFNDNRDPLSSYNIIMDMNGPK 396

Db      465 R-TRYQGVGWAEG-LTLDTSFIPMASPSAGPDPASRCSPECLONEVKSQVQGEVCMIC 522
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY      397 WTTVLGSSWMSVQVNLNINTEKIQMHGKNH-QYPKSYCSSDDCEGHORVYTGHHCCFEC 455

Db      523 IPC-Q-PYEXRLDEFTCADGCLGYW-PNASLTGCFELPOEYIR-WGDA-WAVGPVITACL 577
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      456 VPCGAGTFLLKSELYRQPCGTTEMAPEGSQT-CFPRTVVFLALREHISM-V-LLANTL 512

Db      578 GALATLFLVGVFRHNATPYKASGRELCTILLGVFLCYCMFVFIAKSTAVCTIRL 637
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY      513 LLLLLGTAGLFAMHDDTPVYRASGRLCFMLGSLAAGSGSLYGFGEPTRPACILROA 572

Db      638 GLGTAFCVCSALLTKTNRIARIFG-CAREGAQRPRFISPAQVAIGLALISGLLIVAA 696
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      573 LFLALGFIIFLSCILVRSFQLIIFFKSTKYPTTYHAMVQNHGAGLFWISSAQLLCLT 632

Db      697 WLVEAPAGTKEETAPERREVVTLRCNHRDA-SMLGSLAVNVLIALCTL-YAFKTRCPE 754
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      633 WLWVMPPLPAREYORPFR-LVMLECTETISGLFIALLYGDL-SIAFAFCSYLGXDLPE 690

Db      755 NNEEAFIGTWTTCIIMLAFPIPIFYVSSDYRVOTTTCVSVSLGSLVGLCLAPKL 814
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY      691 NYNEAKCVITSLLENFVSWIAFTTASVYDGYK-LPAAANMAGLS-SLSSGFGYFLPKC 748

Db      815 HILLPOKNNVSH 828
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      749 YVILCRPDLNSTEH 762

RESULT      13
ENTRY      149142 #type complete
TITLE      metabotropic glutamate receptor 8 - mouse
ORGANISM   Mus musculus #common_name house mouse
DATE      02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I49142
```

```
REFERENCE      I49142
#authors      Duvolsin, R.M.; Zhang, C.; Ramonell, K.
#journal      J. Neurosci. (1995) 15:3075-3083
#title        A novel metabotropic glutamate receptor expressed in the
              retina and olfactory bulb.
#cross-references MGIID:9529344
#accession    I49142
#status       preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues     1-908 #label RES
#cross-references EMBL:U17252; NID:9854728; PID:9854729
GENETICS
#gene          mGluR8
#classification superfamily metabotropic glutamate receptor 4
KEYWORDS       neurotransmitter receptor
SUMMARY        #length 908 #molecular-weight 101413 #checksum 2996

Query Match      13.2%; Score 772; DB 2; Length 908;
Best Local Similarity 25.8%; Pred. No. 3.95e-122;
Matches 205; Conservative 221; Mismatches 311; Indels 59; Gaps 51;

Db      69 KEGRIHLEAMLYAIQOTNKDPLLSNITGVRIJLJCCSDITYALQSLTFVQALIEKDA 128
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      6 NEHGYHIFQAMRLGVEINNSTALLPNIITLGQYLDVCS-DSANVYATLR-VLSLPGQH- 62

Db      129 SDVKCANGDPIPTKDPKIGSVIGAAASSYIMVAVNLRFLKIPQISYASTAPELSDNMR 188
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      63 -HIE-IQGLDLHYS-P-VLAVIGPDSINRAATTAALLSFTLV-HISYAASSSTLSVKRO 117

Db      189 YDFESRYVPDSDYQAOAMVDIVTALGMVNYSTLASEGNGEVEAFPTQISRGVCA 248
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      118 YPSFLRTIPNDKYQVETWVLLQKFGMTWISLVGSSDDYQGLQVQALENQAL-VRICIA 176

Db      249 QSQKIPREPPGFEFKT--IKRLLETPNARAVLTFANEDDITGILDAKKLNSGFHWT 305
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY      177 FKDIMPESAQVGD-ERMOCIMRLHQAQATVWVFSSRQLARVFEESVLTNLTKGV-VWV 234

Db      307 GSDSWG-SK-IADVYQOEELAEBAVTLIPKRASIDGDFRFRSRLTANNRRNWFAPFSE 364
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY      235 ASBAMALSRHITGVPGIDRIGVGLVAIQKRA-VPGI-KAFEEYAIRADAEAPR-P-CHK 290

Db      365 GNFQXSGSGEGRKNSHKKCTGLERIARDSYBOEKVQVVIDAVYSMAVALHMKKEIC 424
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      291 GSM-C-SSNQLCREQQAFAHMTPKL-K-AFGSMSSAYN-AYRAVYVAHQLHQL-G-C 342

Db      425 PGYIGLCPKRVITDGRLELGYIAVNFNSAGTPVTFENENGDAFGKIDIFQYIINN-KST 483
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY      343 AS--ELCSR-GRVYPMQLLEQIHKVHFLLHKDT-VAFNDNRDPLSSYNIIMDMNGPKWT 398

Db      484 EYKLIQH--WTN-QLHLKVEDMOMANREHTHPASVCSLPCKPEBKTYGVV-CGMHCG 539
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      399 -FTVLSSSTWSPVQVNLNINTEKIQMHGKNHQPVSVCSSDCLB-HQRYVYTGHHCCFECV 455

Db      540 RCEGVN-QVDEL-SCLEPDLDPQPINIRTC-QR-IPITIKEMHSPMAVVPYLAIIIGI 595
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      457 PCGAGGFIINKSELYRQPCGTTEMAPEGSQTCPRRVVFLALREHISWVLLANLITL 516

Db      596 IATFYIVFVRNNDPYRASGRELSTYLLGIFLCYSTTFIMTAPDTITICSPRIFL 655
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY      517 LIGT-AGL-FAMHLDTPVYRASGRLCFMLGSLAAGSGSLYGFGEPTRPACILLOALF 574

Db      656 GLMGCSYVALTKTNRIHIREFGQKKSVTA-PKFI-SPASQVIFPISLISVOLLEVPW 713
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      575 ALGFTTIFLSCILVRSFQLIIFFKSTKYPTTYHAMVQNHGAGLFWIS-SAQLLCLTW 633

Db      714 FVVDPPHTIIDYGEQRTLPDENAGVLC-DISDLSJCSLGSILMAYCTVYAIKTRG 772
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      634 LVVMTPLPAREY--QR-F-P-HL-VMLECTETISGLFIALFLVNGLLSIAFAFCSYL 687

Db      773 VPETFENAKFIGTWTTCIIMLAFPIPIFFGTAQSEKMTIQCTITLVSKSLASVSLGM 832
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY      688 LPENYNEAKCVITSLLENFVSW--IA-FTTASVYDGYKLPAAANMAGLS-SLSSGFGG 742
```


Db 833 LYMPKVIITFHPEQN 848
: : : : :
QY 743 YFLPKCYIILCRPDLN 758

RESULT 14
ENTRY S71376 #type complete
TITLE glutamate receptor homolog - cherry salmon
ORGANISM #formal_name Oncorhynchus masou #common_name cherry salmon
DATE 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change
01-May-1998

ACCESSIONS
REFERENCE S71376
#authors Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.
#journal FEBS Lett. (1996) 392:71-76
#title Cloning and characterization of a bifunctional metabotropic
receptor activated by both extracellular calcium and
glutamate.
#cross-references M01D:96354880
#accession S71376
#status not compared with conceptual translation
#molecule_type mRNA
#residues 1-1218 #label KUB

KEYWORDS
FEATURE glycoprotein; phosphoprotein

603-625 #domain transmembrane #status predicted #label TM1\
640-660 #domain transmembrane #status predicted #label TM2\
672-690 #domain transmembrane #status predicted #label TM3\
717-737 #domain transmembrane #status predicted #label TM4\
761-782 #domain transmembrane #status predicted #label TM5\
796-817 #domain transmembrane #status predicted #label TM6\
826-850 #domain transmembrane #status predicted #label TM7\
104,233,403,525,
757 #binding site carbohydrate (Asn) (covalent) #status
predicted\
636,699,961 #binding site phosphate (Ser) (covalent) (by protein
kinase C) #status predicted\
705 #binding site phosphate (Thr) (covalent) (by protein
kinase C) #status predicted\
892 #binding site phosphate (Ser) (covalent) (by
cAMP-dependent kinase) #status predicted
SUMMARY #length 1218 #molecular_weight 136838 #checksum 1674

Query Match 12.9%; Score 755; DB 2; Length 1218;
Best Local Similarity 26.2%; Pred. No. 1,01e-118;
Matches 189; Conservative 199; Mismatches 279; Indels 54; Gaps 43;

Db 166 IAGVIGSGSSVALQYONLQLENIPIASATSIDSKTLKFLRYVPSDTLQARAI 225
: : : : :
QY 77 VLAIVGPDSNTNRATYTAALLPFLY-HISYASSETLSVFRQYPSFLRTIPNDKYOVETM 135

Db 226 LDIVKRYMTYVAHTEGNYGESGMEAFKELASQEGICIAHSDKI-YSN-AGEKHPDRL 283
: : : : :
QY 136 VLLQKFGWTWISVSSDDYGGQLGVALDNQALVKGICIAFADIMFSAQVDERMOCL 195

Db 284 LRLRLRLPRARVYVCFCEGTVRGLLMANRLGVAGEFLIGSDGNA-DRDEV-VEGYE 341
: : : : :
QY 196 MRHL-AQ-AGATVYVYSSRQLARVFFESVVLNLTK-VWVASEAMALSRHTIGVGIQ 252

Db 342 QEA-VGGITVYKLS-EVYISFDYFLKRLNTTRNPFEPFQHRQ-CRIGHPLEMNA 338
: : : : :
QY 253 RIGMVGVAIQKRAVPGKLAFFEAFA-RADKDAAPRCHKSGWSSNQQLREC-QAFMAH 309

Db 399 NYKNCSGYSELDENVODSKMGFVIAIYAMOGLDHMSHLCOPGVGLCKAMPIDGS 458
: : : : :
QY 310 TMRKL-KAF-SMSAY--NA---Y--RAYVAVAGHLQHLG--CASE--LC-SRGRYPPW 355

Db 459 QLEFLMRTSFTVSGEDVWFDENGDTPGRYEIMNLQYEPG-AFDYINGSWHEGOLST 517
: : : : :
QY 356 OLLEQIHKVHFL-LHKDYAFNDNRDPLSYNIIAMDMWNPKMTFTYLGSSSTSPVQLNI 414

Db 518 DDYIMQ-INSNDVYL-SYCEPSCSGEIKYIRGENVSCMCITACADNEIVQ-DE-FTCT 573
: : : : :
QY 518 DDYIMQ-INSNDVYL-SYCEPSCSGEIKYIRGENVSCMCITACADNEIVQ-DE-FTCT 573

QY 415 NETKIOMHGKNAHQVPKSVSSDCLGEHQRYV-TGFHHCCEFCVPCGAGFLNKSELYRQ 473

Db 574 ACDLGMWPPDELEGCEPILRLYLE-WGNPESTYQVFAQLGLIVTSFYFIFLYADTQV 632
: : : : :
QY 474 PCGTERRAPBGSTQCFPRVVFALREHTSWVLLANLTLILLD-TGLRWMHLDTPV 532

Db 633 VKSSRELYIILAGIFLIGCFPIILIAOPTVASCYQLRLVGLSATMCSALVTKNRI 692
: : : : :
QY 533 VRASGRGLTLMGSLAASGSG-YGFEGETRACLLRQALFALGTITLSCITVASPDL 592

Db 693 ARLLASKKKICTRKPRFSAMQVIALIVSVQ-LT-LEVTLI-TLE-PPMPVKSYRS 748
: : : : :
QY 593 IIF-----KFSKVPFTFYHAWQNHGAGLFVWISSAOLLICITLWVMTPLPAREYOR 647

Db 749 IRE-VFLIC-NSTVGMVAPLNGILLIMSCRY-YAFKTRNPNANENAKYIAFTMYTTC 805
: : : : :
QY 648 FPHVLMLECTEINSLGFIILAFYLNGLIST-AFACSYLCKDLPENENKCVTFSLFNF 706

Db 806 IWLAF-VPIY-FGSNYKIITTSFVSLS-VTVALGCMFSPKYIILAKPERVRSAPFT 862
: : : : :
QY 707 VSMIAFTTASVYDQKY-LPANMMAGLSLSGFCGYFLPKCYIILCRPDLNSTEHPQA 765

Db 863 S 863
QY 766 S 766

RESULT 15
ENTRY A6742 #type complete
TITLE metabotropic glutamate receptor, mGluR6 - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
29-Jan-1999

ACCESSIONS
REFERENCE A6742
#authors Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto,
R.; Mizuno, N.; Nakanishi, S.
#journal J. Biol. Chem. (1993) 268:11868-11873
#title Molecular characterization of a novel retinal metabotropic
glutamate receptor mGluR6 with a high agonist selectivity
for L-2-amino-4-phosphonobutylate.
#cross-references M01D:93280152
#accession A6742

CLASSIFICATION
KEYWORDS #superfamily metabotropic glutamate receptor 4
#protein-coupled receptor; transmembrane protein
SUMMARY #length 871 #molecular_weight 95088 #checksum 3942

Query Match 12.5%; Score 729; DB 2; Length 871;
Best Local Similarity 26.5%; Pred. No. 1.59e-113;
Matches 215; Conservative 219; Mismatches 308; Indels 70; Gaps 56;

Db 49 RACGAKKFGQVHRLEAMLYALDRVADPELLPGVRLGRLDLDTGSRDYALEQALSFQ 108
: : : : :
QY 1 RSC-SFN-BHGHLFGQMLRGVEEINNSTALLPNTLIGQLDVDS-DSANYATLRL-VL 56

Db 109 ALIRGRGDDEASVRCGPVPLRSAPPRVAVVAGASASSVIMAVNLRFLAIPDISY 168
: : : : :
QY 57 SL---PGQ-HHIELO-GDL--LHISPT--VLAIVGPDSNTNRATTAALLSPFLY-HISY 105

Db 169 ASTAPLSDSTRDYFSRVYPPDSYQAQAVDIVRALGNVYSTLASSENGSGEYAEV 228
: : : : :
QY 106 AASSETLSVYKQYPSFLRTIPNDKYQVETMVLQKFGWTWISVSSDDYGGQLGVAL 165

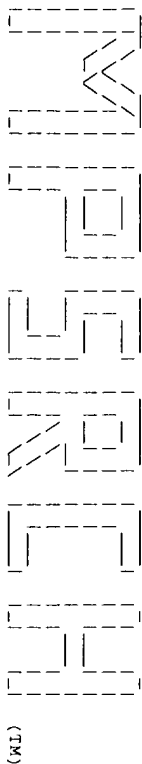
Db 229 QTSREAGYCIASQSIPIPEKPGEFHK-VIRLMETPNARQIILFANDDIRRLVLEATR 287
: : : : :
QY 166 NQAL-VRGICIAFKDIMPQSAQVGDERMOKLMBRLHQAAGATVAVVYSSRQLARVFEESV 224


```

Db 288 OANLGHFLWVSDSMG-SK-ISPILNLEEEA-VGATITLPRKA--SIDGPDQYFMTSL 342
   :||| :||:|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
QY 225 LTNLTGK-VWVASEAMALSRHTGTPGIORIGMVLGVAI-OKRAVPGLKAFEEAT-ARAD 281
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
Db 343 ENNRNINFAEFW-EENFNCKLTSSGQSDSTRKCTGEERIGQDAYEOEGKVOFVIDA 401
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
QY 282 KEAPRPC-HKGSWCSSNOLCR-ECQAFMAH-TMPK-L-KA-FSMSAYN--A--Y-R-A 328
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
Db 402 VYATAHAHSHQALCPGHTGICPAMEPTDGRITLHYIRAVRFGNSAGTPIVAFENGDAP 461
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
QY 329 VYAAVAHGLHOL-LG-CASE--LC-SRGRVYPQLEQIHKVHFLHKDT-VAFNDNRDPL 382
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
Db 462 GRVDIFQOATNGSASGGOAVGOWAEA-LRLDMEVLRMSGDPHEVPPSOCSLPCGPE 520
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
QY 383 SSYNINAMDW-NGRKWTITVAGSSTWSPVQNLINETKIOMHKNHQPCKSVCCSDCLDG- 440
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
Db 521 RKKVKGVP-CQWHEACDGYRF-OVDE-FTCEACPGDMRPTPNHTGCRTPPVRLT-WS 576
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
QY 441 HORVYTGHHCCFECVPCGAGTFLNKSELYRCQPCGTEEMAPESQTCFPRTVVFLALRE 500
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
Db 577 -SPNAALPELLAVLIGIMATTIMATFMRANDTPIYRASGRELSYVLLTGIFLIYAIFLM 635
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
QY 501 HTSWVLLAAN-TLLELLLLGTA-GLFAWHLDTPVVRSAAGRLCLMLGSLAAGSGSLYGF 558
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
Db 636 VAEPQAIICAAARLLLLGTTLSYSALLTKTNRIYRIFEQGRSVTP-PPFI-SPTSOLV 693
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
QY 559 FGEPTRPACLLRQALFALGFTIFLSCLTVRSFOLIIIFKSTKYPTFYHAWYQNHGAGLF 618
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
Db 694 ITFGLTSLQVVGVIAMLGAPPHSVIIDEQORTVDPDQARGVLC-DMSDSLIGCLGYS 752
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
QY 619 VMIS-SAQULLICLITLWLVMTPLPAREX--OR-F-P-HL-VMLECTETNSLGFILAFLYN 671
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
Db 753 LLLMYTCTVYAIKARGVETENEAKPIGFTMYTTCIIMLAEPPIFPGTAQSAEKYIOTT 812
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
QY 672 GLLSISAFACSYLGKDLPENYNEAKCVTFSLFNEFSWIAF---FTTASYVDGKYLPA 727
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
Db 813 TLTVSLASVSLGMLVVPKTYVILFHPDON 844
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
QY 728 NMMAGLS-SLSSGFGGYFLPKCYVILCRPDLN 758
   :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|

```

Search completed: Fri Mar 17 13:29:01 2000
 Job time : 47 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPerch_mp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:36:28 2000; MasPar time 93.42 Seconds

Tabular output not generated. 864.499 Million cell updates/sec

Title: >US-09-361-652-3
Description: (1-777) from US09361652.pep
Perfect Score: 5838
Sequence: 1 RSCSFNENGHYHLFOAMRLGV.....NSTEHFOASIDYTRRCGST 777

Scoring table:
PAM 150
Gap 11

Searched: 666290 segs, 103942017 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-pending
1:Pg 2:060 3:07 4:080 5:081 6:082 7:083 8:084 9:084B
10:085 11:086 12:087 13:088 14:089 15:090 16:091 17:092
18:093 19:094 20:095 21:096 22:097 23:098

Statistics: Mean 42.646; Variance 177.023; scale 0.241

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	5838	100.0	777	23	US-09-361-Sequence 3, Applicatio	0.00e+00
2	5838	100.0	777	1	PCT-US99-1 Sequence 3, Applicatio	0.00e+00
3	4587	78.6	840	2	US-60-172-Sequence 5, Applicatio	0.00e+00
4	4587	78.6	840	23	US-09-361-Sequence 1, Applicatio	0.00e+00
5	4587	78.6	840	1	PCT-US99-1 Sequence 1, Applicatio	0.00e+00
6	4483	76.8	842	1	PCT-US99-1 Sequence 2, Applicatio	0.00e+00
7	4483	76.8	842	23	US-09-361-Sequence 2, Applicatio	0.00e+00
8	1848	31.7	843	18	US-09-361-Sequence 1, Applicatio	1.65e+16
9	1797	30.8	843	18	US-09-361-Sequence 2, Applicatio	2.77e+16
10	1509	25.8	669	18	US-09-361-Sequence 7, Applicatio	7.45e+13
11	1464	25.1	822	2	US-60-172-Sequence 2, Applicatio	2.87e+13
12	1233	21.1	877	2	US-60-172-Sequence 14, Applicati	8.66e+10
13	1182	20.2	1059	16	US-09-134-Sequence 2, Applicatio	1.27e+10
14	1170	20.0	1085	14	US-08-484-Sequence 5, Applicatio	2.08e+10
15	1170	20.0	1085	9	US-08-484-Sequence 2, Applicatio	2.08e+10
16	1170	20.0	1085	9	US-60-172-Sequence 5, Applicatio	2.08e+10
17	1170	20.0	1085	2	US-60-172-Sequence 11, Applicati	2.08e+10
18	1170	20.0	1085	9	US-08-484-Sequence 5, Applicatio	2.08e+10
19	1170	20.0	1085	6	US-08-292-Sequence 5, Applicatio	2.08e+10
20	1163	19.9	1078	2	US-60-172-Sequence 9, Applicatio	1.06e+9
21	1160	19.9	1078	6	US-08-292-Sequence 7, Applicatio	2.14e+9

22	1160	19.9	1078	2	US-60-172-Sequence 6, Applicatio	2.14e+9
23	1160	19.9	1078	9	US-08-484-Sequence 7, Applicatio	2.14e+9
24	1160	19.9	1078	1	PCT-US99-1 Sequence 12, Applicati	2.14e+9
25	1160	19.9	1078	9	US-08-484-Sequence 7, Applicatio	2.14e+9
26	1160	19.9	1078	2	US-60-172-Sequence 7, Applicatio	2.14e+9
27	1160	19.9	1078	2	US-08-484-Sequence 8, Applicatio	2.14e+9
28	1160	19.9	1078	2	US-60-172-Sequence 8, Applicatio	2.14e+9
29	1158	19.8	1079	1	PCT-US98-1 Sequence 59, Applicati	3.41e+9
30	1158	19.8	1079	9	US-08-484-Sequence 8, Applicatio	3.41e+9
31	1158	19.8	1079	9	US-08-484-Sequence 8, Applicatio	3.41e+9
32	1158	19.8	1079	6	US-08-292-Sequence 8, Applicatio	3.41e+9
33	1158	19.8	1079	16	US-09-107-Sequence 59, Applicatio	3.41e+9
34	1158	19.8	1079	9	US-08-484-Sequence 8, Applicatio	3.41e+9
35	1158	19.8	1079	2	US-60-172-Sequence 12, Applicati	3.41e+9
36	1149	19.7	1079	2	US-60-172-Sequence 10, Applicati	2.77e+9
37	1143	19.6	1079	2	US-60-172-Sequence 13, Applicati	1.12e+9
38	1101	18.9	1026	14	US-08-943-Sequence 1, Applicatio	1.97e+9
39	1090	18.7	1001	1	PCT-US99-1 Sequence 8, Applicatio	2.54e+9
40	1074	18.4	1038	1	PCT-US97-0 Sequence 2, Applicatio	1.04e+9
41	1074	18.4	1038	1	PCT-US97-0 Sequence 2, Applicatio	1.04e+9
42	1063	18.2	1088	9	US-08-484-Sequence 6, Applicatio	1.34e+8
43	1063	18.2	1088	9	US-08-484-Sequence 6, Applicatio	1.34e+8
44	1063	18.2	1088	6	US-08-292-Sequence 6, Applicatio	1.34e+8
45	1063	18.2	1088	9	US-08-484-Sequence 6, Applicatio	1.34e+8

ALIGNMENTS

RESULT ID	1	US-09-361-652-3	STANDARD:	PRT:	777 AA.
XX	xxxxxx				
XX		Sequence 3, Application US/09361652			
DE		Sequence 3, Application US/09361652			
CC		GENERAL INFORMATION:			
CC		APPLICANT: Zuker, Charles S.			
CC		APPLICANT: Adler, Jon Elliot			
CC		APPLICANT: Lindemeyer, Juergen			
CC		APPLICANT: Ryba, Nick			
CC		APPLICANT: Hoorn, Mark			
CC		APPLICANT: The Regents of the University of California			
CC		TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor			
CC		FILE REFERENCE: 02307E-088610US			
CC		CURRENT APPLICATION NUMBER: US/09/361,652			
CC		CURRENT FILING DATE: 1999-07-27			
CC		EARLIER APPLICATION NUMBER: US 60/094,465			
CC		EARLIER FILING DATE: 1998-07-28			
CC		NUMBER OF SEQ ID NOS: 8			
CC		SOFTWARE: PatentIn Ver. 2.1			
CC		SEQ ID NO 3			
CC		LENGTH: 777			
CC		TYPE: PRT			
CC		ORGANISM: Homo sapiens			
CC		FEATURE:			
CC		OTHER INFORMATION: human G-protein coupled receptor B3 (GPCR-B3)			
SO		SEQUENCE 777 AA: 86285 MW: 3230984 CN:			
	Query Match	100.0%: Score 5838; DB 23; Length 777;			
	Best Local Similarity	100.0%: Pred. No. 0.00e+00;			
	Matches	777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Dh	1	RSCSFNENGHYHLFOAMRLGVEEINNSTALPNTTIGYOLYDVCSDSANVATRVSLPG 60			
Dh	1	RSCSFNENGHYHLFOAMRLGVEEINNSTALPNTTIGYOLYDVCSDSANVATRVSLPG 60			
Dh	1	RSCSFNENGHYHLFOAMRLGVEEINNSTALPNTTIGYOLYDVCSDSANVATRVSLPG 60			
Dh	61	QHHEIIEGDLHYSPTVLAVIGPDSNTRATTAALLSPFLVHISYAASTETLSEVKRQYPS 120			
Dh	61	QHHEIIEGDLHYSPTVLAVIGPDSNTRATTAALLSPFLVHISYAASTETLSEVKRQYPS 120			
Dh	61	QHHEIIEGDLHYSPTVLAVIGPDSNTRATTAALLSPFLVHISYAASTETLSEVKRQYPS 120			
Dh	61	QHHEIIEGDLHYSPTVLAVIGPDSNTRATTAALLSPFLVHISYAASTETLSEVKRQYPS 120			

Db	121	ELRTLPNDKQYQETWVLLLOKFGWTNLSVGGSDDYQGLQVQALENQALRGICIAFKDI	180
Qy	121	FRTLPNDYQYQETWVLLLOKFGWTNLSVGGSDDYQGLQVQALENQALRGICIAFKDI	180
Db	181	MPFSAQVGBERQCLMRHLQAQATVAVVSSSQLARVFESVLTLTGKVVWASAWA	240
Qy	181	MPFSAQVGBERQCLMRHLQAQATVAVVSSSQLARVFESVLTLTGKVVWASAWA	240
Db	241	LSRHITGVPGIORIGVNLGVALIQRAVPGIKAEAVARADKEAPRCHGSSWCSNQIC	300
Qy	241	LSRHITGVPGIORIGVNLGVALIQRAVPGIKAEAEVAPRADKEAPRCHGSSWCSNQIC	300
Db	301	RSCQAFMATMPLKAFSSMSAAYNAVAYVAHGLHQLLGCASELCSRRVYPMOLLEQ	360
Qy	301	RSCQAFMATMPLKAFSSMSAAYNAVAYVAHGLHQLLGCASELCSRRVYPMOLLEQ	360
Db	361	IKHVFHLLKDDTAFFNDNDPLTSSYNIAMDWNGPKMTFTVLSSSTWSPQOLNINETKIQ	420
Qy	361	IKHVFHLLKDDTAFFNDNDPLTSSYNIAMDWNGPKMTFTVLSSSTWSPQOLNINETKIQ	420
Db	421	WHGKNHQVEKSVCCSDCLEGHQHVWTFGHHCCCECVPCGAGTEFLNKSELYRCOPCGTEW	480
Qy	421	WHGKNHQVEKSVCCSDCLEGHQHVWTFGHHCCCECVPCGAGTEFLNKSELYRCOPCGTEW	480
Db	481	APBSGOTCPRTVYVFLALAEHTSWVLLAANTLLLLLLGTAGLFAWHLDPVYRSAGRL	540
Qy	481	APBSGOTCPRTVYVFLALAEHTSWVLLAANTLLLLLLGTAGLFAWHLDPVYRSAGRL	540
Db	541	CFILMGSLAGSGSIXGFGEPTRPACLLQALFALGFTTFLSCLTVRSFOLIIIFKST	600
Qy	541	CFILMGSLAGSGSIXGFGEPTRPACLLQALFALGFTTFLSCLTVRSFOLIIIFKST	600
Db	601	KVPFTYHAWVQNHGAGLFYWMISSAOLLICTLWLVWTPLPAREYORFPHLVMECTETN	660
Qy	601	KVPFTYHAWVQNHGAGLFYWMISSAOLLICTLWLVWTPLPAREYORFPHLVMECTETN	660
Db	661	SLGFIILAFIYNGLLISARACSTLGGDLPENTYDEACVYTSLLFNYSWIAFFTASVYD	720
Qy	661	SLGFIILAFIYNGLLISARACSTLGGDLPENTYDEACVYTSLLFNYSWIAFFTASVYD	720
Db	721	GXYLPANNAAGLSSISGFGYELPKCYITLCPDPLNSTEHHQASIODYTRRCGST	777
Qy	721	GXYLPANNAAGLSSISGFGYELPKCYITLCPDPLNSTEHHQASIODYTRRCGST	777
RESULT 2 PCT-US99-17099-3 STANDARD; PRT: 777 AA.			
AC	xx	xxxxxx	
DT	xx		
DE	xx		
CC	xx	Sequence 3, Application PC/TUS9917099	
CC	xx	GENERAL INFORMATION:	
CC	xx	APPLICANT: Zuker, Charles S.	
CC	xx	APPLICANT: Adler, Jon Elliott	
CC	xx	APPLICANT: Lindemeier, Juergen	
CC	xx	APPLICANT: Ryba, Nick	
CC	xx	APPLICANT: Hoon, Mark	
CC	xx	APPLICANT: The Regents of the University of California	
CC	xx	TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor	
CC	xx	TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor	
CC	xx	FILE REFERENCE: 02307E-088610PC	
CC	xx	CURRENT APPLICATION NUMBER: PCT/US99/17099	
CC	xx	CURRENT FILING DATE: 1999-07-27	
CC	xx	EARLIER APPLICATION NUMBER: US 60/094,465	
CC	xx	EARLIER FILING DATE: 1998-07-28	
CC	xx	NUMBER OF SEQ ID NOS: 8	
CC	xx	SOFTWARE: PatentIn Ver. 2.1	
CC	xx	SEQ ID NO 3	

CC	LENGTH: 777
CC	TYPE: PRT
CC	ORGANISM: Homo sapiens
CC	FEATURE:
CC	OTHER INFORMATION: human G-protein coupled receptor B3 (GPCR-B3)
CC	SEQUENCE 777 AA; 86285 MW; 3230984 CN;
SQ	
	Query Match 100.0%; Score 5838; DB 1; Length 777; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
D	1 RSCSFNEGHYLLPQAMRGVEINNSTALLPNITLGGQLDYCVSDSANYATLRVLSLPG 60
Q	1 RSCSFNEGHYLLPQAMRGVEINNSTALLPNITLGGQLDYCVSDSANYATLRVLSLPG 60
D	61 QHHIELAGDLLHYSPTYLAIVGPDSINRAATTALSPFLVHISYAASSETLSVKROYPS 120
Q	61 QHHIELAGDLLHYSPTYLAIVGPDSINRAATTALSPFLVHISYAASSETLSVKROYPS 120
D	121 FLRTIPNDKRYEETWMLLKQFGWTWISLVGSSDDYGLGVQALENOALYRGICIAFKDI 180
Q	121 FLRTIPNDKRYEETWMLLKQFGWTWISLVGSSDDYGLGVQALENOALYRGICIAFKDI 180
D	181 MPESAQVEDERMOCLMTHIAQAGTAVVVVSSRRDLAVEFESEVLTNLTKRWVASAWA 240
Q	181 MPESAQVEDERMOCLMTHIAQAGTAVVVVSSRRDLAVEFESEVLTNLTKRWVASAWA 240
D	241 LSRNHTGVPGIQRIGMYLGVAIQRAVPGLKAPEEAAYARADKEAPRECHGSGCSCSNOLC 300
Q	241 LSRNHTGVPGIQRIGMYLGVAIQRAVPGLKAPEEAAYARADKEAPRECHGSGCSCSNOLC 300
D	301 RECCAFAHATMPKIKAFSSMSAYNAAYAVAAGHLGOLLGCASELCSSRRVYPWOLLEQ 360
Q	301 RECCAFAHATMPKIKAFSSMSAYNAAYAVAAGHLGOLLGCASELCSSRRVYPWOLLEQ 360
D	361 IHKHFELIHKRTVAFNNRPDPLSYNTIIADMNGPKMTFTVLSSSTSPVOLINNETKIQ 420
Q	361 IHKHFELIHKRTVAFNNRPDPLSYNTIIADMNGPKMTFTVLSSSTSPVOLINNETKIQ 420
D	421 WHGNKHQVPKSVCSDDLCEGHQRPVTGFHHCCECYVCAGATEFLNKSELYRCOPCGTEEW 480
Q	421 WHGNKHQVPKSVCSDDLCEGHQRPVTGFHHCCECYVCAGATEFLNKSELYRCOPCGTEEW 480
D	481 APESGQCPTPTVVFALARHETSVMLLAANTLLILLTAGLFAWHLDTPVVRSAAGRL 540
Q	481 APESGQCPTPTVVFALARHETSVMLLAANTLLILLTAGLFAWHLDTPVVRSAAGRL 540
D	541 CFIMLGSLAAAGSSLVXPFGEPTPPACLLNQALFALGFTIFLSCLYVRSQOLIIFPEST 600
Q	541 CFIMLGSLAAAGSSLVXPFGEPTPPACLLNQALFALGFTIFLSCLYVRSQOLIIFPEST 600
D	601 KVPFFYHAMVONHBAGLFVYMISSAQAOLICTLMVLVYVTPLPAREYORFPPLVMLECTETN 660
Q	601 KVPFFYHAMVONHBAGLFVYMISSAQAOLICTLMVLVYVTPLPAREYORFPPLVMLECTETN 660
D	661 SLGFLTLAEFLNYGLGISAFACSYLGKDLPENYNBAKCVTESLLFNFSWIATFTASVVD 720
Q	661 SLGFLTLAEFLNYGLGISAFACSYLGKDLPENYNBAKCVTESLLFNFSWIATFTASVVD 720
D	721 GKYLPAAMMAAGLISSSGFGGYTLPRPCYIILCPDLNSTEHQOASIQDYTRRCGST 777
Q	721 GKYLPAAMMAAGLISSSGFGGYTLPRPCYIILCPDLNSTEHQOASIQDYTRRCGST 777
RESULT 3 STANDARD: PRT; 840 AA.	
ID US-60-172-600-5	xxxxxx
XX AC	
XX AC	
XX DE	Sequence 5, Application US/60172600

CC Sequence 5, Application US/60172600
CC GENERAL INFORMATION:
CC APPLICANT: Bonazzi, Vivien
CC TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
CC TITLE OF INVENTION: RECEPTOR, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
CC TITLE OF INVENTION: PROTEIN, AND USES THEREOF
CC FILE REFERENCE: C1000178
CC CURRENT APPLICATION NUMBER: US/60/172,600
CC CURRENT FILING DATE: 1999-12-20
CC NUMBER OF SEQ ID NOS: 14
CC SOFTWARE: FastSeq for Windows Version 4.0
CC SEQ ID NO 5
CC LENGTH: 840
CC TYPE: PRT
CC ORGANISM: UNKNOWN
CC FEATURE:
CC OTHER INFORMATION: SEE GENE BANK REPORT
CC
CC
CC
SQ SEQUENCE 840 AA: 93496 MW: 3932001 CN.

Query Match 78.6%; Score 4587; DB 2; Length 840;

Best Local Similarity 75.2%; Pred. No. 0.00e+00; Mismatches 93; Indels 1; Gaps 1;
Matches 585; Conservative 99;

Db 63 RPDSENGHGHLEFOAMFTEEEINNSALLPNTLIGELYDYVCSANVATLRLALOG 122
1 RSCSFNEHGHLEFOAMRLGVEINNSTALLPNTLIGELYDYVCSANVATLRLVLSLP 60
Cc 123 PRHLEIKDLRNHSSKVAFAFGPNTDHAVTALLGPFIMPLVSYEASSVLSAKRKP 182
Cc 61 QHHEILOGDHLHYSPVLAVIGPSTNRAATLALSPFLVH-ISTYASSETLSVKRQYP 119
Db 183 SFLRTVPSDRHOVEVMYVQLLOSFGWVWISLIGSGDYGOGLVQALEELAVRGICVAFKD 242
Cc 120 SFLRTVPSDRHOVEVMYVQLLOSFGWVWISLIGSGDYGOGLVQALEELAVRGICVAFKD 179
Cc 243 IVPFSARVGPBRMOSXMOHLAQAARTVYVFSNRHLARVFEFSVLANLTGKVVASEDM 302
Cc 180 IMPFSAVGBGRMOCMLRHHLAQAAGATVYVFSNRHLARVFEFSVLANLTGKVVASEDM 239
Cc 303 AISTYITSVTIGIGITVGLVAVQROVPGKKEFEESYRAVTAAPSACPGSMCSTNOL 362
Cc 240 ALSHHTIGVGIORIGVLAIGVLAIOKRAVPGKAFEEAVYARADKEAPRCHSGSMCSTNOL 299
Cc 363 CRECHFTTRMPTLGAFFMSAAYRVEAVYVAHGHOLIGTSEICSRGPVPMOULO 422
Cc 300 CRECHFTTRMPTLGAFFMSAAYRVEAVYVAHGHOLIGTSEICSRGPVPMOULO 359
Cc 423 QIYKVNFLHENTVAFPDNDGTGLGYDIIAMDNGPEMTEEEIIGSASLSPVHLDINKTKI 482
Cc 360 QIHKVHFLKMDVAFNDNDPLSSYNIIAMDNGPKMTFTVLGSSITWSPVQULINETKI 419
Cc 483 QHMKKNQVPSVCTTDCLAGHRVYVGSHHCCFEVPCGAGTFLNKSGLITCOPCGTEE 542
Cc 420 QHMKKNQVPSVCTTDCLAGHRVYVGSHHCCFEVPCGAGTFLNKSGLITCOPCGTEE 479
Cc 543 WAPKESTCEPRTRYEFLLAMEPILSLVLAANTLILLLVAGLFAHGHHTPVYRSAGR 602
Cc 480 WAPKESTCEPRTRYEFLLAMEPILSLVLAANTLILLLVAGLFAHGHHTPVYRSAGR 539
Cc 603 LCFMLGSLVAGSCSFYFGEPTVPACLLRQPLSLGFAFLSCLTIRSFOLVITKFS 662
Cc 540 LCFMLGSLVAGSCSFYFGEPTVPACLLRQPLSLGFAFLSCLTIRSFOLVITKFS 599
Cc 663 TKYPTFRTAONHAGALFIVSVTHLLICLTILVMTTPRTREYQRFPLVILECTEV 722
Cc 600 TKYPTFRTAONHAGALFIVSVTHLLICLTILVMTTPRTREYQRFPLVILECTEV 659
Cc 723 NSVGFLLAFTNHLISITFVCSYGLKELPENYEAACVFSLLNLTNVSMAFTMASIY 782
Cc 660 NSVGFLLAFTNHLISITFVCSYGLKELPENYEAACVFSLLNLTNVSMAFTMASIY 719
Cc 783 QGSYLPVAVNLAGLTLLSGGFSGFLEPKCYVILCRPELNTNEHQASIODYTRRCGTT 840
Cc 719 QGSYLPVAVNLAGLTLLSGGFSGFLEPKCYVILCRPELNTNEHQASIODYTRRCGTT 783

Qy 720 DGKYLPAANMAGLSLSSGFGCYFLEPKCYVILCRPDLNTEHQASIODYTRRCGTT 777

RESULT 4
ID US-09-361-652-1 STANDARD: PRT: 840 AA.

AC xxxxxx

DE Sequence 1, Application US/09361652

CC Sequence 1, Application US/09361652

CC GENERAL INFORMATION:

CC APPLICANT: Zuker, Charles S.

CC APPLICANT: Adler, Jon Elliot

CC APPLICANT: Lindemeyer, Juerger

CC APPLICANT: Ryba, Nick

CC APPLICANT: Hoon, Mark

CC APPLICANT: The Regents of the University of California

CC TITLE OF INVENTION: Nucleic Acids Encoding a G-protein Coupled Receptor

CC TITLE OF INVENTION: Involved in Sensory Transduction

CC FILE REFERENCE: 02307E-0886100S

CC CURRENT APPLICATION NUMBER: US/09/361,652

CC CURRENT FILING DATE: 1999-07-27

CC EARLIER APPLICATION NUMBER: US 60/094,465

CC NUMBER OF SEQ ID NOS: 8

CC SOFTWARE: PatentIn Ver. 2.1

CC SEQ ID NO 1

CC LENGTH: 840

CC TYPE: PRT

CC ORGANISM: Rattus sp.

CC FEATURE:

CC OTHER INFORMATION: rat G-protein coupled receptor B3 (GPCR-B3)

CC SEQUENCE 840 AA: 93496 MW: 3932001 CN;

Query Match 78.6%; Score 4587; DB 23; Length 840;

Best Local Similarity 75.2%; Pred. No. 0.00e+00; Mismatches 93; Indels 1; Gaps 1;

Matches 585; Conservative 99;

Db 63 RPDSENGHGHLEFOAMFTEEEINNSALLPNTLIGELYDYVCSANVATLRLALOG 122
1 RSCSFNEHGHGHLEFOAMRLGVEINNSTALLPNTLIGELYDYVCSANVATLRLVLSLP 60
Cc 123 PRHLEIKDLRNHSSKVAFAFGPNTDHAVTALLGPFIMPLVSYEASSVLSAKRKP 182
Cc 61 QHHEILOGDHLHYSPVLAVIGPSTNRAATLALSPFLVH-ISTYASSETLSVKRQYP 119
Db 183 SFLRTVPSDRHOVEVMYVQLLOSFGWVWISLIGSGDYGOGLVQALEELAVRGICVAFKD 242
Cc 120 SFLRTVPSDRHOVEVMYVQLLOSFGWVWISLIGSGDYGOGLVQALEELAVRGICVAFKD 179
Cc 243 IVPFSARVGPBRMOSXMOHLAQAARTVYVFSNRHLARVFEFSVLANLTGKVVASEDM 302
Cc 180 IMPFSAVGBGRMOCMLRHHLAQAAGATVYVFSNRHLARVFEFSVLANLTGKVVASEDM 239
Cc 303 AISTYITSVTIGIGITVGLVAVQROVPGKKEFEESYRAVTAAPSACPGSMCSTNOL 362
Cc 240 ALSHHTIGVGIORIGVLAIGVLAIOKRAVPGKAFEEAVYARADKEAPRCHSGSMCSTNOL 299
Cc 363 CRECHFTTRMPTLGAFFMSAAYRVEAVYVAHGHOLIGTSEICSRGPVPMOULO 422
Cc 300 CRECHFTTRMPTLGAFFMSAAYRVEAVYVAHGHOLIGTSEICSRGPVPMOULO 359
Cc 423 QIYKVNFLHENTVAFPDNDGTGLGYDIIAMDNGPEMTEEEIIGSASLSPVHLDINKTKI 482
Cc 360 QIHKVHFLKMDVAFNDNDPLSSYNIIAMDNGPKMTFTVLGSSITWSPVQULINETKI 419
Cc 483 QHMKKNQVPSVCTTDCLAGHRVYVGSHHCCFEVPCGAGTFLNKSGLITCOPCGTEE 542
Cc 420 QHMKKNQVPSVCTTDCLAGHRVYVGSHHCCFEVPCGAGTFLNKSGLITCOPCGTEE 479

QY	180	IMPE\$AQVGBERMQCLMRHLAQAGATVVVVV\$SSRQLARFEFESVYLTNLTGKVVVASEAM	239
Db	303	AI\$TYIT\$V\$TGIGIGITVU\$GVA\$Q\$Q\$V\$D\$G\$K\$E\$F\$E\$E\$S\$V\$R\$A\$V\$T\$A\$P\$A\$S\$C\$P\$B\$G\$M\$C\$S\$T\$N\$Q\$L	362
QY	240	AL\$H\$H\$T\$G\$V\$G\$D\$R\$I\$O\$R\$I\$M\$V\$G\$V\$A\$I\$O\$K\$R\$A\$V\$D\$G\$A\$F\$E\$E\$A\$A\$R\$A\$D\$K\$E\$P\$R\$C\$H\$G\$M\$S\$C\$S\$N\$Q\$L	299
Db	363	CR\$E\$H\$T\$F\$T\$T\$N\$M\$D\$T\$L\$A\$F\$S\$M\$S\$A\$A\$Y\$R\$V\$E\$V\$V\$V\$A\$V\$G\$L\$H\$Q\$L\$G\$T\$S\$E\$I\$S\$R\$G\$P\$V\$P\$M\$O\$L\$Q	422
QY	300	CR\$E\$Q\$A\$M\$A\$T\$T\$M\$K\$L\$A\$F\$S\$M\$S\$Y\$N\$A\$Y\$R\$V\$A\$V\$A\$G\$L\$H\$Q\$L\$G\$A\$S\$E\$L\$S\$R\$R\$A\$Y\$P\$M\$O\$L\$E	359
Db	423	Q\$I\$K\$V\$N\$F\$L\$E\$H\$T\$V\$A\$F\$D\$N\$G\$T\$L\$G\$Y\$D\$I\$A\$M\$D\$N\$G\$P\$E\$W\$F\$E\$I\$G\$S\$A\$S\$I\$P\$V\$H\$D\$I\$N\$K\$T\$K\$I	482
QY	360	Q\$I\$K\$H\$V\$E\$L\$L\$K\$D\$I\$V\$A\$F\$N\$D\$R\$P\$L\$S\$S\$Y\$N\$I\$A\$M\$D\$N\$G\$P\$K\$M\$T\$F\$V\$G\$S\$T\$W\$P\$Q\$V\$M\$N\$E\$T\$K\$I	419
Db	483	Q\$H\$G\$K\$N\$Q\$V\$V\$S\$C\$T\$D\$C\$A\$G\$H\$R\$V\$V\$G\$S\$H\$C\$C\$E\$C\$V\$C\$E\$A\$G\$T\$F\$L\$M\$S\$E\$L\$I\$Q\$P\$C\$G\$T\$E\$	542
QY	420	Q\$H\$G\$K\$N\$Q\$V\$P\$K\$S\$C\$S\$D\$C\$E\$G\$H\$Q\$R\$V\$T\$G\$F\$H\$C\$C\$E\$C\$V\$C\$G\$A\$G\$T\$F\$L\$N\$K\$S\$E\$L\$Y\$R\$C\$O\$P\$C\$G\$T\$E\$	479
Db	543	W\$P\$R\$E\$S\$T\$C\$P\$R\$V\$E\$F\$L\$A\$H\$E\$P\$I\$S\$V\$L\$A\$N\$T\$L\$L\$L\$L\$V\$G\$T\$A\$G\$L\$F\$A\$H\$F\$H\$P\$V\$V\$R\$S\$A\$G\$R	602
QY	480	W\$P\$R\$G\$S\$T\$C\$P\$R\$V\$V\$L\$A\$R\$E\$H\$T\$S\$W\$L\$A\$N\$T\$L\$L\$L\$L\$G\$T\$A\$G\$L\$F\$A\$H\$H\$D\$I\$P\$V\$R\$S\$A\$G\$R	539
Db	603	L\$C\$F\$L\$M\$G\$S\$L\$V\$A\$G\$S\$C\$S\$Y\$F\$E\$F\$E\$P\$P\$A\$C\$H\$R\$O\$P\$L\$F\$S\$L\$G\$A\$I\$F\$L\$S\$C\$I\$T\$R\$S\$Q\$V\$I\$Y\$K\$F\$S	662
QY	540	L\$C\$F\$L\$M\$G\$S\$L\$A\$G\$S\$S\$L\$X\$G\$F\$F\$E\$P\$T\$R\$A\$C\$H\$R\$A\$L\$A\$G\$T\$F\$F\$L\$S\$C\$U\$T\$R\$S\$Q\$V\$I\$Y\$K\$F\$S	599
Db	663	T\$K\$V\$E\$F\$F\$R\$W\$A\$O\$N\$H\$G\$A\$G\$L\$F\$V\$I\$V\$S\$T\$V\$H\$L\$I\$C\$L\$T\$W\$L\$V\$M\$T\$P\$R\$T\$R\$E\$Y\$Q\$R\$P\$H\$V\$I\$E\$C\$T\$E\$V	722
QY	600	T\$K\$V\$E\$F\$F\$H\$A\$W\$O\$N\$H\$G\$A\$G\$L\$F\$V\$M\$I\$S\$A\$Q\$Q\$L\$I\$C\$L\$T\$W\$L\$V\$V\$M\$T\$P\$L\$P\$A\$R\$E\$Y\$Q\$R\$P\$H\$V\$I\$E\$C\$T\$E\$	659
Db	723	N\$V\$S\$O\$F\$L\$A\$F\$H\$N\$I\$L\$I\$S\$T\$F\$V\$C\$S\$Y\$G\$K\$E\$L\$P\$E\$N\$Y\$N\$A\$K\$O\$V\$T\$S\$I\$L\$N\$F\$S\$W\$A\$F\$T\$M\$A\$S\$I\$Y	782
QY	660	N\$S\$G\$F\$I\$A\$F\$Y\$N\$D\$L\$I\$S\$I\$A\$F\$A\$C\$S\$Y\$G\$K\$D\$P\$E\$N\$Y\$N\$A\$K\$O\$V\$T\$S\$I\$L\$N\$F\$S\$W\$A\$F\$T\$M\$A\$S\$I\$Y	719
Db	783	Q\$G\$S\$T\$P\$A\$V\$N\$V\$I\$A\$G\$T\$L\$L\$G\$G\$S\$G\$Y\$F\$E\$L\$P\$K\$C\$Y\$V\$I\$L\$C\$R\$E\$L\$N\$T\$E\$H\$F\$Q\$A\$S\$I\$Q\$D\$T\$R\$R\$C\$G\$T	840
QY	720	D\$G\$T\$P\$A\$N\$N\$A\$M\$A\$D\$L\$S\$S\$G\$F\$G\$Y\$F\$L\$P\$K\$C\$Y\$V\$I\$L\$C\$R\$P\$D\$N\$S\$T\$H\$F\$A\$S\$I\$Q\$D\$T\$R\$R\$C\$G\$S	777
RESULT	6	STANDARD;	PRT; 842 AA.
ID	PCN-US99-17099-2		
AC	xxxxxx		
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DT			
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DE			
XX			
Sequence 2, Application PC/TUS9917099			
CC	Sequence 2, Application PC/TUS9917099		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Zuker, Charles S.		
CC	APPLICANT: Adler, Jon Elliot		
CC	APPLICANT: Lindemeier, Juergen		
CC	APPLICANT: Ryba, Nick		
CC	APPLICANT: Hoon, Mark		
CC	APPLICANT: The Regents of the University of California		
CC	TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor		
CC	TITLE OF INVENTION: Involved in Sensory Transduction		
CC	FILE REFERENCE: 02307E-088610PC		
CC	CURRENT APPLICATION NUMBER: PCN/TUS99/17099		
CC	CURRENT FILING DATE: 1999-07-27		
CC	EARLIER APPLICATION NUMBER: US 60/094,465		
CC	EARLIER FILING DATE: 1998-07-28		
CC	NUMBER OF SEQ ID NOS: 8		
CC	SOFTWARE: PatentIn Ver. 2.1		
CC	SEQ ID NO 2		
CC	LENGTH: 842		
CC	TYPE: PRT		
CC	ORGANISM: Mus sp.		
CC	FEATURE:		
CC	OTHER INFORMATION: mouse G-protein coupled receptor B3 (GPCR-B3)		
CC	SEQUENCE 842 AA: 93455 MW: 3909917 CN:		

Query Match 76.8%; Score 4483; DA 1; Length 842;
Best Local Similarity 74.2%; Pred. No. 0.00e+00;
Matches 577; Conservative 101; Mismatches 99; Indels 1; Gaps 1;

Db 65 RSDSFNGHGYHLFOAMRFTVEEINNSTALLPNTLIGELYDYVCSSESSNVATLRVPAOOG 124
1 RSCSFNEHGYHLFOAMRGLVEEINNSTALLPNTLIGELYDYVCSANVATLRVLSLPG 60

Qy 125 TGHLEMRDLRNHSSKVVALLIGPNTDHATTALLESFIMPLVSYDASSVYLSGKRKFP 184
61 QHHELEGGDLHYSPYLAIVGPDSTINRAATTAALLSPFLVH-ISTYASSETLSVKRQYP 119

Db 185 SFLRTIPSDKYQVEVIVIRLLQSFQWWSILVSGYDYGQGLQVQALDELATPRGICVAFKD 244
120 SFLRTIPNDKYQVEETVLLQKFGMTWISLVGSSDDYQGLQVQALEQALVRGICIAFKD 179

Qy 245 VVPLSAQAGDPRMQRMRLARARTVYVFSNNHLAGVFFRSVYLANLTKWVIASEDW 304
180 IMPFSAGVGERMOCIMRHLAQAGATVYVFSRQLAEVFESVYLTLNIGKVVWASEAW 239

Db 305 AISTYITNVPDIOGIGTVLGVAIQROVPGIKFEFEESYVQAVMGAPRTCPBGSNGCTNOL 364
240 ALSRHITGVPDIOIRIGVLAIGVAIQRAVPGIKAEFEAYARADKEAPRCHGKSSNOL 299

Qy 365 CRECHAFITNMMPDLGAFSMAAYNVEAYAVAHGLHQLIGCTSGTCARGPVYPMOLQ 424
300 CREQOAMAHMTPKLFKAFSSANAYRAVAVAHGLHQLIGCSELCSRRVYPMOLLE 359

Db 425 QIYVNFLLHKTYAFDDKGPGLCYDIIAMDNGPEKTFEVIGSASISPVHLDINKTKI 484
360 QIHVHFLLHRDVTAFNDNRDPLSSYNIIAMDNGPKWTFEVLGSSITSPVQULINETKI 419

Qy 485 OMHCKNNQVPYSVCTRCLBGGHRLVNGSHHCCEPCMGCEGTFLNSELTCOPCGTEE 544
420 OMHCKNNQVPYSVCSDDLBSGHQVVTGFHHCCEVPCGAGTFLNSELTCOPCGTEE 479

Db 545 WAPGSSACFSRTVEFLGWHEPISLVLLAANTLLLLIGTAGLFAFARLHTPVYRSAGR 604
480 WAPGSSQTCFRTVYFLALREHTSMVLLAANTLLLLIGTAGLFAFARLHTPVYRSAGR 539

Qy 605 LCFLMLGSLVAGSCSLYSFEGKPTVPACLLRQPLFSLGFAIFLSCLTIRSFQULVIIFKFS 664
540 LCFLMLGSLVAGSCSLYGFEGEPTRPACLLRQALFALGFIIFLSCLTIRVSQULVIIFKFS 599

Db 665 TKVPTFYHTAQNHNAGIFIVYSTVHLFCLTLMAMTTPRTREYORFPHLVLECEY 724
600 TKVPTFYHTAQNHNAGIFIVMISSAQLLICTLWLVMTPLPAREYORFPHLVLECEY 659

Qy 725 NSVGFVAFANHILISTEVCSTLGKELPENYNEAKCVFSLIHFVSWIAFTMSIY 784
660 NSLGFITLAFLYNGLISTISAFACSTLIGKDLPENYNEAKCVFSLIHFVSWIAFTTASVY 719

Db 785 QGSYLPANVNLAGLATLSGFGSGYFLPKCYVILCRPELINTEHFOASIQDYTRRCGT 842
720 DGKYLPAANMAGLSSSGFGGYFLPKCYVILCRPDLNSTEHFOASIQDYTRRCGST 777

RESULT 7
ID US-09-361-652-2 STANDARD: PRT; 842 AA.

AC xxxxxx
XX
DT
XX Sequence 2, Application US/09361652
DE
XX
CC Sequence 2, Application US/09361652
CC GENERAL INFORMATION:
CC APPLICANT: Zucker, Charles S.
CC APPLICANT: Adler, Jon Elliot
CC APPLICANT: Lindemeier, Juergeen
CC APPLICANT: Ryba, Nick
CC APPLICANT: Hoon, Mark

CC APPLICANT: The Regents of the University of California
CC TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
CC TIME OF INVENTION: Involuted in Sensory Transduction
CC FILE REFERENCE: 02307E-086610US
CC CURRENT APPLICATION NUMBER: US/09/361,652
CC EARLIER FILING DATE: 1999-07-27
CC EARLIER APPLICATION NUMBER: US 60/094,465
CC NUMBER OF SEQ ID NOS: 8
CC SOFTWARE: Patent'n Ver. 2.1
CC SEQ ID NO 2
CC LENGTH: 842
CC TYPE: PRT
CC ORGANISM: Mus sp.
CC FEATURE:
CC OTHER INFORMATION: mouse G-protein coupled receptor B3 (GPCR-B3)
CC SEQUENCE 842 AA; 93455 KW; 3909917 CN;

Query Match 76.8%; Score 4483; DA 23; Length 842;
Best Local Similarity 74.2%; Pred. No. 0.00e+00;
Matches 577; Conservative 101; Mismatches 99; Indels 1; Gaps 1;

Db 65 RSDSFNGHGYHLFOAMRFTVEEINNSTALLPNTLIGELYDYVCSSESSNVATLRVPAOOG 124
1 RSCSFNEHGYHLFOAMRGLVEEINNSTALLPNTLIGELYDYVCSANVATLRVLSLPG 60

Qy 125 TGHLEMRDLRNHSSKVVALLIGPNTDHATTALLESFIMPLVSYDASSVYLSGKRKFP 184
61 QHHELEGGDLHYSPYLAIVGPDSTINRAATTAALLSPFLVH-ISTYASSETLSVKRQYP 119

Db 185 SFLRTIPSDKYQVEVIVIRLLQSFQWWSILVSGYDYGQGLQVQALDELATPRGICVAFKD 244
120 SFLRTIPNDKYQVEETVLLQKFGMTWISLVGSSDDYQGLQVQALEQALVRGICIAFKD 179

Qy 245 VVPLSAQAGDPRMQRMRLARARTVYVFSNNHLAGVFFRSVYLANLTKWVIASEDW 304
180 IMPFSAGVGERMOCIMRHLAQAGATVYVFSRQLAEVFESVYLTLNIGKVVWASEAW 239

Db 305 AISTYITNVPDIOGIGTVLGVAIQROVPGIKFEFEESYVQAVMGAPRTCPBGSNGCTNOL 364
240 ALSRHITGVPDIOIRIGVLAIGVAIQRAVPGIKAEFEAYARADKEAPRCHGKSSNOL 299

Qy 365 CRECHAFITNMMPDLGAFSMAAYNVEAYAVAHGLHQLIGCTSGTCARGPVYPMOLQ 424
300 CREQOAMAHMTPKLFKAFSSANAYRAVAVAHGLHQLIGCSELCSRRVYPMOLLE 359

Db 425 QIYVNFLLHKTYAFDDKGPGLCYDIIAMDNGPEKTFEVIGSASISPVHLDINKTKI 484
360 QIHVHFLLHRDVTAFNDNRDPLSSYNIIAMDNGPKWTFEVLGSSITSPVQULINETKI 419

Qy 485 OMHCKNNQVPYSVCTRCLBGGHRLVNGSHHCCEPCMGCEGTFLNSELTCOPCGTEE 544
420 OMHCKNNQVPYSVCSDDLBSGHQVVTGFHHCCEVPCGAGTFLNSELTCOPCGTEE 479

Db 545 WAPGSSACFSRTVEFLGWHEPISLVLLAANTLLLLIGTAGLFAFARLHTPVYRSAGR 604
480 WAPGSSQTCFRTVYFLALREHTSMVLLAANTLLLLIGTAGLFAFARLHTPVYRSAGR 539

Qy 605 LCFLMLGSLVAGSCSLYSFEGKPTVPACLLRQPLFSLGFAIFLSCLTIRSFQULVIIFKFS 664
540 LCFLMLGSLVAGSCSLYGFEGEPTRPACLLRQALFALGFIIFLSCLTIRVSQULVIIFKFS 599

Db 665 TKVPTFYHTAQNHNAGIFIVYSTVHLFCLTLMAMTTPRTREYORFPHLVLECEY 724
600 TKVPTFYHTAQNHNAGIFIVMISSAQLLICTLWLVMTPLPAREYORFPHLVLECEY 659

Qy 725 NSVGFVAFANHILISTEVCSTLGKELPENYNEAKCVFSLIHFVSWIAFTMSIY 784
660 NSLGFITLAFLYNGLISTISAFACSTLIGKDLPENYNEAKCVFSLIHFVSWIAFTTASVY 719

Db 785 QGSYLPANVNLAGLATLSGFGSGYFLPKCYVILCRPELINTEHFOASIQDYTRRCGT 842
720 DGKYLPAANMAGLSSSGFGGYFLPKCYVILCRPDLNSTEHFOASIQDYTRRCGST 777

RESULT	ID	US-09-361-631-1	STANDARD;	PRT;	843 AA.
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XX	DT				
XX	DE	Sequence 1, Application US/09361631			
CC	CC	Sequence 1, Application US/09361631			
CC	CC	GENERAL INFORMATION:			
CC	CC	APPLICANT: Zuker, Charles S.			
CC	CC	APPLICANT: Adler, Jon Elliot			
CC	CC	APPLICANT: Lindemeyer, Juergen			
CC	CC	APPLICANT: The Regents of the University of California			
CC	CC	TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor			
CC	CC	FILE REFERENCE: 02307E-08872005			
CC	CC	CURRENT APPLICATION NUMBER: US/09/361,631			
CC	CC	CURRENT FILING DATE: 1999-07-27			
CC	CC	EARLIER APPLICATION NUMBER: US 60/095,464			
CC	CC	EARLIER FILING DATE: 1998-07-28			
CC	CC	EARLIER APPLICATION NUMBER: US 60/112,747			
CC	CC	EARLIER FILING DATE: 1998-12-17			
CC	CC	NUMBER OF SEQ ID NOS: 10			
CC	CC	SOFTWARE: Patentln Ver. 2.0			
CC	CC	SEQ ID NO 1			
CC	CC	LENGTH: 843			
CC	CC	TYPE: PRT			
CC	CC	ORGANISM: Rattus sp.			
CC	CC	FEATURE:			
CC	CC	OTHER INFORMATION: rat G-protein coupled receptor (GPCR) B4 amino			
CC	CC	OTHER INFORMATION: acid sequence			
CC	CC	SEQUENCE 843 AA: 95799 MW: 4010925 CN;			

Query Match	31.7%;	Score 1848;	DB 18;	Length 843;
Best Local Similarity	37.5%;	Pred. No. 1.65e-169;		
Matches	293;	Mismatches 269;	Indels 26;	Gaps 22;

Db	71	GINIMQARFVVEEINNCSSLLPGVLKEADVDCYSSNNTHPGXYFLA--ODDDLILK	122
Qy	9	GYNLEQARLVEEELNNSTALLPNTLTGOLYDXDCSDSANATLRVLSLPGQHIELQG	68
Db	130	DYSQIMPHVAVIGPDNSESATVSNILSHFLDQITYSATSDLRKDRKHPMSMLRTVPS	189
Qy	69	DLIHSPTVLAVIGPDSSTINRAATTAALSPPLY-HISVAASESTLSYKQPSFLRTIPN	127
Db	190	ATHHIEAVVOLAHFGHOMWIVLVVSDSDGEGNSHLLSQRLTKSDICIAOEVLPIES	249
Qy	128	DKYQETVAVLLQKFGKWTWISLVGSSDDYGGOLGYALENO-ALYRGICIAFKDIMP--S	184
Db	250	SQVNRSEEQRLDNLILDKLRTTSARVVYVESP-ELSYFPEHEYLKNNFTGFWVIAESW	308
Qy	185	AQV--GDE-R-MQCLIMRLHAQAGATVVYVFESSROLAR-VFESVVLNLTGKVVVASEAW	239
Db	309	AIDPVLAHLTLELRHTGTFGLTGIQVRSIPGSSOR--VRDRKGYPPVNTNIRTCNQ	365
Qy	240	ALSRHITGVPGCIQIGVLGVAIQDRAAPGAKAEAEVAYARDKEA-PAPCRGKSGWCSNQ	298
Db	366	DCDACLN-TKFSFNILLTSGSERVYVYSAVAVVAHALHRLTLCNRRYCKQKQVEMQL	424
Qy	299	LCREQQAAMATMKRLKFAKFSMSA-YNNYRAVYVAVHOLHLLCSASBLSRGVAYVQQL	357
Db	425	LREIHWAVFTLLGNRLFFDQOGDPMUL-LDIIQOMDISQNPQSIASYSFTSKRLTYIN	483
Qy	358	LEQIKRVFFLLHKDTVAENDNRD-PLSESYNIADMDWNPCKMTFFVLGSSSTSPQVLNINE	418
Db	484	NVSYTEPNTNIVPVMSCSKSQCPQGMKKSVALHPCCEFCIDCMGTILNRSDAFENLSC	544
Qy	417	TKIQHGKNNHOVPSVCSDDLQEGHQRVYVTFHHCCECEVCGAGTFLNKS-ELYRCQPC	475

DB	543	PGSMWYKNDITCFORRPTFLEMEVEPTIYVAIIAAAGFSTALIEIF-WRHQFPMVR	601
Oy <td>476</td> <td>GTEKAPBGSOTCFPRIVYFALBREHNSWILLANLTLLLLGLTAGLPM- HLDIPYR</td> <td>534</td>	476	GTEKAPBGSOTCFPRIVYFALBREHNSWILLANLTLLLLGLTAGLPM- HLDIPYR	534
Db <td>602</td> <td>SAGGDMCFMLVPLLLAFGMVPIYVGPPTVSCFQRAFFTCISLCITVRSFQIVC</td> <td>661</td>	602	SAGGDMCFMLVPLLLAFGMVPIYVGPPTVSCFQRAFFTCISLCITVRSFQIVC	661
Oy <td>535</td> <td>SAGGALCFMLGMSLAAGSGSYGFGGEPTRPACLLRQALFALGFTIPLSCLTVRSFOLII</td> <td>594</td>	535	SAGGALCFMLGMSLAAGSGSYGFGGEPTRPACLLRQALFALGFTIPLSCLTVRSFOLII	594
Db <td>662</td> <td>VEKMARLRPSAYSPWMVYHGPYVFAITLAKVALVYGNMLATTINIGRTDDDDPIMII</td> <td>721</td>	662	VEKMARLRPSAYSPWMVYHGPYVFAITLAKVALVYGNMLATTINIGRTDDDDPIMII	721
Oy <td>595</td> <td>IFKSTKATPIYTHAMVQHGAGLGVMTSSAQOLICTLWLVTPLP- ABEYQAFPLVM</td> <td>653</td>	595	IFKSTKATPIYTHAMVQHGAGLGVMTSSAQOLICTLWLVTPLP- ABEYQAFPLVM	653
Db <td>722</td> <td>LSCHPNYRNGLENTSMDLLSYLGFSPAYMGKELPTNYNEAKFTILSMTEFSTSISLC</td> <td>781</td>	722	LSCHPNYRNGLENTSMDLLSYLGFSPAYMGKELPTNYNEAKFTILSMTEFSTSISLC	781
Oy <td>654</td> <td>LECTETNSLGFTLAFLYNGLSTISAFACSYLGRDLPENYNEAKVTPSLDFNFWIAFE</td> <td>713</td>	654	LECTETNSLGFTLAFLYNGLSTISAFACSYLGRDLPENYNEAKVTPSLDFNFWIAFE	713
Db <td>782</td> <td>TFMSVHOCVLTIMDLVTVLNFALICLG-YFGKCKMILFEPBRNRSATFNSMIGQYTM</td> <td>840</td>	782	TFMSVHOCVLTIMDLVTVLNFALICLG-YFGKCKMILFEPBRNRSATFNSMIGQYTM	840
Oy <td>714</td> <td>TTASATYDEKYLPAANMAG-LSSLSSQGGFELPKCYVILLCRDPLNSTEHFQASIDQYTR</td> <td>772</td>	714	TTASATYDEKYLPAANMAG-LSSLSSQGGFELPKCYVILLCRDPLNSTEHFQASIDQYTR	772
Db <td>841</td> <td>R 841</td> <td></td>	841	R 841	
Oy <td>773</td> <td>R 773</td> <td></td>	773	R 773	
RESULT	9		
ID	US-09-361-631-2	STANDARD:	PRT; 843 AA.
XX	xxxxxx		
XX			
DT			
XX			
DE	Sequence 2, Application US/09361631		

CC Sequence 2: Application US/09361631
CC GENERAL INFORMATION:
CC APPLICANT: Zuker, Charles S.
CC APPLICANT: Adler, Jon Elliot
CC APPLICANT: Lindemeyer, Juergen
CC APPLICANT: The Regents of the University of California
CC TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein
CC TITLE OF INVENTION: Involved in Sensory Transduction

CC CURRENT APPLICATION NUMBER: US/09/361,631
CC CURRENT FILING DATE: 1999-07-27
CC EARLIER APPLICATION NUMBER: US 60/095,464
CC EARLIER FILING DATE: 1998-07-28
CC EARLIER APPLICATION NUMBER: US 60/112,747
CC EARLIER FILING DATE: 1998-12-17
CC NUMBER OF SEQ ID NOS: 10
CC SOFTWARE: PatentIn Ver. 2.0
CC SEQ ID NO 2
CC LENGTH: 843
CC TYPE: PRT
CC ORGANISM: Mus sp.
CC FEATURE:
CC OTHER INFORMATION: mouse G-protein coupled receptor (GPCR) B4 amino
CC OTHER INFORMATION: acid sequence
CC SEQUENCE 843 AA: 95/52 MW: 399656 CN;

Query Match	30.88;	Score 1797;	DB 18;	Length 843;
Best Local Similarity	37.0%;	Pred. No. 2.77e-164;		
Matches	289;	Conservative 191;	Mismatches 275;	Indels 26;
				Gaps 23;

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Db      71 GYNLMQAMRAVEEINNCSLLPGVLLGYEMDVCYLSNNIQPGLYFLSQIDDFLPILK- 12
      ||:|||||:||||:||||:||||:| |:| |:| |:|
QY      9 GYHLFQAMRGVEEINNSTALLPNITLGYQLYDVCSDSANVYATLRVLSTLPQHIIELQG 68

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[illegible]

[illegible]

CY	3	C-STENHGCHYLFOAMRLQVEEELNSTALLPRITTLGQLDYDVCSSANVATLRYLSLPQC	61
Db	118	NKIDSLNDIFENCNSEHIPS--IAVGATGCSTAVANLLGLFYIPOVSYASSRLLSNK	1777
OY	62	HHE-LO-GDLLHYG---PTVLAVIGPOSTNRATTAALLSPFLV-HISYAASETLSVK	1195
Db	178	NOFKSFLETRPDEHQATMAADIEFFRMWNGTIIAADDDYGPGICEKFEALAEERDICI	2337
OY	116	ROYPSFLETRIPDKQOVBETWLLLOKFEMTWISLVGSSDDYGQGVQVALENQAIVRGICI	1757
Db	238	DESELISOYSQE--EEIQ-Q-VVENIQTAVIVVFESSGGPLEBLINE-IYRRNTIKIW	293
OY	176	AFKDIMP-FSAQOVGERMQCMRHHAQGAQAVVVFS-ROLARVFESVLTNLTKKW	233
Db	294	LASEMASSSLIAMPEEFRRVIGSTIGFAKKAGQIPGEFEELOKYHPKKSANGAKFEWE	3535
OY	234	VASEAMA---L-SR----HIIGVP-GID-RIGMWLG---VA-IQ-KRAV-GL-KAF-E	274
Db	354	EFFNCYLDESSEKNSPASASFRKAHEBGLGAGNGTAARPPCTGDENTSVETPYMDTHL	4133
OY	275	EA---YARAD-KEAP-RPC-HKG--SWCSSN-OLC-RE-C-OAFMAHTPKLKAFS-M	3195
Db	414	RISTVYLYAVYSIAAHODITYTCGKGLFTNGSCADIKKYEAQVULKHLHLNFISMG	4737
OY	320	SSAIVAYAVYAVAAGHLQQLGACSE-L-----CS-RGRYPQMLLEQHKKVFLHK-	3707
Db	474	EVDVDERGDLVGNYSINIMWLSPEDGSVVEEVGYNVYAKKGERLFINEKILMGFS	5333
OY	371	DTVANNDNRBDLSVNITIAMOMNPK-WT-FTVLGS-STWSP-VQ-LINNETKIOWHGN	4225
Db	534	KEVPSSNCRDCLPOTRKGIIEGPTECCFECVDCPDGEYSDETIDASADCPCEDYMSNEN	5935
OY	426	HOVPKSYVCSDDLGHOR-VVTGFHHCCFCEVPCGAGTFLNKSELYRCOPCGEEMAPEG	484
Db	594	HTSCPKQIEELSMTERPG-TALLFNVLGFIPLFPVLAGVTKRNRPYKATNRELSTYL	6555
OY	445	SOTCPKR-VVFLACLREHTSMVLLANTILLLLDGL-TAGLEAMHLDPVVSAGRLCFL	5433
Db	653	LLFSLLCFSSSLF-ETGEPOMWTCRLROPAGISFVLCISCIJVKTNRVLVE-AKI	7095
OY	544	MUGSLAAG-SSGVGFPEBPTRPACLRQALFALGFIIPLSCLVRSFOLLIIKFEKTV	6002
Db	710	PTSLHRKWWGLNFLVFLFCITPVQIVICVIWXTAPSSYRNHELDEIIFITCHE-GS	7685
OY	603	PT-FYHANVQHGAEGLEYMISSAQDLICTHVLVMTPLPARERYQRPHLYMLECTETS	6655
Db	769	L-MALGELIGTCLLAACEFFAKSRKLBNPNFNEARFITFSMLIFTWISFPAATAST	827
OY	662	LGFIILAFL-YNGLISISAFCSTLGDPLPENYEACVTFSLFTNFVSWIAFFT-ASY	718
Db	828	X-YGREVASVEVIALIAA-SFGLLACIFENKYYILLFXPSRTIE	869
OY	719	YDGKULPANMMAGLSLSSGFGY-FLPKCYVILCLRDLNSTE	761
RESULT	14		
ID	US-08-484-719-5	STANDARD:	PRT; 1085 AA.
XX	xxxxxx		
Sequence	5,	Application	US/08484719
GENERAL INFORMATION:			
CC	APPLICANT:	Edward F. Nemeth, Edward M.	
CC	APPLICANT:	Brown, Steven C. Hebert,	
CC	APPLICANT:	Bradford C. Van Wageningen,	
CC	APPLICANT:	Manuel F. Balandrin,	
CC	APPLICANT:	Forrest H. Fuller, Eric G.	
CC	APPLICANT:	Delmar, Scott T. Moe	
CC	TITLE OF INVENTION:	CALCIUM RECEPTOR-ACTIVE	

MUSE RELEASE
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MSEARCH protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Mar 17 13:35:41 2000; MSEARCH time 13.42 Seconds
Tabular output not generated.

Title: >US-09-361-652-3
Description: (1-777) from US09361652.pep
Perfect Score: 5838
Sequence: 1 RSCSFNEGHYHLPQAMRLGV.....NSTEHFOASIDYTRRCGST 777

Scoring table: PAM 150
Gap 11

Searched: 134018 seqs, 13297625 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT9_COMB 5:backfiles1

Statistics: Mean 35.945; Variance 174.591; scale 0.206

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1170	20.0	1085	1	US-08-484-	Sequence 5, Applicatio	3.80e-88
2	1170	20.0	1085	1	US-08-485-	Sequence 5, Applicatio	3.80e-88
3	1170	20.0	1085	2	US-08-480-	Sequence 5, Applicatio	3.80e-88
4	1170	20.0	1085	2	US-08-943-	Sequence 5, Applicatio	3.80e-88
5	1170	20.0	1085	3	US-08-353-	Sequence 5, Applicatio	3.80e-88
6	1160	19.9	1078	2	US-08-943-	Sequence 7, Applicatio	2.82e-87
7	1160	19.9	1078	3	US-08-353-	Sequence 7, Applicatio	2.82e-87
8	1160	19.9	1078	1	US-08-485-	Sequence 7, Applicatio	2.82e-87
9	1160	19.9	1078	1	US-08-484-	Sequence 7, Applicatio	2.82e-87
10	1160	19.9	1078	1	US-08-480-	Sequence 7, Applicatio	2.82e-87
11	1158	19.8	1079	1	US-08-484-	Sequence 8, Applicatio	4.21e-87
12	1158	19.8	1079	2	US-08-480-	Sequence 8, Applicatio	4.21e-87
13	1158	19.8	1079	3	US-08-353-	Sequence 8, Applicatio	4.21e-87
14	1158	19.8	1079	2	US-08-943-	Sequence 8, Applicatio	4.21e-87
15	1158	19.8	1079	1	US-08-485-	Sequence 8, Applicatio	4.21e-87
16	1063	18.2	1088	1	US-08-484-	Sequence 6, Applicatio	7.62e-79
17	1063	18.2	1088	3	US-08-353-	Sequence 6, Applicatio	7.62e-79
18	1063	18.2	1088	2	US-08-480-	Sequence 6, Applicatio	7.62e-79
19	1063	18.2	1088	2	US-08-943-	Sequence 6, Applicatio	7.62e-79
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22	951	16.3	1058	2	US-08-687-	Sequence 5, Applicatio	3.88e-69
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AC	xxxxxx			
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DT				
XX	Sequence 5, Application US/08484565			
DE				
XX	Sequence 5, Application US/08484565			
CC	Patent No. 5763569			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Edward M. Brown			
CC	APPLICANT: Steven C. Hebert			
CC	APPLICANT: James E. Garrett, Jr.			
CC	TITLE OF INVENTION: CALCULUM RECEPTOR-ACTIVE			
CC	TITLE OF INVENTION: MOLECULES			
CC	NUMBER OF SEQUENCES: 20			
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESS: Lyon & Lyon			
CC	STREET: First Interstate World Center			
CC	STREET: Suite 4700			
CC	STREET: 633 West Fifth Street			
CC	CITY: Los Angeles			
CC	STATE: California			
CC	COUNTRY: USA			
CC	ZIP: 90071			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage			
CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC	SOFTWARE: FASTSEQ			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: US/08/484,565			
CC	FILING DATE: 7 June, 1995			
CC	CLASSIFICATION: 435			
CC	PRIOR APPLICATION DATA:			
CC	PRIOR APPLICATION DATA: Including application			
CC	PRIOR APPLICATION DATA: described below: 9			
CC	APPLICATION NUMBER: 08/353,784			
CC	FILING DATE: 9 December, 1994			
CC	APPLICATION NUMBER: PCT/US/94/12117			
CC	FILING DATE: 21 October, 1994			
CC	APPLICATION NUMBER: U.S. 08/292,827			
CC	FILING DATE: 23 August, 1994			
CC	APPLICATION NUMBER: U.S. 08/141,248			
CC	FILING DATE: 22 October, 1993			

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	1085 AA.
ID	US-08-484-565-5			
AC	xxxxxx			
XX				
DT				
XX	Sequence 5, Application US/08484565			
DE				
XX	Sequence 5, Application US/08484565			
CC	Patent No. 5763569			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Edward M. Brown			
CC	APPLICANT: Steven C. Hebert			
CC	APPLICANT: James E. Garrett, Jr.			
CC	TITLE OF INVENTION: CALCULUM RECEPTOR-ACTIVE			
CC	TITLE OF INVENTION: MOLECULES			
CC	NUMBER OF SEQUENCES: 20			
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESS: Lyon & Lyon			
CC	STREET: First Interstate World Center			
CC	STREET: Suite 4700			
CC	STREET: 633 West Fifth Street			
CC	CITY: Los Angeles			
CC	STATE: California			
CC	COUNTRY: USA			
CC	ZIP: 90071			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage			
CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC	SOFTWARE: FASTSEQ			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: US/08/484,565			
CC	FILING DATE: 7 June, 1995			
CC	CLASSIFICATION: 435			
CC	PRIOR APPLICATION DATA:			
CC	PRIOR APPLICATION DATA: Including application			
CC	PRIOR APPLICATION DATA: described below: 9			
CC	APPLICATION NUMBER: 08/353,784			
CC	FILING DATE: 9 December, 1994			
CC	APPLICATION NUMBER: PCT/US/94/12117			
CC	FILING DATE: 21 October, 1994			
CC	APPLICATION NUMBER: U.S. 08/292,827			
CC	FILING DATE: 23 August, 1994			
CC	APPLICATION NUMBER: U.S. 08/141,248			
CC	FILING DATE: 22 October, 1993			

[illegible]

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CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: First Interstate World Center
CC STREET: Suite 4700
CC STREET: 633 West Fifth Street
CC City: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: FASTSEQ
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/353,784
CC FILING DATE: 9 December, 1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC PRIOR APPLICATION DATA: Including application
CC PRIOR APPLICATION DATA: described below: 8
CC APPLICATION NUMBER: PCT/US/94/12117
CC FILING DATE: 21 October, 1994
CC APPLICATION NUMBER: U.S. 08/292,827
CC FILING DATE: 23 August, 1994
CC APPLICATION NUMBER: U.S. 08/141,248
CC FILING DATE: 22 October, 1993
CC APPLICATION NUMBER: U.S. 08/009,389
CC FILING DATE: 23 February, 1993
CC APPLICATION NUMBER: U.S. 08/017,127
CC FILING DATE: 12 February, 1993
CC APPLICATION NUMBER: U.S. 07/934,161
CC FILING DATE: 21 August, 1992
CC APPLICATION NUMBER: U.S. 07/634,044
CC FILING DATE: 11 February, 1992
CC APPLICATION NUMBER: U.S. 07/749,451
CC FILING DATE: 23 August, 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Heber, Sheldon O.
CC REGISTRATION NUMBER: 38,179
CC REFERENCE/DOCKET NUMBER: 209/069
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ. ID NO.: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1085 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE: 1085 AA, 121170 MW, 6189757 CN;
SQ

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D	b	356	TFNCHLOEGANGPLVPDFTFLGHEGEGARLSNSETAPRPLCTGGENISVETPYMDYTHL	4155
O	y	276	AYA-R-AD-P-----RPHCG-SWCSNOJC-RE-C-QAFMAHTMPKJAKRS-M	3195
D	b	416	RISYVYIAYYSIAALDDIYTCIPGRFLFNGSCADIKKAYMOUYKHLRHLNFTSNMG	4755
O	y	320	SSAYAYRAYVAYAVAHGLHQLLGC-AS-EL-----CS-RGRVYPMOLLEOJHKVHFLHK-	3705
D	b	476	BOYFDEEGCDLAGNYSIINMHLSPEDSGIVKEYGVYVYAKKGERFLINDERKILWGSFS	5355
O	y	371	DYVANDNRDPLSSNITIAMDMNGKP-WT-FTVLGS-STWSP-VQ-LININETKIQWGNK	4255
D	b	536	REVPFSNCSRDCLAGTRKGIIEGBPTCCFECEVEDPDEHSDETDASADCPCDDFWNEN	5955
O	y	426	HOVPKSVCSODLEBHQH-VYTGPHHCCFECEVPCGAGFELKSKLSLYHCQCGTEEMAPEG	4845
D	b	596	HTSCIAKEIEFLSMTEPRG-TALILFANVLGIFLAFVLGVFIKRNTPYKAINRELSYL	6545
O	y	485	SOTCEPRVYVFLAHEHNSWLLANLITLILLGLG-TAGLEAMHLDPYVRSAGGRCLFL	5435
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O	y	544	MIGSLIAG-SSSLYGFGESEPRPCLLQALFALGFTTFUSCLTVKRSFOLLITIFKSTKY	6025
D	b	712	PTSEHRKMGWGLNFLVFLCTFMQVICALWLTAPPSYRNHLEDELEIFITICHE-GS	7705
O	y	603	PT-FYHAWVQHNGAGLEFYMISSAQLLTCLWLVVWPIPLAREYQRPHLMLECEPTNS	6615
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D	b	830	Y-KRVSAYEVIATILAA-SFGLLCIFENKYIILFPPSRTEIE	8715
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ID	US-08-943-986-7			
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XA				
DJ				
XX				
DE	Sequence 7, Application US/08943986			
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CC	Sequence 7, Application US/08943986			
CC	Patent No. 5962314			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Edward M. Brown			
CC	APPLICANT: Steven C. Hebert			
CC	APPLICANT: James E. Garrett, Jr.			
CC	TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE			
CC	TITLE OF INVENTION: MOLECULES			
CC	NUMBER OF SEQUENCES: 20			
CC	CORRESPONDENCE ADDRESSES:			
CC	ADDRESSEE: Lyon & Lyon			
CC	SPEED: First Interstate World Center			
CC	STREET: Suite 4700			
CC	STREET: 633 West Fifth Street			
CC	CITY: Los Angeles			
CC	STATE: California			
CC	COUNTRY: USA			
CC	ZIP: 90071			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage			
CC	COMPUTER: IBM PC compatible			
CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC				

[illegible]


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Dd      474 GE0VTFDCCGLVGVYVSITNNHLSPEBDSIYFKREVGYNYAKKGBRLFINEXILMSGF   5333
Oy      371 -DTVAFNBNRDPLOSSYNIIAMDNGPK-WT-FTVLGS-STWSP-VQ-LNTNEIKIQHGK    424
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Oy      425 NHOVPKSVSSDCLEGHOR-VVTGFHHOCFECVCAGATFLNKSELYRCOPCG:EEMAPE     4833
Db      594 NHTSCIAKEIFELSWTEPFG-IATLFAVLDFPLTAFLVGFIKERNTPIVKATNBELSY    6528
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Db      653 LLFSFLCCFESSSLF-FIGEPODMTCRLROPAEGISEYLICSLIVYTNRYLVFE--AK       7099
Oy      543 LMLGSLAANG-SGSLYGFGEPTRPACULROALFALGFIETPLSCTLVRSFOLIIKFSTX      6010
Db      710 IPTSHRRKMWLNLQGLFLVFCTMOVICVMICYVTAAPSSRNQOEDELDEFITCHE-G       7688
Oy      602 VPT-FYAHMVONHGAGLFVM:ISSAQOLLICTLWTUVMTPLPARYQRPHIMVMEJETN      6606
Db      769 SL-MALGFLIGYTCLLAAICEFFAFKRKLDPENENEAKFITFSMLIFFIWISFPAYAS     8279
Oy      661 SIGFILARL-YINGLTSISAFACYLGKDLENNEAKCVFSLLENFVSGIAFFT-AS          7177
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RESULT      7             STANDARD:      PRT;      1078 AA.
ID US-08-353-784-7
XX AC xxxxxx
XX DT
XX ST
Sequence 7, Application US/08353784
De Sequence 7, Application US/08353784
Cc Patent No. 6011068
Cc GENERAL INFORMATION:
Cc APPLICANT: Edward F. Nemeth, Edward M.
Cc APPLICANT: Brown, Steven C. Hebert,
Cc APPLICANT: Bradford G. Van Wageningen, Manuel
Cc APPLICANT: F. Balandrin, Forrest H. Fuller,
Cc APPLICANT: Eric G. Delmar, and Scott T. Moe
Cc TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
Cc TITLE OF INVENTION: MOLECULES
Cc NUMBER OF SEQUENCES: 20
Cc CORRESPONDENCE ADDRESSES:
Cc ADDRESSEE: Lyon & Lyon
Cc STREET: First Interstate World Center
Cc STREET: Suite 4700
Cc CITY: Los Angeles
Cc STATE: California
Cc COUNTRY: USA
Cc ZIP: 90071
Cc COMPUTER READABLE FORM:
Cc MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
Cc COMPUTER: IBM PC compatible
Cc OPERATING SYSTEM: PC-DOS/MS-DOS
Cc SOFTWARE: FASTSEQ
Cc CURRENT APPLICATION DATA:
Cc APPLICATION NUMBER: US/08/353,784
Cc FILING DATE: 9 December, 1994
Cc CLASSIFICATION: 514
Cc PRIOR APPLICATION DATA:
Cc PRIOR APPLICATION DATA: including application
Cc PRIOR APPLICATION DATA: described below: 8
Cc APPLICATION NUMBER: PCT/US/94/12117
Cc FILING DATE: 21 October, 1994
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CC	APPLICATION NUMBER: U.S. 08/292,827	
CC	FILING DATE: 23 August, 1994	
CC	APPLICATION NUMBER: U.S. 08/141,248	
CC	FILING DATE: 22 October, 1993	
CC	APPLICATION NUMBER: U.S. 08/009,389	
CC	FILING DATE: 23 February, 1993	
CC	APPLICATION NUMBER: U.S. 08/017,127	
CC	FILING DATE: 12 February, 1993	
CC	APPLICATION NUMBER: U.S. 07/934,161	
CC	FILING DATE: 21 August, 1992	
CC	APPLICATION NUMBER: U.S. 07/834,044	
CC	FILING DATE: 11 February, 1992	
CC	APPLICATION NUMBER: U.S. 07/749,451	
CC	FILING DATE: 23 August, 1991	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME: Heber, Sheldon O.	
CC	REGISTRATION NUMBER: 38,179	
CC	REFERENCE/DOCKET NUMBER: 209/069	
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE: (213) 489-1600	
CC	TELEFAX: (213) 955-0440	
CC	TELEX: 67-3510	
CC	INFORMATION FOR SEQ. ID NO: 7:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH: 1078 amino acids	
CC	TYPE: amino acid	
CC	TOPOLOGY: linear	
CC	MOLECULE TYPE: protein	
CC	SEQUENCE 1078 AA; 120573 MW; 6153012 CN;	
Query Match	19.9%; Score 1160; DB 3; Length 1078;	
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QY	3 C-SFHEGHYHLEFQARKLVEELINSTALLPITIGCYCYVCSDSANAVATLRILSLPQ 61	
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D	b		653	L L S E L I C C F S S S L F - F I G E P O D M T W C R L R O P A F G I S F V L C S I L Y T N R V L W F E - - A K	709
O	y		543	I M I G S L A N G - S G S L Y G F G E P T R C L L R Q M L F A L G F I I F I S C L Y V S F O I I I F K R S T K	601
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Q	y		602	V P T - F Y H A M V O N H G A G L E V M I S S A O L L I C L T L W V M P L P A R E Y O R F P H L V M E C T E T N	660
D	b		769	S L - M A L G F L I G Y T C L A I C F F P A S S K R L E P E N N E A K F I F S M L I P F I Y I W I S F I P A Y S	827
Q	y		661	S U G F L I A L - Y N G L I S I S A P A C S T L G D P E N T N E A K C V F S L F N F V S H I A F T T - A S	717
D	b		828	T Y - G N F A S V A E V I A I L A A - S F G L L A C I F P N K Y I I L K P S R N T I E	870
Q	y		718	Y V D G K Y L P A A N M M A G L S S I S G F G Y - F L P R C Y I L C R P D L N S T E	761
R	E	S	U	8	PRT; 1078 AA.
I	D	X		US-08-485-588-7	
A	C	X		xxxxxx	
D	e			Sequence 7, Application US/08485588	
X	x			Sequence 7, Application US/08485588	
C	c			Patent No. 5688938	
C	c			GENERAL INFORMATION:	
C	c			APPLICANT: Edward M. Brown	
C	c			APPLICANT: Steven C. Hebert	
C	c			APPLICANT: Forrest H. Fuller	
C	c			APPLICANT: James B. Garrett, Jr.	
C	c			TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE	
C	c			TITLE OF INVENTION: MOLECULES	
C	c			NUMBER OF SEQUENCES: 20	
C	c			CORRESPONDENCE ADDRESS:	
C	c			ADDRESSEE: Lyon & Lyon	
C	c			STREET: First Interstate World Center	
C	c			STREET: Suite 4700	
C	c			STREET: 633 West Fifth Street	
C	c			CITY: Los Angeles	
C	c			STATE: California	
C	c			COUNTRY: USA	
C	c			ZIP: 90071	
C	c			COMPUTER READABLE FORM:	
C	c			MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage	
C	c			COMPUTER: IBM PC compatible	
C	c			OPERATING SYSTEM: PC-DOS/MS-DOS	
C	c			SOFTWARE: FASTSEQ	
C	c			CURRENT APPLICATION DATA:	
C	c			APPLICATION NUMBER: US/08/485,588	
C	c			FILING DATE: 7 June, 1995	
C	c			CLASSIFICATION: 435	
C	c			PRIOR APPLICATION DATA:	
C	c			Prior Application Data: described application	
C	c			Prior Application Data: included below: 9	
C	c			APPLICATION NUMBER: 08/335,784	
C	c			FILING DATE: 9 December, 1994	
C	c			APPLICATION NUMBER: PCT/US/94/12117	
C	c			FILING DATE: 21 October, 1994	
C	c			APPLICATION NUMBER: U.S. 08/292,827	
C	c			FILING DATE: 23 August, 1994	
C	c			APPLICATION NUMBER: U.S. 08/141,248	
C	c			FILING DATE: 22 October, 1993	
C	c			APPLICATION NUMBER: U.S. 08/009,389	
C	c			FILING DATE: 23 February, 1993	
C	c			APPLICATION NUMBER: U.S. 08/017,127	
C	c			FILING DATE: 12 February, 1993	
C	c			APPLICATION NUMBER: U.S. 07/934,161	
C	c			FILING DATE: 21 August, 1992	
C	c			APPLICATION NUMBER: U.S. 07/834,044	

CC	FILED DATE: 11 February, 1992
CC	APPLICATION NUMBER: U.S. 07/749,451
CC	FILING DATE: 23 August, 1991
CC	ATTORNEY/AGENT INFORMATION:
CC	NAME: Heber, Sheldon O.
CC	REGISTRATION NUMBER: 38,179
CC	REFERENCE/DOCKET NUMBER: 213/005
CC	TELECOMMUNICATION INFORMATION:
CC	TELEPHONE: (213) 489-1600
CC	TELEFAX: (213) 955-0440
CC	TELEX: 67-3510
CC	INFORMATION FOR SEQ ID NO: 7:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 1078 amino acids
CC	TYPE: amino acid
CC	TOPOLOGY: linear
CC	MOLECULE TYPE: protein
CC	SEQUENCE 1078 AA; 120573 MW; 6153012 CN;
CC	Query Match 19.9%; Score 1160; DB 1; Length 1078;
CC	Best Local Similarity 31.9%; Pred. No. 2,82e-87;
CC	Matches 263; Conservative 232; Mismatches 250; Indels 80; Gaps 57;
Db	60 CIRNRFGRFLQAMITAEIENSPPALLNLGIRYIPDTCNTVSALAA--TLSPVAQ 117
QY	3 C-SNEHYHLFLQAMRGRGVEINNSTLNLPTITGYQJYVCDSANAVYATLRYLSLPQ 61
Db	118 NKDISLNDEFCNCSSEHPSPIAVGATGSGSTAVANLGLFIYPOVSASSRLLSNK 177
QY	62 HHIE-LQ-GDLLHS---PYLAIAGDSITNRATTAALLSPPLY-HISTAASETLTVK 115
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QY	116 RQYSFSLTIPNDEHQATAMADIIEYFRMVMVGTTIAADDYGRPGIEKFEAEEDRDI 175
Db	238 DESLEISQYSE--EE-IQHVVEIQTSTKVIYVESGSDPLEIKE-IVRANITGKIW 293
QY	176 AFKIDMF-FSQVQDEDMKQCLMRLAQAGATVYVES-RQLARVFESVYLLNLGKVM 223
Db	294 LASBAMASSSLIAMPQYFHHVVGITGFALAGQIPGRREFLKYVPRKSYHNGFAKEFWE 353
QY	224 VASEAMA--L-S--R-R-HITGVF-GIQ-RIGWVLGV-A-IQK--R-AVP-GL-KAF-E 274
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Db	534 SREVPFNSQSDCLAGRRKGIIEEPKTCCEVCYCPGGEYSDETFDASACKCPDDEFSNE 593
QY	425 NHQYPKSYSCSDCLCEGNOR-VITGFHNCCCEYPCGCGTGLNKSSELYRCOPCGTEKAP 483
Db	594 NHTSCIAKEIFLSTWTEPFG-IALTLEPAVLGIFLTAFLVGFIFKFRNTPIYKATNRELSY 652
QY	484 GSGQCFPRTYVFLALREHTSMVLLAANTLLLLLLLG-TAGLFAMHLDTPVRSAGRLCF 542
Db	653 LLLSLSLCCFSSSLF-FIGEPQDMTCYLROPAGISVLCISCLVKTNNVLYFE--AK 709
QY	543 LMLSLSLAAG--SGSLYGFGEFTRPACLLRQALFALGFTPLSCLTVNRSFLLIIIFKSTK 601
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QY	602 VPT-FYHMYQVNHGAGLFVMISSAQOILLICITLWLYVTPPLPAREYQFPHLYMECTETN 660
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0y	661	SLGFIILAL--YNGLLISARACYLKGDLPENNNEAKVCYFSLLEFVSWIAEFTT--AS	717
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0y	718	YVDGKYLPAANMMAGLSLSSGFGY-FLPRCYILLCPDLNSTE	761

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ID	US-08-484-565-7				
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DT					
De	Sequence 7, Application US/08484565				
XX					
CC	Sequence 7, Application US/08484565				
CC	Patient No. 5763569				
CC	GENERAL INFORMATION:				
CC	APPLICANT: Edward M. Brown				
CC	APPLICANT: Steven C. Hebert				
CC	APPLICANT: James E. Garrett, Jr.				
CC	TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE				
CC	TITLE OF INVENTION: MOLECULES				
CC	NUMBER OF SEQUENCES: 20				
CC	CORRESPONDENCE ADDRESSES:				
CC	ADDRESSEE: Lyon & Lyon				
CC	STREET: First Interstate World Center				
CC	STREET: Suite 4700				
CC	STREET: 633 West Fifth Street				
CC	CITY: Los Angeles				
CC	STATE: California				
CC	COUNTRY: USA				
CC	ZIP: 90071				
CC	COMPUTER READABLE FORM:				
CC	MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage				
CC	COMPUTER: IBM PC compatible				
CC	OPERATING SYSTEM: PC-DOS/MS-DOS				
CC	SOFTWARE: FASTSEQ				
CC	CURRENT APPLICATION DATA:				
CC	APPLICATION NUMBER: US/08/484,565				
CC	FILING DATE: 7 June, 1993				
CC	CLASSIFICATION: 435				
CC	PRIOR APPLICATION DATA:				
CC	Prior Application Data: including application				
CC	Prior Application Data: described below: 9				
CC	APPLICATION NUMBER: 08/353,784				
CC	FILING DATE: 9 December, 1994				
CC	APPLICATION NUMBER: PCT/US/94/12117				
CC	FILING DATE: 21 October, 1994				
CC	APPLICATION NUMBER: U.S. 08/292,827				
CC	FILING DATE: 23 August, 1994				
CC	APPLICATION NUMBER: U.S. 08/141,248				
CC	FILING DATE: 22 October, 1993				
CC	APPLICATION NUMBER: U.S. 08/009,389				
CC	FILING DATE: 23 February, 1993				
CC	APPLICATION NUMBER: U.S. 08/017,127				
CC	FILING DATE: 12 February, 1993				
CC	APPLICATION NUMBER: U.S. 07/934,161				
CC	FILING DATE: 21 August, 1992				
CC	APPLICATION NUMBER: U.S. 07/834,044				
CC	FILING DATE: 11 February, 1992				
CC	APPLICATION NUMBER: U.S. 07/749,451				
CC	FILING DATE: 23 August, 1991				
CC	ATTORNEY/AGENT INFORMATION:				
CC	NAME: Hebert, Sheldon O.				
CC	REGISTRATION NUMBER: 38,179				
CC	REFERENCE/DOCKET NUMBER: 213/006				
CC	TELECOMMUNICATION INFORMATION:				
CC	TELEPHONE: (213) 489-1600				
CC	TELEFAX: (213) 955-0440				
CC	TELEX: 67-3510				
CC	INFORMATION FOR SEO ID NO: 7:				

CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 1078 amino acids
CC	TYPE: amino acid
CC	TOPOLOGY: linear
CC	MOLECULE TYPE: protein
CC	SEQUENCE 1078 AA; 120573 MW; 6153012 CN;
CC	Query Match 19.9%; Score 1160; DB 1; Length 1078;
CC	Best Local Similarity 31.9%; Pred. No. 2,82e-87;
CC	Matches 263; Conservative 232; Mismatches 250; Indels 80; Gaps 57;
CC	60 CIRYFRGFRKLOAMIRAIEEINSSPLLNLGRIEPTCTVSKALEA--TISEFVAQ 117
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CC	118 NKIDSLNDECONSEHPSPIAVAGTSGVSAVANNLGLIYIPQVSASSRLTSNK 177
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CC	319 MSSAVNAVRAYAAVAGHGHQLG-AS-EL-----CS-RGRVYPMQDLQIHKVHFLHK 370
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CC	371 -DTAFENDNRDPLSSYNIIMADMWGPK-WT-FYVLGS-STWSP-VQ-LNINETRIQWHRK 424
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CC	425 NHQVPKSYCSDSLCEGHQR-VVIGFHHCCEDCYPCGAGTFLNKSSELYKROPCGTEMADE 483
CC	594 NHTSCIAKEIEFLSWTEPFG-IALLTEPAVLGIFLTAFLVGVFIKFRNPPIVAKTNELSY 652
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CC	653 LLHLSLLOCSSSLF-FIGEPQDTCILROPAGISVLCSSILYKTRNVLVFE--AK 709
CC	543 LMLGSLAAG-SGSLYGEFGEPTBPACLLROALFALGTFILSLCTVRSQLLIIEFSTK 501
CC	720 IPTSHRKMWMLQNLQFLVLCPTQMOLVIOVMYLTAPSPSYNOLEDEDIITTCHE-G 768
CC	602 VPT-FYHAMVONHAGCFPMIISAQOLLITLIMVYTPPLANEYORFRLVWLEDETEIN 660
CC	769 SL-VALGFLIGLYTCLLAICFFFAFKRSRKLPENFNEAKFTFMSMLLIFFWISFIPAVAS 827
CC	661 SLGFLIARL--YNCLLSISAFACGYLJKDLPENVNNEAKCVTFSLLENFWSIAWFPTT-AS 717
CC	828 TY-GKFSVAEYVIAIILAA-SFGLLACIFENKIIYIILFKPSRNTIE 870
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CC	RESULT 10
CC	ID US-08-480-751-7 STANDARD: PRT: 1078 AA.
CC	AC xxxxxx
CC	XX

DT Sequence 7, Application US/08480751
 XX Patent No. 5858684
 CC Sequence 7, Application US/08480751
 CC Patent No. 5858684
 CC GENERAL INFORMATION:
 CC APPLICANT: Edward F. Nemeth
 CC APPLICANT: Edward M. Brown
 CC APPLICANT: Steven C. Hebert
 CC APPLICANT: Forrest H. Fuller
 CC APPLICANT: James E. Garrett, Jr.
 CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
 CC NUMBER OF SEQUENCES: 20
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Lyon & Lyon
 CC STREET: First Interstate World Center
 CC STREET: Suite 4700
 CC STREET: 633 West Fifth Street
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90071
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: FASTSEQ
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/480,751
 CC FILING DATE: 7 June, 1995
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC PRIOR APPLICATION DATA: including application
 CC PRIOR APPLICATION DATA: described below: 9
 CC APPLICATION NUMBER: 08/353,784
 CC FILING DATE: 9 December, 1994
 CC APPLICATION NUMBER: PCT/US/94/12117
 CC FILING DATE: 21 October, 1994
 CC APPLICATION NUMBER: U.S. 08/292,827
 CC FILING DATE: 23 August, 1994
 CC APPLICATION NUMBER: U.S. 08/141,248
 CC FILING DATE: 22 October, 1993
 CC APPLICATION NUMBER: U.S. 08/009,389
 CC FILING DATE: 23 February, 1993
 CC APPLICATION NUMBER: U.S. 08/017,127
 CC FILING DATE: 12 February, 1993
 CC APPLICATION NUMBER: U.S. 07/934,161
 CC FILING DATE: 21 August, 1992
 CC APPLICATION NUMBER: U.S. 07/834,044
 CC FILING DATE: 11 February, 1992
 CC APPLICATION NUMBER: U.S. 07/749,451
 CC FILING DATE: 23 August, 1991
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Heber, Sheldon O.
 CC REGISTRATION NUMBER: 38,179
 CC REFERENCE/DOCKET NUMBER: 213/004
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (213) 489-1600
 CC TELEFAX: (213) 955-0440
 CC TELETYPE: (213) 955-0440
 CC INFORMATION FOR SEQ ID NO: 7:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 1078 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 1078 AA; 120573 MW; 6153012 CN;
 CC
 CC Query Match 19.98; Score 1160; DB 2; Length 1078;
 CC Best Local Similarity 31.98; Pred. No. 2.82e-87;
 CC Matches 263; Conservative 232; Mismatches 250; Indels 80; Gaps 57;

Db 60 CIRNFRGRFRLQAMIFALEEINSPALLPNLTIGRIFPTGCTVSKALEA--TISFVAQ 117
 QY 3 C-SFNEHGHLVQAMRLGYEINNTALLPNITLIGQLVDVSDSNVATRLVSLPQ 61
 Db 118 NKIDSLNDEPNCSEHIPSTIAVVGATSGSVAVANILGLFYIPQVYASSRLLSK 177
 QY 62 HITE-LQ-GDLHY--PTVLAVIPDSNTNRAATFALLSPFLV-HISYASSSETLSVK 115
 Db 178 NQKSLRTIPNDEHQTAMADIEFFRMNVTGTIADDDYGRPGLEKREAREEDICI 237
 QY 116 RQPSFLRTIPNDKYQVETVMTLLQKFGWTWISLWSSDDYQQLGVALLENALVNGICI 175
 Db 238 DFEELISOYSD--EE-IQHVVEVIONSTAKYIVVSSGPDLELKE-IYVRNIGIKI 293
 QY 176 AFKDIMP-TSAQVGDERMOCMLRHIAQATVYVFS--RQLARVFEVSLTNLIGKYM 233
 Db 294 LASEANASSSLAMPQYFHVVGTTIGFALKAQIPGFRFLKVKHPRKSVHNGFAKEWE 353
 QY 234 VASEAWA--L-S--R--R--HITGVP-GIQ-RIGMVLGV-A-IQK--R-AVP-GL-KAF-E 274
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 QY 275 EAYA-R-ADKE-APRCH--RGSWCSNQLCRECAF--M-A--HTMKRLA---FS- 318
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 QY 371 -DTVAENDRNDPLSSYNIITAMDMNGPK-WT-FTVLGS-STWSP-VQ-LINETKIQHGK 424
 Db 534 SREVPNSNRCPLGSTRKIIEGEPTCCFCEVCGDGSSETASAKNPKDDWMS 593
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 Db 594 NHTSCIATKEIEFLSWTEPRG-IALTFAVLGIFLAFVGVFIKFRNPYVATNRELSY 652
 QY 484 GSOTCPFRVVFALREHNSWLLANITLLILLLG-TGLRPMHMDTVVASAGRLCF 542
 Db 653 LILFSLCCPSSSLF-FIEPDQWTCRLRQAPAGISFVLCISCIKYNRVLLVFE--AK 709
 QY 543 LMGSLAAG-SGSLYGFEEPTRPACLLRQALFALGFTTFLSLCYVRSQLIIIEFSTK 601
 Db 710 IPSEHRKMGVNLQFLVLCFTFMQIVICVIMLTAPSSVRNQLDEEIIFFICHE-G 768
 QY 602 VPT-FYHANVQNHGAGLEFVWISSAQLICTLWLVMTLPAREYORFPHVLWLBCTETN 660
 Db 769 SL-MALGFILGYTCLLAACFEFAFSRKLPEFNFAKFIPTFSMLFFIWTISFIPAVAS 827
 QY 661 SLGFIILAF--YNGLLISAFACSYIGKDLPENYNKAKVTISLLENFWSIAFFTT-AS 717
 Db 828 TY-GKFSVAVEVIAITAA-SGLLACIFPNKIYIIIFKRSNTIE 870
 QY 718 VYDGKYLPAANNMAGLSLSGFGY-FLPKCYVILCRPDLNSTE 761
 RESULT 11
 ID US-08-484-565-8 STANDARD; PRT; 1079 AA.
 AC xxxxxx
 XX
 XX
 DT Sequence 8, Application US/08484565
 CC Patent No. 5763569
 CC GENERAL INFORMATION:
 CC APPLICANT: Edward M. Brown
 CC APPLICANT: Steven C. Hebert
 CC APPLICANT: James E. Garrett, Jr.

CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
CC TITLE OF INVENTION: MOLECULES
CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: First Interstate World Center
CC STREET: Suite 4700
CC STREET: 633 West Fifth Street
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: FASTSEQ
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/484,565
CC FILING DATE: 7 June, 1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC PRIOR APPLICATION DATA: including application
CC PRIOR APPLICATION DATA: described below: 9
CC APPLICATION NUMBER: 08/353,784
CC FILING DATE: 9 December, 1994
CC APPLICATION NUMBER: PCT/US/94/12117
CC FILING DATE: 21 October, 1994
CC APPLICATION NUMBER: U.S. 08/292,827
CC FILING DATE: 23 August, 1994
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CC FILING DATE: 12 February, 1993
CC APPLICATION NUMBER: U.S. 07/934,161
CC FILING DATE: 21 August, 1992
CC APPLICATION NUMBER: U.S. 07/834,044
CC FILING DATE: 11 February, 1992
CC APPLICATION NUMBER: U.S. 07/749,451
CC FILING DATE: 23 August, 1991
CC AFFORNEY/AGENT INFORMATION:
CC NAME: Heber, Sheldon O.
CC REGISTRATION NUMBER: 38,179
CC REFERENCE/DOCKET NUMBER: 213/006
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 955-0440
CC TELEFAX: (213) 489-1600
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1079 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: Protein
CC SEQUENCE 1079 AA; 120867 MW; 6054255 CN;
SQ
Query Match 19.88; Score 1158; DB 1; Length 1079;
Best Local Similarity 31.48; Pred. No. 4,21e-87;
Matches 262; Conservative 233; Mismatches 261; Indels 78; Gaps 55;
Db 60 C1VYNGRGEFMIQAMIFAIKEINSSPILNMTGRIPTGNTVSKALAA--TLSPVAQ 117
QY 3 C-SFNEHGILFLPAMRLGVEINNSTALLPNTILGOLYVCSDSANVYATLRYLSLPGQ 61
Db 118 NKIDSLNDFCNCSEHPISTIAVAGTSGSTAVANLGLFYIPQVYASSRLSNK 177
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Db 178 NQKSPFRTIPNDEHQATLAADIIIEFRKMWVGITIAADDYGRPGIETKEFEAEFRDICI 237
QY 116 RQYSPFLRIPNDKYQVETWVLLQKFGMTWISLVGSSDDYDGLQVQALENOALVRGICI 175

Db 238 DFESELIQVSGDE--EEIQQ-VVEVIONSTAKVIYVSSGPDLEPIKE-IVRRNITGRIV 293
QY 176 AFDIIMP-FSAQVDEDMQCLMRHIAQAGATVVVSSS-QOLARVFESVYLTNITGRIV 233
Db 294 LASEWASSSLIAKFEYEHVVGIGTIGG-LKAGQIPGRREFLOKHVPKSYHNGFAKEFEWE 353
QY 234 VASEWAA--L-SR----HITGVP-GIQ-RIGVWLGV-A-IQK---R-AVP-GL-KAF-E 274
Db 354 ETEFCHLOEAKGPELPVDTVRSHESGNRLNLSIAFRPLCTGDEININSEVP-YYDYE 412
QY 275 EAYV-R-AD--KEA-P-----RCHKGS-W---CSSX-Q-LCEHCQAFMAHTMPKLAFS 318
Db 413 HIRSYVYLAIVSIAIALODITCLPGRGLFENGSG--DJKRYEAMQVLTKHRLNTNN 472
QY 319 -MSAINAYRAVAVAGHGLHQLGC-AS-EL-----CS-RGRVPMWOLHQRHVLHLH 369
Db 473 MGEQVPEDECGDLVGNYSIINWHLSPEDSGSIVEKEYVYVYAKGGRFLFINEKILMSG 532
QY 370 K-DIVAFNDNRDPLSSYNIITAMDMNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIOMHG 423
Db 533 FSRVFPNSGSRDQAGIRKGIIEGPTCCFCEVCEPDGEGYSGETDASACDPCDFWSN 592
QY 424 KNHQVPRKVSQSCLEBGR-VYTGFIHCCFCEVPCGAGTFILKSELXRCQPCGTEEMAP 482
Db 593 ENHTSCIARKEIFLAAMEPRG-IATLFLAVLGIFLAIVGVLFKFRNTPIVATNELS 651
QY 483 EGSGTCEPRIVFLALREHTSWVLANTLLDLLG-TAGLEFAMHIDTVVNSAGRLC 541
Db 652 YLLFSLLCFSSSLF-FIGEPDWTGRLRQPAFGISEVLCISCIATKINRVLVEF--A 708
QY 542 FLMGSLAAG-SSGLVGFEPETPRACLLQALFALGFTIFLCLYVRSGLIITFEFST 600
Db 709 KIPSPFRKMWGLNQLVFLCTFMQILCIITWLYTAPSSYRNHELEDEITFITCHEG 768
QY 601 KVPF-FYHAWQNHGAGLFEVMISSAOLLICLTWLVMTPLPAREYORFPHLVLECTET 659
Db 769 SIMAGSLIGYTLALACFEPAFKSRKLPENFNENKFTIFSMILFIPIVTSFPAVAST 828
QY 660 NSLGFILAFIYNGILISAFACSYLGKDPENENAKCVIFSLDFNVSAIAFTT-ASV 718
Db 829 Y-GKEVSAVEVIAILA-SFGLACIFENKVIYIILKPSRNITEVYSSATAHA 880
QY 719 YDGKYLPLAAMWAGLSLSSGFGGY-FLPCYVILCRPDLNENHQAISIQDYT 771
RESULT 12
ID US-08-480-751-8 STANDARD; PRT; 1079 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 8, Application US/08480751
XX
CC Sequence 8, Application US/08480751
CC Patent No. 5858684
CC GENERAL INFORMATION:
CC APPLICANT: Edward F. Nemeth
CC APPLICANT: Edward M. Brown
CC APPLICANT: Steven C. Hebert
CC APPLICANT: Forrest H. Fuller
CC APPLICANT: James E. Garrett, Jr.
CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: First Interstate World Center
CC STREET: Suite 4700
CC STREET: 633 West Fifth Street
CC CITY: Los Angeles
CC STATE: California

[illegible]

```

01      :||| | || | : : : | |||| | | : : | : | : |
02 424 KNOQPKVCSDDCLEGHQR-VWGFHHCCFECVPCCAGTFLNKSELYRCOPCGETEMAP 4822
03 Db 593 ENHTGCIKAKEIEFLAMTEHPFG-IALTUFVAIGIFLFAVGFIKFNPTIVYKATNELS 651
04   : : : : | | | : : : | : : : : | : | :||| : : : |
05 483 ESSQCFCFRIVYFLALRHTISMVLLAANTLLLLLLLG-TAGLFMHLDTPIVBSAGRLC 5411
06 Db 652 VALLFSLICSSSSLE-FIGEPODWTCRLQRPAGFISVCISCILVKTNRVLLVE--A 708
07   : : | : | : : | : | : | : | : | : | : | : | : | : |
08 542 FLMLSLAAG-SGSLVFGEPEPTPACLLROALPALGFTIIFLSCLTIVRSFOLLIIFFXST 600
09 Oy 709 KPPTFHKKMGMLNIQFLVLVLCFEHQJLIIMLVYTPAPSSYNHNLDEIIITHEG 768
10   : : | : | : : | : | : | : | : | : | : | : | : | : |
11 601 KAPT-FYIAWQUNQOAGLFYMISAQOLLIJLTVLVYTPAREYORPHLVMLEDET 659
12 Db 769 SLMASGLIGYTCLAAICPFEEAFKSRKLPEPENEAKTFEPMLEFPYIWISFIPAVAST 828
13   : : : : | | | : : | : | : | : | : | : | : | : | : |
14 Oy 660 NSLGTILAFVLNGLISTIAFACSLTGKDLPENYNEACVTFSLFNFVSMTAFETT-ASY 718
15 Db 829 Y-GKFVASVEVZAILAA-SFGLACIFFEKVYIILFKPSRNTIBEVRSSTAHA 880
16   | : | : | : | : | : | : | : | : | : | : | : | : | :
17 Oy 719 YDGKYLPAANMMAGLSLSSGFGV-FLPKCYVILCRPDINSTBFOASIDDY 771
18
19 RESULT 14
20 ID US-08-943-986-8 STANDARD: PRT; 1079 AA.
21 AC xxxxxx
22 Dx
23 Xx
24 Sequence 8, Application US/08943986
25 DE
26 xx
27 CC
28 CC Patent No. 5962314
29 CC GENERAL INFORMATION:
30 CC APPLICANT: Edward M. Brown
31 CC APPLICANT: Steven C. Hebert
32 CC APPLICANT: James E. Garrett, Jr.
33 CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
34 CC TITLE OF INVENTION: MOLECULES
35 CC NUMBER OF SEQUENCES: 20
36 CC CORRESPONDENCE ADDRESS:
37 CC ADDRESSEE: Lyon & Lyon
38 CC STREET: First Interstate World Center
39 CC STREET: Suite 4700
40 CC STREET: 633 West Fifth Street
41 CC CITY: Los Angeles
42 CC STATE: California
43 CC COUNTRY: USA
44 CC ZIP: 90071
45 CC COMPUTER READABLE FORM:
46 CC MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
47 CC COMPUTER: IBM PC compatible
48 CC OPERATING SYSTEM: PC-DOS/MS-DOS
49 CC SOFTWARE: FASTSO
50 CC CURRENT APPLICATION DATA:
51 CC APPLICATION NUMBER: US/08/943,986
52 CC FILING DATE: 03-OCT-1997
53 CC CLASSIFICATION: 530
54 CC PRIOR APPLICATION DATA:
55 CC APPLICATION NUMBER: 08/484,565
56 CC FILING DATE: 7-June-1995
57 CC APPLICATION NUMBER: 08/353,784
58 CC FILING DATE: 9 December, 1994
59 CC APPLICATION NUMBER: PCT/US/94/12117
60 CC FILING DATE: 21 October, 1994
61 CC APPLICATION NUMBER: U.S. 08/292,827
62 CC FILING DATE: 23 August, 1994
63 CC APPLICATION NUMBER: U.S. 08/141,248
64 CC FILING DATE: 22 October, 1993
65 CC APPLICATION NUMBER: U.S. 08/009,389
66 CC FILING DATE: 23 February 1993

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Sun Mar 26 09:26:12 2000

US-09-361-652-3.rai

Page 15

Search completed: Fri Mar 17 13:36:11 2000
Job time : 30 secs.

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CC REFERENCE/POCKET NUMBER: 213/005
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1079 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1079 AA: 120867 MW: 6054255 CN:

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Query Match	19.8%;	Score 1158;	DB 1;	Length 1079;
Best Local Similarity	31.4%;	Pred. NO. 4.21e-87;		
Matches	262;	Conservative	233;	Mismatches 261; Indels 78; Gaps 55;

Db	60	CIRNRFCEPRLQIMAFIAEIEINSSPRLTGMTGTYIEPTCNVSXALBA--TISVAO	11
Qy	3	C-SFNEHRYHFLQAMRLQVEIEINNSTALLPITITGTYGOLDYVCSANAVYITLRYLSIPGO	61
Db	118	NKIDSLNDEFQCNSEHPISTIAVAVGATGSGVSTAVANLLGLEFIPOVSYASSRLSNK	177
Qy	62	HHIE-IQ-GDLLHYS---PTLVAVIGDSTNRATTAALLSPFLV-HISVASSETLSYK	115
Db	178	NOXSFLLRTIINDEHQATAMADITEYFRMMVNGIADDDOYGRGITEKFEZEABERDICI	237
Qy	116	ROYBFELETTIPNDYQYQVETWILLQKRGKWTISLVGSSDDYGGOLGVALNOALYRGICI	175
Db	238	DFSELISOYSE--EEIOQ--VEVIONKSTAKVIVFSSGGDLEPLIKE-IVRANITGRW	293
Qy	176	AFKIDMP-FSMQVODERMOCLMRRLAQAATVAVVSS-RQLARVFESVYLTNLGKW	233
Db	294	LASEAMASSLIAMPEYFHVVGITIGFGLKAGQIPGRREFLOKVHPKSVYHGFANEFEWE	353
Qy	234	VASEMA---L-SR---HITGV-P-GIO-RIGMWLVY-A-IQK---R-AVP-GL-KAF-E	274
Db	354	ETFNCHLOEGAKGPLVDTPFRSHBEGGNRLNSTAFRLCTGDEINSEVLP-YMDYE	412
Qy	275	EAYA-R-AD-KEA-P-----RPHCKS-W---CSSN-Q-LCREQAFMAHTYKPKLAES	318
Db	413	HLRISYNYVLAVYSIAHALODIYCLDEGRGLFTNGSCADIKRYEAMOVNLKHLNLTNN	472
Qy	319	MSSAVNAYRAVYAVAHGLHQLLCC-AS-EL-----CS-RGRVYPMQLDQIHKVHFLH	369
Db	473	MGEQYTDEDCDLDVGNSTIINHSLSPDGSLVKEVGYVYVYAKKGRLEFINEKILMSG	522
Qy	370	K-DIVANENDNDPLSSYNIIAMDNGPK-WT-FYVLDS-STWSP-VQ-LININETKIQWHE	423
Db	533	FSREVPENCSRDQACGRKGIIEGEPTCECECECECDGSEYSDMASADCKPDQFSN	592
Qy	424	KNHOVPASVCSDDLQEGHOR-VYIGFHHCCFECYPCAGAFIINKSELRYCOPCGTEWMA	482
Db	593	ENHSTCIAKEIEFLAMTEPEG-IALLTFAVYGLTFAVGVETKERNPPIVATNRELS	651
Qy	483	EGSOTCEPRTVAFALREHTHSWVLLANTLLILLILG-TAGLEAMHMDTPVVSAGRLC	541
Db	652	YLLFSLDCCSSSLF-FIGEPQWOTRLQAPAGISFVLCISGILVKTARVLVEE-A	708
Qy	542	FLLMGSILAAG-SGSLYGFEGEPTRPACLERQALFALFETFLSCLTAVRSQLLIFKFS	600
Db	709	KIPTSFHRKMGMLQJLFLVFLCFMFOILCIILVLYAPASSYRNHLEDEIIFICHG	768
Qy	601	KVPI-FTHAWQNNQAGLLFWMISSAQLDILCTMLVYMTPLPAREYORFHYLMLECTE	659
Db	769	SLMALSLIGTCLLAAICFFPAKSKRLDPENNEAKFITFSMLIPIYIISTIPAYAST	828
Qy	660	NSLQFILLAFNLGLLSTSAACSYLGDLPENYNEACVTFSLFLFNVSIMAFETT-ASY	718
Db	829	Y-GRFVSVEVYIALA-SGLLACIFENYVYIILFSPNSITIEEVYSSGTAAMA	880
Qy	719	YDGRYILPRANMAGLSSLSGFGGY-FLPKCYILLCAPDLNSTHEDFASIDYDT	771

 WATSON
 (TM)

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 Msearch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Fri Mar 17 13:26:21 2000; Maspar time 39.48 Seconds
 Tabular output not generated. 466.217 Million cell updates/sec

Title: >US-09-361-652-3
 Description: (1-777) from US09361652.pep
 Perfect score: 5838
 Sequence: 1 RSCSFNHCYHLFQAMRLGV.....NSTEHFQASIDYTRRCGST 777

Scoring table: PAM 150
 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq36
 1:geneseqp

Statistics: Mean 38.193; Variance 172.438; scale 0.221

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1170	20.0	1085	1	M89563	Bovine parathyroid cal
2	1170	20.0	1085	1	M54844	Bovine parathyroid cal
3	1170	20.0	1085	1	M38272	Bovine parathyroid cal
4	1160	19.9	1078	1	M54846	Human parathyroid calc
5	1160	19.9	1078	1	M89565	Human parathyroid calc
6	1160	19.9	1078	1	M11889	Parathyroid calcium re
7	1160	19.9	1078	1	M38274	Human parathyroid cell
8	1158	19.8	1079	1	M94828	Rat kidney extracellular
9	1158	19.8	1079	1	M54847	Rat kidney calcium rec
10	1158	19.8	1079	1	M89565	Rat parathyroid calcin
11	1158	19.8	1079	1	M38275	Rat kidney cell calcin
12	1101	18.9	1026	1	M32059	Dogfish shark kidney c
13	1064	18.2	1088	1	M38273	Human parathyroid cell
14	1063	18.2	1088	1	M54845	Human parathyroid calc
15	1063	18.2	1088	1	M89564	Human parathyroid calc
16	1063	18.2	1088	1	M11888	Parathyroid calcium re
17	992	17.0	1219	1	M25763	Amino acid sequence of
18	992	17.0	1219	1	M25762	Amino acid sequence of
19	915	15.7	779	1	M94931	Rat pheromone receptor
20	845	14.5	912	1	M82558	Human mgluR4.
21	845	14.5	912	1	R72092	Human mgluR4.
22	801	13.7	1056	1	M25764	Amino acid sequence of
23	796	13.6	906	1	R25081	GLU-G-R subtype 1b.

24	796	13.6	1199	1	R25080	GLU-G-R subtype 1a.
25	790	13.5	906	1	R64250	Human mgluR3B.
26	786	13.5	1056	1	M25765	Amino acid sequence of
27	787	13.5	1194	1	R42199	HSMGRL1.
28	781	13.4	872	1	R95052	Human metabotropic glu
29	771	13.2	850	1	M94901	Mouse pheromone recept
30	769	13.2	1180	1	R64253	Human mgluR5a.
31	770	13.2	1212	1	R64250	Human mgluR5b.
32	763	13.1	877	1	R64255	Human mgluR5c.
33	761	13.0	872	1	R89580	Metabotropic glutamate
34	757	13.0	908	1	M41568	Human metabotropic glu
35	756	12.9	908	1	M49928	Human metabotropic glu
36	731	12.5	866	1	M94920	Rat pheromone receptor
37	731	12.5	877	1	M01099	Metabotropic glutamate
38	718	12.3	803	1	M94903	Mouse pheromone recept
39	714	12.2	548	1	M94917	Rat pheromone receptor
40	714	12.2	667	1	M94919	Rat pheromone receptor
41	711	12.2	877	1	R82657	Human mgluR3.
42	713	12.2	879	1	R64252	Human mgluR3.
43	703	12.0	768	1	M94918	Rat pheromone receptor
44	676	11.6	605	1	M94925	Rat pheromone receptor
45	675	11.6	867	1	R72093	Human mgluR4 clone cmR

ALIGNMENTS

RESULT 1
 ID M89563 standard; Protein: 1085 AA.
 AC W89563;
 DT 19-MAR-1999 (first entry)
 DE Bovine parathyroid calcium receptor BOPCAR 1.
 KW Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;
 KW calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;
 KW spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;
 KW neonatal distress; neurodegenerative disease; Alzheimer's disease;
 KW Huntington's disease; Parkinson's disease; dementia; muscle tension;
 KW depression; anxiety.
 OS Bos sp.
 PN US658684-A.
 PD 12-JAN-1999.
 PF 07-JUN-1995; 480751.
 PR 23-AUG-1991; US-749451.
 PR 11-FEB-1992; US-834044.
 PR 21-AUG-1992; US-934161.
 PR 12-FEB-1993; US-017127.
 PR 23-FEB-1993; US-009389.
 PR 22-OCT-1993; US-141248.
 PR 19-AUG-1994; US-292827.
 PR 21-OCT-1994; WO-012117.
 PR 08-DEC-1994; US-353784.
 PA (BGM) BRIGHAM & WOMEN'S HOSPITAL.
 PA (NPSF-) NPS PHARM INC.
 PI Balandrin MF, Brown EM, Del Mar EG, Garrett JE,
 PI Hebert SC, Nemeth EF, Van Wagenen BC;
 DR MPI: 99-119871/10.
 DR N-PSDB; V82483.
 PT Screening for calcium receptor-active compounds - by recombinant
 PT expression of nucleic acid encoding calcium receptor and determining
 the effect of compounds on calcium receptor activity
 PS Claim 1: Fig 47: 176pp: English.
 CC A method has been developed of screening for a compound able to affect
 CC one or more activities of a calcium receptor (CR) comprises: (A)
 CC contacting a recombinant cell with a test compound, where the
 CC recombinant cell comprises a recombinant nucleic acid expressing the CR,
 CC provided that the cell does not have functional CR expression from
 CC endogenous nucleic acid; (3) determining the ability of the test
 CC compound to affect one or more activities of the calcium receptor; and
 CC (C) comparing the ability with the ability of the test compound to
 CC affect the one or more CR activities in a cell not comprising the
 CC recombinant nucleic acid. The present sequence represents bovine
 CC parathyroid CR, designated a BOPCAR 1. The nucleic acid sequence of
 CC BOPCAR 1 can be used as part of the recombinant nucleic acid in the

CC method described above. The compounds identified can be used to treat CC diseases or disorders characterized by abnormal calcium homeostasis, e.g. hyperparathyroidism, osteoporosis and other bone and mineral-related disorders. They can also be used for the treatment of diseases and disorders associated with disrupted Ca²⁺ responses, e.g. seizures, stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in cardiac arrest or neonatal distress, epilepsy, neurodegenerative diseases such as Alzheimer's disease, Huntington's disease and Parkinson's disease, dementia, muscle tension, depression, and anxiety. Sequence 1085 AA.

Query Match 20.0%; Score 1170; DB 1; Length 1085;
Best Local Similarity 31.9%; Pred. No. 4,34e-94;
Matches 263; Conservative 227; Mismatches 256; Indels 78; Gaps 56;

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Db 61 C1YNNRGRWLOAMTAFEBEINSSPALLPMTLGRITDONTYSKALEA--TISFVAQ 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   3 C-SFNEHGYHLFOAMRGVEINNSTALLPNTLGYQLDYVCSDSANVATLRLVSLPQ 61

Db 119 NKIDSLNIDFECNCSEHPISTIAVVGATGSGISTAVANLGLFYIPQVYASSRLLSNK 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   62 HHEF-LQ-GDLHYS---PVLAVIGDSTNRATTAALLSPFLV-HISTAASSETLSVK 115

Db 179 NQKSFRLTIPNDEHOATAMADIEFRMNVGTIAADDYGRPGIEKFEBAERDICI 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   116 ROYPSFLRTIPNDKYQVETWLLQKFGMTWISLVSSDDYQQLGQALLENQALVRGICI 175

Db 239 DFESE-L-ISQYDEERKIQVVEVIONSTAKIVYVSSGDPLEPIKE-IYRNINGRIWL 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   176 AFEDIMFSAQVDERMOCIMRHLAQAGATVVVSS-RQLARFFESVYLTNLGKVVW 234

Db 296 ASEAMASSSLIAMPEYHVVGITIGFLKAGQIPGREFREOKYPRKSVNGFAKEEMEE 355
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   235 ASEAMA---L-SR---HITGVP-GIQ-RIGMVLGV-A-IQK---R-AVP-GL-KAF-EE 275

Db 356 TFNCQLQEGAKGPLVDTLRGHEEGARLNSPTAFRPLCTGGENISVEETPYMDYTHL 415
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   276 AVA-R-AD-KEA-P-----RPCCHK-SWCSNQLC-RE-C-QAFMAHTMPKILKAFS-M 319

Db 416 RISYNYTLAVYSTAHADQITICIRGRGLFTNGSCADIKVEMOVAKHLRLNFTSNMG 475
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   320 SSAYNARAVYVAHGHQLGCG-AS-EL-----CS-RGRVYPWOLLEQIHRVHFLHK- 370

Db 476 EGYTFDECGDLAGNYSTIINMHLSPEDSGIVFEKGYNYAVAKKERLFIINDEXLMSGFS 535
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   371 DYAFNDNRPLPSYNTIANDMNGPK-WT-FYVLGS-STMSP-VQ-LINETRIQMHGKN 425

Db 536 REVPFNSGSDCLAGTRKGIIESEPTCCFEVCEDPGEYSDETASACDKCPDDEMSNEN 595
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   426 HQVPKSYVSSDCLGEGHOR-VVTGFHHCCEFCVCGAGTFLNKSLEYRCQCGTEEMAPDG 484

Db 596 HTSCIAKEIEFLMTEPEFG-IALTFLFAVLGIELFAVLGYEIKFRNPIKATNRELSTYL 654
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   485 SQCFPPTVFLVLRRETSVALLAANTLTLTLG-TAGLFAMWLDTPVVRSSAGRLCFL 543

Db 655 LIFSLLCESSSLF-FIGEPDWTCLROPAGISFVLCISCIIVKTRVLVEE-AKI 711
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   544 MGSLLAAG-SGSLYGFGEPTPRACLLRLQALFALGFIIFLSCLTVRSFOLLIIFFKSTKV 602

Db 712 PISFHRKMGMLNLOFLVLCFMQIVCAIWLNTAPSSYRNHELEDEIIFITCHE-GS 770
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   603 PT-FYHAWQNHGAGLFWMISSAQLDICTLWLVWTPPLDAREQRPHPLVMECTETNS 661

Db 771 L-MALGFLIGYLLAALICFFPAKSRKLPENNEAKFIIFSMILFIIVISFIPAST 829
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   662 LGTILFLV--YNGILSTISAPCSGLGKDPENNEACVFSLLFNFSVIAFEFTT-ASY 718

Db 830 Y-SKEVASVEVIAIIAA-SFGLACIFPNKYIILFKPSNTIE 871
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   719 YDKKYLPAAMMAGLSLSSGFGY-FLPKCYILCRPLDNSTE 761

```

RESULT 2

ID W54844 standard; Protein; 1085 AA.
AC W54844;
DT 01-SEP-1998 (first entry)
DE Bovine parathyroid calcium receptor 1 protein 5kb fragment.
KW Calcium ion concentration; parathyroid hormone; homeostasis;
KW kidney; calcium receptor; detection.
OS Bos sp.
PN US5763569-A.
PF 09-JUN-1998.
PD 07-JUN-1995; 484565.
PR 07-JUN-1995; US-484565.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-017127.
PR 23-FEB-1993; US-009389.
PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (BGMH) BRIGHAM & WOMEN'S HOSPITAL.
PI (NPSF-); NPS PHARM INC.
PI Brown EM, Garrett JE, Hebert SC;
DR MPI; 98-347412/30.
DR N-PSDB; V26962.
PT calcium receptor poly:peptide(s) - useful for drug screening or antibody production
PS Claim 5; Fig 47; 17app; English.
CC The bovine parathyroid calcium receptor gene encodes a 1085 amino acid protein. The tissue from which this receptor and receptors from human parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulates Ca²⁺ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca²⁺ levels in juxtaglomerular and proximal tubule cells in the kidney. The purified receptors (produced recombinantly) can be used to screen for compounds that modulate calcium receptor activity, especially those that can be used to treat diseases CC associated with the receptors in these tissues. They can also be used CC to raise antibodies for use in detection assays.
SQ Sequence 1085 AA;

Query Match 20.0%; Score 1170; DB 1; Length 1085;
Best Local Similarity 31.9%; Pred. No. 4,34e-94;
Matches 263; Conservative 227; Mismatches 256; Indels 78; Gaps 56;

```

Db 61 C1YNNRGRWLOAMTAFEBEINSSPALLPMTLGRITDONTYSKALEA--TISFVAQ 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   3 C-SFNEHGYHLFOAMRGVEINNSTALLPNTLGYQLDYVCSDSANVATLRLVSLPQ 61

Db 119 NKIDSLNIDFECNCSEHPISTIAVVGATGSGISTAVANLGLFYIPQVYASSRLLSNK 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   62 HHEF-LQ-GDLHYS---PVLAVIGDSTNRATTAALLSPFLV-HISTAASSETLSVK 115

Db 179 NQKSFRLTIPNDEHOATAMADIEFRMNVGTIAADDYGRPGIEKFEBAERDICI 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   116 ROYPSFLRTIPNDKYQVETWLLQKFGMTWISLVSSDDYQQLGQALLENQALVRGICI 175

Db 239 DFESE-L-ISQYDEERKIQVVEVIONSTAKIVYVSSGDPLEPIKE-IYRNINGRIWL 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   176 AFEDIMFSAQVDERMOCIMRHLAQAGATVVVSS-RQLARFFESVYLTNLGKVVW 234

Db 296 ASEAMASSSLIAMPEYHVVGITIGFLKAGQIPGREFREOKYPRKSVNGFAKEEMEE 355
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   235 ASEAMA---L-SR---HITGVP-GIQ-RIGMVLGV-A-IQK---R-AVP-GL-KAF-EE 275

Db 356 TFNCQLQEGAKGPLVDTLRGHEEGARLNSPTAFRPLCTGGENISVEETPYMDYTHL 415
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   276 AVA-R-AD-KEA-P-----RPCCHK-SWCSNQLC-RE-C-QAFMAHTMPKILKAFS-M 319

Db 416 RISYNYTLAVYSTAHADQITICIRGRGLFTNGSCADIKVEMOVAKHLRLNFTSNMG 475
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   320 SSAYNARAVYVAHGHQLGCG-AS-EL-----CS-RGRVYPWOLLEQIHRVHFLHK- 370

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D	b	61	CARNPEGRLOAMITAEIENSPPALNMTLGVIEDICTMVSALDA--TISFVQ	118
O	y	3	C-SENEHYELFQAMRRGVEIDENINSTLNLITLGOLIVDCSSANAVYATLVNLSIPGO	61
D	b	119	NKIDSLNDEPCNCSSEHPISTHIAVVGATGSGISTAVANLGLFEYIPDVSAYSSSRLSNK	178
O	y	62	HHIE-LQ-GDLLHYS--PVLAVIGPDSINRAAT ⁺ AALLSPVLV-HISYAAASETLISVK	115
D	b	179	NOFSPLRTINDSHQ ⁺ TAAADIEYRRKMWG ⁺ IIAACDDYGRGIEKFEDEBERDICI	238
O	y	116	ROYSPFLRTIPNDYQYETWVLLQ ⁺ KGWMTISLVGSSDDYGGDLGVALENQALVIGICI	175
D	b	239	DFSE-L-ISOYSDERKIQOAVEVYIONSTAKIVYESSGSDPEJELIKE-YYRRAITGRIML	295
O	y	176	AFKIMPPSAQVGBERRQCMRLHQAQAVVYFSS-RQNAVFFPSVLTNLTKVWY	234
D	b	296	ASEMASSSLIAMPETHYHHVVGITIGELKAGQIDGFEPILOKVHPKXSVNGFAKFEWE	355
O	y	235	ASEMA--L-SR---HITGP-GIQ-RIGWLVG ⁺ -V-IQK--R-AVP-GL-KAF-EE	275
D	b	356	TFNCHLDGAGCPVPDPTFLRGHEGAGRLNSPTARPLCTGDEINSSVETPYMYTHL	415
O	y	276	AYA-R-AD--KEA-P-----RPCKKG-SWSSNDLC-RE-C--QAFMAHTPPLKAFS-M	319
D	b	416	RISYNYLAVYS ⁺ AAHALODIYTCTIPSGLETNGSCADIKREAVOMVLKHLRH ⁺ NFTSNMG	475
O	y	320	SSAANAVRAYAAVAGHGLHLLGC-AS-EL-----CS-RGVHYVPMOLLEQIHKHVFLHK-	370
D	b	476	EQVTFDEGDLGAYSTIINHLSPEDSIYFKEVGYNYNAKKGERLFINDEKILMSGFS	535
O	y	371	DTVAENDRDPLSSYNIITAMDMNPK-WT-FIVLGS-STWSP-VQ-LINLETIOMHGKN	425
D	b	536	REVPFNSCRDLCTGTRKGIIEGPTCCFCEVCEPDCSYGDETFDASACDPCDPFMSNEN	595
O	y	426	HQVKKSVSSCDLEGHQR-VTGRHHCCFCGCVPGACETPLNKSELYNQCGGHEWAPEG	484
D	b	596	HTSCAKIEPLSTPEPG-IALTFLPVLGIIETLAVLYGVFIKFRNTPYIKATNRELSTYL	654
O	y	485	SQCEPFRVYFLA ⁺ REHTSWL ⁺ LAANTLLLELLLG-TAGLFAWHLDPVVRASAGRLCFL	543
D	b	655	LLFSLTCCFSSSLF-FIGEPODMTC ⁺ ROPAGISFVLICSLIKVKNRLVAFE--AKI	711
O	y	544	MLGSLANG-SSSYXGFGEPTRPACLLRLQALFNLGFIITFSLCLVRSFOLLIIIFKPSKV	602
D	b	712	PTSHRRKMWGLNLFVLVCTEQVYICAIWLTAPSSYRNHELEDEIIFTTCH-GS	770
O	y	603	PT-FYHAWOVQHAGLTVMSAALQILCTLWVW ⁺ PLPAREQRP ⁺ PHLMIECTETNS	661
D	b	771	L-MLGLIGTCLLAICFPFAKRSKRLDENFEAKETIFSMILPFIWISLIPVAST	829
O	y	652	LGLTIAFL--YNGLLISAPACSLTGADLENNEACVTFSLFNFVSNIAFTT ⁺ ASV	718
D	b	830	Y-GKEVSAVEVIALIAA-SFGLACIFENFVYIIIFKPSRNTIE	871
O	y	719	YDKGYLPANMMAGLSLSSGFGY-FLPCYCV ⁺ ILCRPDLNSTE	761
RESULT		4		
AC		WS4846	standard; Protein; 1078 AA.	
AC		WS4846;		
DT		01-SEP-1998	(first entry)	
DE			Human parathyroid calcium receptor 4.0 protein 4kb fragment.	
KM			Calcium ion concentration; parathyroid hormone; homeostasis;	
KM			kidney; calcium receptor; detection.	
PS			Homo sapiens.	
PN		US5763569-A.		
PN		09-JUN-1998.		
PF		07-JUN-1995;	484565.	

PR 23-FEB-1993; US-009389.
 PR 22-OCT-1993; US-141248.
 PR 19-AUG-1994; US-292827.
 PR 21-OCT-1994; WO-012117.
 PR 08-DEC-1994; US-353784.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PA (NPSB-) NPS PHARM INC.
 PI Brown EM, Garrett JE, Hebert SC;
 DR WPI: 98-347412/30.
 DR N-PDB: V26964.
 PT Calcium receptor poly:peptide(s) - useful for drug screening or
 PT antibody production
 PS Claim 7; Fig 49; 174pp; English.
 CC The tissue from which the human parathyroid calcium receptor and
 CC receptors from bovine parathyroid and rat kidney are derived, respond to
 CC changes, and control changes, in calcium ion concentration,
 CC e.g. parathyroid hormone regulates Ca²⁺ homeostasis in blood and
 CC extracellular fluid, and kidney function alters through changes in Ca²⁺
 CC levels in juxtaglomerular and proximal tubule cells in the kidney. The
 CC purified receptors (produced recombinantly) can be used to screen for
 CC compounds that modulate calcium receptor activity, especially those that
 CC can be used to treat diseases associated with the receptors in these
 CC tissues. They can also be used to raise antibodies for use in detection
 CC assays.
 SQ Sequence 1078 AA;

Query Match 19.9%; Score 1160; DB 1; Length 1078;
 Best Local Similarity 31.9%; Pred. No. 3,73e-93;

Matches 263; Conservative 232; Mismatches 250; Indels 80; Gaps 57;

DB 60 CTRNRRGRWLOAMFAIEINSSPALPNTLGRIPDTCTVSKALEA--TISFVAO 117
 QY 3 C-SFNHGHLFCQMRKLGVEINNSTALPNTILGQLDYVCSDSANVYATLVLSPGQ 61
 DB 118 NKDSINLDFEFCGSHPISTIVAGTSGSTAVANILGLTYIOYVASSSSRLT 177
 QY 62 HHE-LQ-GDLHYS---PVLAVIGPDSINRAITTAALSPVLY-HISFAASETLVSK 115
 DB 178 NOFKSELTIPNDEHQAAMADIIEFRNMVGTIAADDYGRPGIEKFEAEEDICT 237
 QY 116 RQPSFLRTIPNDKYQVETVLLQKFGTWISLVGSSDYGGLQVLAENQALVAGICT 175
 DB 238 DSELSISQSD--EE-IQHVVEVIONSTAKVIVFSSGDEPLEIKE-IVRNITGKIW 293
 QY 176 AFDIDMP-FSAQGDERMOCIMRHLAQAGATVYVFS--RQLARVEESVTLNLGKW 233
 DB 294 LASEMASSSLAMPYFHVVGSTIGFALKAGIIPFRERLKVHRKSHNFAEFWE 353
 QY 234 VASEAFA--L-S--R-HITGP-6IQ-RIGVLDV-A-IQR--R-AVP-GL-KAF-E 274
 DB 354 EYFNCHLQAGAKGPLVDYDFLNGHESGDRFSSSTAFLPCTGDENISSEVETPIDYTH 413
 QY 275 EAYV-R-AJKE-APRCH--KSGWSSNQLCREQAF--M-A--HMPRLKA----FS- 318
 DB 414 LRISVNYAVYSIAHALDIYCLPGRGLFTNGSCADIKKVAOVYLKHLRLNFTNNK 473
 QY 319 MSSAVNAYAVYAAVAGHLQDLGC-AS-EL-----DS-RGRVYPMQDLQIHRYVFLHK 370
 DB 474 GEGVTEDEGDYVGNYSIINMHLSPEDGSTVEKEGVYNNYAKGRRLTNEKILMSGP 533
 QY 371 -DVAANDNRDPSSSTNITIAMDNNGK-R-WT-FVLDS-STWSP-VQ-LNINERKIOWHG 424
 DB 534 SREVPSNCRDCLAGTRKGIIEGPEPTCEVEYCPDEGSDTDSACNCKDDPMNSN 593
 QY 425 NQGVPSVSSSCLBEHQH-R-VYGFHHCCEYCPGAGITLMSSELYKROPCTEMARE 483
 DB 594 NHTSCIAKTIEFLSWTEPRG-IALLFAVLGIFLFAVLGVETIKFRNTPIVATNBLST 652
 QY 484 GSGTCEPRVVFALREHSHWVLLANTLILLILG-TAGLFAMHDDTPVRSAGGRLCG 542
 DB 653 LLLFSLICESSSLF-FIGEPDMTCRLQRPAGISFVLCISILYKTNVLLVFE--AK 709
 QY 543 LMGSLAAG-SGSLVGFEGEPTRPACLLRLQALFALGFTIFLSCLTVRSFOLIIIFKSTK 601

DB 710 IPTFHRKWMGINTLOFLVFLCTFMQIVICVIMLYTAPSSYRNOLEDEIFITCHE-G 768
 QY 602 VPT-FYHAWQVHAGLGFWMISSAQLLICLWLVWTPDLPAREQRPHVLMLECTEN 660
 DB 769 SL-MALGFLIGYTCILMAICFFAFKSRRLPENNEAKETFSMTLFIWISFIPAYAS 827
 QY 661 SLGFIILAFI--YNGILISTISAFKCSYLGKLPENNYNEAKETFSLLFNFVSWIAFFT--AS 717
 DB 828 TY-GKVSAYEVIALIAA-SPLLCIFENFKYIILFKSRNTIE 870
 QY 718 VIDGKTLPANMAGLSSLSGFGGI-FUPKCYVILCRPDLNSTE 761

RESULT

ID W89565 standard; Protein; 1078 AA.

AC W89565;
 DT 19-MAR-1999 (first entry)
 DE Human parathyroid calcium receptor phupcar 4.0.
 KW Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;
 KW calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;
 KW spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;
 KW neonatal distress; neurodegenerative disease; Alzheimer's disease;
 KW Huntington's disease; Parkinson's disease; dementia; muscle tension;
 KW depression; anxiety.
 OS Homo sapiens.
 PN US5858684-A.
 PD 12-JAN-1999.
 PF 07-JUN-1995;
 PR 07-JUN-1995; US-480751.
 PR 23-AUG-1991; US-749451.
 PR 11-FEB-1992; US-834044.
 PR 21-AUG-1992; US-934161.
 PR 12-FEB-1993; US-017127.
 PR 23-FEB-1993; US-009389.
 PR 22-OCT-1993; US-141248.
 PR 19-AUG-1994; US-292827.
 PR 21-OCT-1994; WO-012117.
 PR 08-DEC-1994; US-353784.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PA (NPSB-) NPS PHARM INC.
 PI Balandrin MF, Brown EM, Del Mar EG, Garrett JE,
 PI Hebert SC, Nemeth EF, Van Wagenen BC;
 DR WPI: 99-119871/10.
 DR N-PDB: V82485.
 PT Screening for calcium receptor-active compounds - by recombinant
 PT expression of nucleic acid encoding calcium receptor and determining
 PT the effect of compounds on calcium receptor activity
 PS Claim 1; Fig 49; 176pp; English.
 CC A method has been developed of screening for a compound able to affect
 CC one or more activities of a calcium receptor (CR) comprises: (A)
 CC contacting a recombinant cell with a test compound, where the
 CC recombinant cell comprises a recombinant nucleic acid expressing the CR,
 CC provided that the cell does not have functional CR expression from
 CC endogenous nucleic acid; (B) determining the ability of the test
 CC compound to affect one or more activities of the calcium receptor; and
 CC (C) comparing the ability with the ability of the test compound to
 CC affect the one or more CR activities in a cell not comprising the
 CC recombinant nucleic acid. The present sequence represents human
 CC parathyroid CR, designated a phupcar 4.0. The nucleic acid sequence of
 CC phupcar 4.0 can be used as part of the recombinant nucleic acid in the
 CC method described above. The compounds identified can be used to treat
 CC diseases or disorders characterized by abnormal calcium homeostasis, e.g.
 CC hyperparathyroidism, osteoporosis and other bone and mineral-related
 CC disorders. They can also be used for the treatment of diseases and
 CC disorders associated with disrupted Ca²⁺ responses, e.g. seizures,
 CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in
 CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative
 CC diseases such as Alzheimer's disease, Huntington's disease and
 CC Parkinson's disease, dementia, muscle tension, depression, and anxiety.
 SQ Sequence 1078 AA;

Query Match 19.9%; Score 1160; DB 1; Length 1078;


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      : : | | | | | : : : | : | : : | : : : : | : : :
QY 319 MSAYNNAVRAVAAVAGHGLGCG-AS-EL-----CS-RGRVYPMQLLEQIHKYFLLHK 370

Db 474 GEQVTFDECGDLVGNYSIINMHLSPEDGSIVFEKGYNNYAKGERLFIINEKILMSGF 533
      : : | : : : : : : : : : : : : : : : : : : : :
QY 371 -DTAFNDNRDPLSSYNIIMDMNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIOMHGK 424

Db 534 SREVPFNSCRDCLAGTRKGIIEGPTCCFCEVCPDGEYDETDASACNKPDDFWSNE 593
      : : | : : | | | | | : : : | : : : : : : : : :
QY 425 NHQPKSVCSDDCLEGHR-VVTGFHCCFCFCVPCGAGTFLNKSLSLYCQCGRTEMAPE 483

Db 594 NHTSCIAKEIEFLSWTEPFG-IALTFLAVLGIFLTAFLVGVFIKFRNTPYKATNRELSY 652
      : : : : : : : : : : : : : : : : : : : : :
QY 484 GSQCFEPTVVEFLAREHTSWLLAANTLILLLLIG-TAGLFAMHLDPVVRSGGRICF 542

Db 653 LLLFSLCCFSSSLF-FIGEPQDWTCTLRQAPAGISFLCISCLVKNRLVLFEE-AK 709
      : : | : | : | : | : | : | : | : | : | : | : |
QY 543 LMLGSLAAG-SGSLYGFGEPTRPCLRLQALFALGFITFLSCLTVRSFQILILFKFSTK 601

Db 710 IPTSFHKKMWGLNQFLVFLCTFMQIVICVIMLYTAPSSYRNQLEDEIIFITCHE-G 768
      : : | : : | : : : : : : : : : : : : : : :
QY 602 VPT-FYHAWQNHGAGLFVMISSAQLICLTWLVTPLPAREYQRPFLVMECTETN 660

Db 769 SL-MALGFLIGYTCLLAICFFFAFKSRKLPDENNEAKETIFPSMIEFIWISPIPAYAS 827
      : : | : | : | : : : : : : : : : : : : : :
QY 661 SLGFLIAFL--YNGLLSISAFACSYLGKDLPEYNEAKCVTFSLFNFVSWIAEFTT-AS 717

Db 828 TY-GKFSAVEVIAIILAA-SFGLLACIFENKIYIILFKPSRNTIE 870
      : : | : : : : : : : : : : : : : : : : :
QY 718 YDCKYILPAAANMAGLSSLSGFGGY-FLPKCYVILCRPDLNSTE 761

RESULT
ID W38274 standard: Protein: 1078 AA.
AC W38274:1998 (first entry)
DT 08-MAY-1998
DE Human parathyroid cell calcium receptor 4.0 (Hupcar 4.0).
KW Human parathyroid cell calcium receptor 4.0; Hupcar 4.0;
   calcium homeostasis; hyperparathyroidism; osteoporosis.
OS Homo sapiens.
PN US5688938-A.
PD 18-NOV-1997.
PE 07-JUN-1995; 485588.
PR 07-JUN-1995; US-485588.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-017127.
PR 23-FEB-1993; US-009389.
PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (BGM ) BRIGHAM & WOMENS HOSPITAL.
PI (NPS-) NPS PHARM INC.
PI Brown EM, Fuller FH, Garrett JE, Hebert SC;
DR WPI: 98-008040/01.
DR N-PSDB: T95859.
PT DNA encoding calcium receptor polypeptide(s) - useful for
   therapeutic purposes, e.g. hyperparathyroidism and osteoporosis
PS Claim 20: Columns 125-134; 174pp; English.
CC The present sequence is human parathyroid cell calcium
   receptor 4.0 (Hupcar 4.0).
CC The specification includes details of molecules that can modulate
   one or more inorganic ion receptor activities, and antibodies and
   antibody fragments targeted to inorganic ion receptor proteins. The
   proteins, nucleic acids and antibodies may be used to treat
   disorders by modulating one or more inorganic ion receptor
   activities, preferably disorders of calcium homeostasis, e.g.
   hyperparathyroidism and osteoporosis.
SQ Sequence 1078 AA:

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Query Match

19.9%; Score 1160; DB 1; Length 1078;

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      : : | | | | | : : : | : | : : | : : : : | : : :
Best Local Similarity 31.9%; Pred. No. 3,73e-93;
Matches 263; Conservative 232; Mismatches 250; Indels 80; Gaps 57;

Db 60 CIRNFGFRLQAMITAIETINSSPALLPNIIGVIFPTCTVSAALAA--TLSEVAQ 117
      : : | : : : : : : : : : : : : : : : : : : : :
QY 3 C-SENEGTHLFOAMRGVEINNSTLIPNITLGYCLYVCSDSAVAVATLRLSLPGQ 61

Db 118 NKIDSLNIDFCONCSEHIPTIAVAGTSGSVAVANVLGLFIPVVSASSRLSNK 177
      : : | : : | : : | : : | : : | : : | : : | : : |
QY 62 HHIE-LQ-GDLNHS---PVLAVIGPDSINRAATIALLSPLY-HISTAASETISVK 115

Db 178 NQKFSPLRTIPNDEHQATAMADIIIEYFRMWVGTIAADDYGRPGIEKFEAEEDIC 237
      : : | : | : | : | : | : | : | : | : | : | : |
QY 116 RQYSPFLRTIPNDRQYETWVLLQKFGMTWISLYGSSDDYQGLVQALENQALVRGCI 175

Db 238 DFEELIQYDE--EE-IQHVVEIQNSTAKVIVYESSGDLDELKIE-IVRRITGKI 293
      : : | : : : : : : : : : : : : : : : : : : :
QY 176 AFKQIMP-FSAQVDEDMQCLMRHLAQAGATVYVFS--QLARVFESVYVLTNLTKW 233

Db 294 LASBAMASSLIAMPQYFHYVGTIGFALAKAGIIPGREFLKVHPKSYHNGFAKEFE 353
      : : | : : | : : | : : | : : | : : | : : | : : |
QY 234 VASEAMA---L-S--R-HITGVF-GIQ-RIGWLVG-A-IQK--R-AYP-GL-KAF-E 274

Db 354 ETFNCHLQEGAKGELPVDTFLRGHEESGDRFSNSTAFRLCTGDENISSVETPYDIT 413
      : : | : : | : : | : : | : : | : : | : : | : : |
QY 275 EAYR-R-ADKE-APRPGH---KSGMCSNQLCREQAF--M-A--HTMPKLA---FS- 318

Db 414 LRISYNYLVAVYSIAHALDQIYTCLPGRGLFTNGSCADIKVEMOVLKRLHNFNNM 473
      : : | : | | | | | : : : | : : : : : : : : :
QY 319 MSAYNNAVRAVAAVAGHGLGCG-AS-EL-----CS-RGRVYPMQLLEQIHKYFLLHK 370

Db 474 GEQVTFDECGDLVGNYSIINMHLSPEDGSIVFEKGYNNYAKGERLFIINEKILMSGF 533
      : : | : : | : : | : : | : : | : : | : : | : : |
QY 371 -DTAFNDNRDPLSSYNIIMDMNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIOMHGK 424

Db 534 SREVPFNSCRDCLAGTRKGIIEGPTCCFCEVCPDGEYDETDASACNKPDDFWSNE 593
      : : | : : | | | | | : : : | : : : : : : : : :
QY 425 NHQPKSVCSDDCLEGHR-VVTGFHCCFCFCVPCGAGTFLNKSLSLYCQCGRTEMAPE 483

Db 594 NHTSCIAKEIEFLSWTEPFG-IALTFLAVLGIFLTAFLVGVFIKFRNTPYKATNRELSY 652
      : : : : : : : : : : : : : : : : : : : : :
QY 484 GSQCFEPTVVEFLAREHTSWLLAANTLILLLLIG-TAGLFAMHLDPVVRSGGRICF 542

Db 653 LLLFSLCCFSSSLF-FIGEPQDWTCTLRQAPAGISFLCISCLVKNRLVLFEE-AK 709
      : : | : | : | : | : | : | : | : | : | : | : |
QY 543 LMLGSLAAG-SGSLYGFGEPTRPCLRLQALFALGFITFLSCLTVRSFQILILFKFSTK 601

Db 710 IPTSFHKKMWGLNQFLVFLCTFMQIVICVIMLYTAPSSYRNQLEDEIIFITCHE-G 768
      : : | : : | : : : : : : : : : : : : : : :
QY 602 VPT-FYHAWQNHGAGLFVMISSAQLICLTWLVTPLPAREYQRPFLVMECTETN 660

Db 769 SL-MALGFLIGYTCLLAICFFFAFKSRKLPDENNEAKETIFPSMIEFIWISPIPAYAS 827
      : : | : | : | : : : : : : : : : : : : : :
QY 661 SLGFLIAFL--YNGLLSISAFACSYLGKDLPEYNEAKCVTFSLFNFVSWIAEFTT-AS 717

Db 828 TY-GKFSAVEVIAIILAA-SFGLLACIFENKIYIILFKPSRNTIE 870
      : : | : : : : : : : : : : : : : : : : :
QY 718 YDCKYILPAAANMAGLSSLSGFGGY-FLPKCYVILCRPDLNSTE 761

RESULT
ID W94928 standard: Protein: 1079 AA.
AC W94928:
DT 04-MAY-1999 (first entry)
DE Rat kidney extracellular calcium/polyvalent cation-sensing receptor.
KW Pheromone receptor; signal transduction; fertility; behaviour;
   reproduction; rodent; insect; rat.
OS Rattus sp.
PN WO9900423-A1.
PD 07-JUN-1999.
PE 30-JUN-1997; US-051284.
PR 30-JUN-1997; US-051284.
PA (HARD ) HARVARD COLLEGE.

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QY 275 EAYV-R-AD--KEA-P-----RPOHKG-S-W---CSSN-Q-LCRECOAFMAHMPKILKAFS 318
DB 413 HLRISYNYVLAIVYSIAHALODIYTCLPGRGFTNGSCADIKKEVAMOVYKHLRLNFTNN 472
QY 319 -MSAIVNAVYAVAHGJHOLLGC-AS-EL-----CS-RGRVYPMQJLEQJHVKHFLH 369
DB 473 MGEQVTFDECGDLGVNTSIIMHLSPEDEGSIVFEVGYNYAKGERLFINDEKILMSG 532
QY 370 K-DIVAENDNDPLSYNIIMDMNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQMHG 423
DB 533 FSRVFPNSCRDQACGRKIIIGEPICCECEVCECPDGEISGETDASADCKCPDDWSN 592
QY 424 KNHQVPKSVCSDDLEGHQR-VVTFGHHCCFECVPCGAGTFLNKSLEYRCQPCGTEEMAP 482
DB 593 ENHTSCIAKEIEFLAMTEPFG-IALTFLFAVLGIFLAFVGIKFRNTPIYKATNRELS 651
QY 483 EGSQTCFPRVYFLARHETSMVLAANTLLLLLLG-TAGLFAMHLDTPVRSAGGRIC 541
DB 652 YLLFSLLCFSSSLF-FIGEPDWTCLRQAPAGISFVLICISILVKNRVLLVFE--A 708
QY 542 FLMLGSLAAG-SGSLYGFEPGPTPACILRQALFALGFTIFLSCLTVRSFQJLIIFKST 600
DB 709 KIPTSFHRKMGMLQFLVFLCTFMQILICITMLYAPSSYRNHEDELIITFCHG 768
QY 601 KVPF-FYHAMVQNHGAGLFVMTSSAQLICLTWLVWTPLPAREYORFPHLVMECTET 659
DB 769 SLMLAGSLIGYCLLAACIFFFAKSRKLPENNEAKFIPEFSLIFETWISFIPAYAST 828
QY 660 NSLGILAFILNGLISAFACSTLGDLPENYNEACVITSLFNVSMIAFEIT--ASV 718
DB 829 Y-GKFSVAEYIALIA-SFGLACIFENKVIYILFPRNTIEVRSSTAHA 880
QY 719 YDKYFLPAANMAGLSSISGFGYV-FLPKCYVILCRPDLNSTEHFQASIDYT 771

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RESULT 10
ID W89566 standard: Protein: 1079 AA.
AC W89566;
DE 19-MAR-1999 (first entry)
DB Rat parathyroid calcium receptor prakcar 3A.
KW Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;
KW calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;
KW spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;
KW neonatal distress; neurodegenerative disease; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; dementia; muscle tension;
KW depression; anxiety.
OS Rattus sp.
PN US5858684-A.
PD 12-JAN-1999.
PE 07-JUN-1995; 480751.
PR 07-JUN-1995; US-480751.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-011127.
PR 23-FEB-1993; US-009389.
PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (BGM) BRIGHAM & WOMENS HOSPITAL.
PA (NPS) NPS PHARM INC.
PI Balandrin MF, Brown EM, Del Mar EG, Garrett JE,
PI Hebert SC, Nemeth EF, Van Wagenen BC;
DR WPI: 99-119871/10.
DR N-PDB: W82486.
PT Screening for calcium receptor-active compounds - by recombinant
PT expression of nucleic acid encoding calcium receptor and determining
PT the effect of compounds on calcium receptor activity
CC Claim 1: Fig 50: 17pp; English.
CC A method has been developed of screening for a compound able to affect
CC one or more activities of a calcium receptor (CR) comprises: (A)

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CC contacting a recombinant cell with a test compound, where the
CC recombinant cell comprises a recombinant nucleic acid expressing the CR,
CC provided that the cell does not have functional CR expression from
CC endogenous nucleic acid; (B) determining the ability of the test
CC compound to affect one or more activities of the calcium receptor; and
CC (C) comparing the ability with the ability of the test compound to
CC affect the one or more CR activities in a cell not comprising the
CC recombinant nucleic acid. The present sequence represents rat
CC parathyroid CR, designated a prakcar 3A. The nucleic acid sequence of
CC prakcar 3A can be used as part of the recombinant nucleic acid in the
CC method described above. The compounds identified can be used to treat
CC diseases or disorders characterized by abnormal calcium homeostasis, e.g.
CC hyperparathyroidism, osteoporosis and other bone and mineral-related
CC disorders. They can also be used for the treatment of diseases and
CC disorders associated with disrupted Ca2+ responses, e.g. seizures,
CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in
CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative
CC diseases such as Alzheimer's disease, Huntington's disease and
CC Parkinson's disease, dementia, muscle tension, depression, and anxiety.
SQ Sequence 1079 AA;

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Query Match 19.8%; Score 1158; DB 1; Length 1079;
Best Local Similarity 31.4%; Pred. No. 5,73e-93;
Matches 262; Conservative 233; Mismatches 261; Indels 78; Gaps 55;

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DB 60 CINYRGRFMTQAMTFALEINSSPSLLPMTLGYRIFDTONTVSKALEA--TISFVAO 117
QY 3 C-SFNEGHYFLPMALGVEINSSALLPNTLIGVQLDVCSDSNVYATIRVLSPEQ 61
DB 118 NKIDSLNDFEFCSCSHITSTAVCATGSGVSTAVANLLGLYIPOVSYASSRLSK 177
QY 62 HHIE-LQ-GDLHYV--FTVLAVIGPDSITNRAATFALLSFLV-HISYASSESLTSYK 115
DB 178 NOKSFLETPNDENHATAMADIEEFERNWVGTIAADGPGGIEKREAEEDIDCI 237
QY 116 RQYPSFLRTPNDKYVERVWLLQKFMTWISLSSDYGQVLAENQALVRGIC 175
DB 238 DFSELISQYSD--EEDIQ-VVEVIONSTAKYIVFSSGPDLEPIKE-IVRNITGRIT 293
QY 176 AFDQIMP-PSAQYGDGRMQCLMRHLAQAATVYVSS-RQLARVEFEEVVLNLGKWM 233
DB 294 LASEANASSLIMPEYFVAVGTTGFGKAGIOPGFREFLOKHPKRVNNGFAKEPE 353
QY 234 VASEANA--L-SR---HITGP-GIQ-RIGWLVAV-A-IOK--R-AVP-GL-KAF-E 274
DB 354 ETNCHLQEGAKPLVDVDFVRSHEGGRRLNSSFAPFLCTGDENISVETP-YMDE 412
QY 275 EAYV-R-AD--KEA-P-----RPOHKG-S-W---CSSN-Q-LCRECOAFMAHMPKILKAFS 318
DB 413 HLRISYNYVLAIVYSIAHALODIYTCLPGRGFTNGSCADIKKEVAMOVYKHLRLNFTNN 472
QY 319 -MSAIVNAVYAVAHGJHOLLGC-AS-EL-----CS-RGRVYPMQJLEQJHVKHFLH 369
DB 473 MGEQVTFDECGDLGVNTSIIMHLSPEDEGSIVFEVGYNYAKGERLFINDEKILMSG 532
QY 370 K-DIVAENDNDPLSYNIIMDMNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQMHG 423
DB 533 FSRVFPNSCRDQACGRKIIIGEPICCECEVCECPDGEISGETDASADCKCPDDWSN 592
QY 424 KNHQVPKSVCSDDLEGHQR-VVTFGHHCCFECVPCGAGTFLNKSLEYRCQPCGTEEMAP 482
DB 593 ENHTSCIAKEIEFLAMTEPFG-IALTFLFAVLGIFLAFVGIKFRNTPIYKATNRELS 651
QY 483 EGSQTCFPRVYFLARHETSMVLAANTLLLLLLG-TAGLFAMHLDTPVRSAGGRIC 541
DB 652 YLLFSLLCFSSSLF-FIGEPDWTCLRQAPAGISFVLICISILVKNRVLLVFE--A 708
QY 542 FLMLGSLAAG-SGSLYGFEPGPTPACILRQALFALGFTIFLSCLTVRSFQJLIIFKST 600
DB 709 KIPTSFHRKMGMLQFLVFLCTFMQILICITMLYAPSSYRNHEDELIITFCHG 768
QY 601 KVPF-FYHAMVQNHGAGLFVMTSSAQLICLTWLVWTPLPAREYORFPHLVMECTET 659

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CC the plasma membranes of aquatic species, especially on the apical
 CC membrane of epithelial cells of elasmobranch fish, particularly
 CC from cells found in the collecting duct or late distal tubule in
 CC the kidney, intestine, gill, rectal gland, gonad or brain; an
 CC antibody that specifically binds to a PVCr; and a method of
 CC screening for aquatic PVCr agonists and antagonists. Modulation of
 CC the expression of the aquatic PVCr activates or inhibits aquatic
 CC PVCr mediated ion transport and endocrine changes that permit fish
 CC to adapt to fresh or salt water. The method facilitates the
 CC aquaculture of marine fish and can provide for the development of
 CC marine fish that are easily adaptable to fresh water aquaculture.
 SQ Sequence 1026 AA;

Query Match 18.9%; Score 1101; DB 1; Length 1026;
 Best Local Similarity 31.2%; Pred. No. 1,20e-87;
 Matches 256; Conservative 231; Mismatches 253; Indels 81; Gaps 54;

DB 64 CRYNFRGFWLQAMFALEINNSMTLPNLTGRIPTQNTVSKALAA--TLSEVAQ 121
 QY 3 C-SFNEHGYHLFOAMRGLVEEINNSTALLPNTLGQYDVCSDSANVATLRLVSLPQ 61
 DB 122 NKIDSLNIDFCNCSDHPISTIANVAGTSGISTAVANLGLFTPIQVYASSRLSNK 161
 QY 62 HHE-LQ-GDLHYS--PTVLAVIGPDSNRATTAALSPFLV-HISYASSETLSVK 115
 DB 182 NEYKAFRTIPNDEQATAAEIEHFQMMWVGTIADDDYGRPGDKFREAVKRDICI 241
 QY 116 RQYPSLRTIPNDKYQVETVLLQKRGWTVISLVSDDYDGLQVQALNQALVRCICI 175
 DB 242 DSEF-M-ISQYVQKOLEFIADYIQNSANVYVSSGPDLEPLI-QEIVRNITDRIWL 298
 QY 176 AFDIDPFSAQVDERQCMRLHQAQATVYVSS-RQLARVFEESVLTMLTGKVV 234
 DB 299 ASRAMASSSLIAPEYFHVVGITIGFALRAGRIPGEKFIKEVHPAPRMGSLRSSGR 358
 QY 235 ASRAMA--L-SR---HITGVP-GID-RIGMVLGVA-IQK--RAV-P--GL-KA--- 272
 DB 359 LQDLHREDLTQKNSKVPSPHGAQDGSKAGNSRRTALRHPGTGENTISVETPLYD 418
 QY 273 FEFAVARAD---KEA--P-R-PC-H-KSGMCS-SNQ--LCRDE--QAFAMHMPKAKF 317
 DB 419 THLRISTNVYVYVSTAHADIDHSCKPGTGIFANGSCADIKYEAQVQVNLHLKFTN 478
 QY 318 S-MSSAYNAAYVAVAHGHLQGLGC--ASEL-----CS-RGRVYPMQLEQIHKVFLL 368
 DB 479 SMEQVDEPDQGLKGYTILNMQLSADESVLFHEVGNNAVAKPSDRNLNINEKILMS 538
 QY 369 HK-DYAFANDNRPLSYNIIAMDMPK-WT-FYVLGS-STWS-PVO-LINETKIQWH 422
 DB 539 GFSGVVPFNSCDVCPVGRKGIIEGPTCCFCMACABGEFSDENDASACTCPDNFWS 598
 QY 423 GKHWQPKSVCSGDCLEGNHR-VYTFHNCFCPEVPCGATFLNKSLSYKQCGTEWMA 481
 DB 599 NEHTSCIAKEIYLSWTEFG-IALTIFAVLGLITSEVLGVFIFKRNTPYKAINREL 657
 QY 482 PEGSQCFPTVYVTLRLRETSWLLAANTLLDLLLG-TAGLFAMHLDTPVVSAGRL 540
 DB 658 SYLLSILCOFSSSLI-FIGEPRDMTCRLKOPAFGSFVLCSILYKTNRLVAVE-- 714
 QY 541 CFMLDSLSAAG-SGLKFGFGEPTRPACLRQALFALGFTIFLSCLVRSFOLLIFKFS 599
 DB 715 AKIPTSLHRKWLNLQFLVLCIYQVITCIIMLYTAPSSRYNHELDEVEYFICDE 774
 QY 600 TKVPT-FYHAWQNHGAGLVMSAQLICLTLWLVMPFLAREVQRPHVMECTE 658
 DB 775 -GSL-MALGFLITCLLAICFPFAKSKRLPENNEAKFTPSMIFITWISPIAY 832
 QY 659 TNSLIGFLAFL--YNGILSTSAFACSYLGRDLPENNEACVTSILFNVSIAFETL- 715
 DB 833 VSTY-GKFSVAVEVIALAS-SFGLGCIIFENCCYILFEP 871
 QY 716 ASYVDGKYLPAANMAGLSLSSGFGY-FLPCYVILCRP 755

RESULT 13
 ID M38273 standard; Protein: 1088 AA.

AC M38273;
 DT 08-MAY-1998 (first entry)
 DE Human parathyroid cell calcium receptor 5.2 (HupCar 5.2).
 KW Human parathyroid cell calcium receptor 5.2; HupCar 5.2;
 KW calcium homeostasis; hyperparathyroidism; osteoporosis.
 OS Homo sapiens.
 PN US5688938-A.
 PD 18-NOV-1997.
 PE 07-JUN-1995; 485588.
 PR 23-AUG-1991; US-749451.
 PR 11-FEB-1992; US-834044.
 PR 21-AUG-1992; US-934161.
 PR 12-FEB-1993; US-017127.
 PR 23-FEB-1993; US-009389.
 PR 22-OCT-1993; US-141248.
 PR 19-AUG-1994; US-292827.
 PR 21-OCT-1994; WO-012117.
 PR 08-DEC-1994; US-353784.
 PA (BGM) BRIGHAM & WOMENS HOSPITAL.
 PA (NPSF-) NPS PHARM INC.
 PI Brown EM, Fuller FH, Garrett JE, Hebert SC;
 DR WPI; 98-008040/01.
 DR N-PDSB; T95858.
 PT DNA encoding calcium receptor polypeptide(s) - useful for
 PT therapeutic purposes, e.g. hyperparathyroidism and osteoporosis
 PS Claim 20; Columns 117-126; 174pp; English.
 CS The present sequence is human parathyroid cell calcium
 CC receptor 5.2 (HupCar 5.2).
 CC The specification includes details of molecules that can modulate
 CC one or more inorganic ion receptor activities, and antibodies and
 CC antibody fragments targeted to inorganic ion receptor proteins. The
 CC proteins, nucleic acids and antibodies may be used to treat
 CC disorders by modulating one or more inorganic ion receptor
 CC activities, preferably disorders of calcium homeostasis, e.g.
 CC hyperparathyroidism and osteoporosis.
 SQ Sequence 1088 AA;

Query Match 18.2%; Score 1064; DB 1; Length 1088;
 Best Local Similarity 31.6%; Pred. No. 3.37e-84;
 Matches 264; Conservative 231; Mismatches 250; Indels 90; Gaps 59;

DB 60 CRYNFRGFWLQAMFALEINNSPALPNTLGRIDTQNTVSKALAA--TLSEVAQ 117
 QY 3 C-SFNEHGYHLFOAMRGLVEEINNSTALLPNTLGQYDVCSDSANVATLRLVSLPQ 61
 DB 118 NKIDSLNIDFCNCSDHPISTIANVAGTSGYSTAVANLGLFTPIQVYASSRLSNK 177
 QY 62 HHE-LQ-GDLHYS--PTVLAVIGPDSNRATTAALSPFLV-HISYASSETLSVK 115
 DB 178 NQKSFRTIPNDEHQATMAADIEEYFVNWVGTIADDDYGRPGIEKFEAREEDICI 237
 QY 116 RQYPSLRTIPNDKYQVETVLLQKFGWTVISLVSDDYDGLQVQALNQALVRCICI 175
 DB 238 DPEELLISQSDS--EE-IGHVEVIONSTAKYIVVSSPDLEPLIKE-IYVRNITGKIW 293
 QY 176 AFDIDMP-FSAQVGDGRMQLMRHLQAQATVYVSS-RQLARVFEESVLTMLTGKWW 233
 DB 294 LASEAASSSLTAMPQYFVAVGTIGIFALKAGQIPDFRFLKVVHRRKVVHNGFAKEFE 353
 QY 234 VASEAANA--L-S--R--HITGVP-GIQ-RIGMVLGVA-IQK--RAV-GL-KAF-E 274
 DB 354 EFNCHLQGGANGPLVDVDFLGRHESGDRFNSSTAFLPRLCTGDNISVETPYIDYTH 413
 QY 275 EAVA-R-ADKE-APRCH--KSGMCSNQLOCRECAF--M-A--HTMPKLLA---FS- 318
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 QY 319 MSSAYNAAYVAVAHGHLQGLGC-AS-EL-----CS-RGRVYPMQLEQIHKVFLLK 370

PF 07-JUN-1995; 480751.
 PR 07-JUN-1995; US-480751.
 PR 23-AUG-1991; US-749451.
 PR 11-FEB-1992; US-834044.
 PR 21-AUG-1992; US-934161.
 PR 12-FEB-1993; US-017127.
 PR 23-FEB-1993; US-009389.
 PR 22-OCT-1993; US-141248.
 PR 19-AUG-1994; US-292827.
 PR 21-OCT-1994; MO-012117.
 PR 08-DEC-1994; US-353784.
 PA (BGHM) BRIGHAM & WOMEN'S HOSPITAL.
 PA (NPSF) NPS PHARM INC.
 PI Balandrin MF, Brown EM, Del Mar EG, Garrett JE,
 PI Hebert SC, Nemeth EF, Van Wagenen BC;
 DR WPI: 99-119871/10.
 DR N-PSDB: 982484.
 PT Screening for calcium receptor-active compounds - by recombinant
 PT expression of nucleic acid encoding calcium receptor and determining
 PT the effect of compounds on calcium receptor activity
 PS Claim 1; Fig 48; 176pp; English.
 CC A method has been developed of screening for a compound able to affect
 CC one or more activities of a calcium receptor (CR) comprises: (A)
 CC contacting a recombinant cell with a test compound, where the
 CC recombinant cell comprises a recombinant nucleic acid expression from
 CC provided that the cell does not have functional CR expression from
 CC endogenous nucleic acid; (B) determining the ability of the test
 CC compound to affect one or more activities of the calcium receptor; and
 CC (C) comparing the ability with the ability of the test compound to
 CC affect the one or more CR activities in a cell not comprising the
 CC recombinant nucleic acid. The present sequence represents human
 CC parathyroid CR, designated a pParCar 5.2. The nucleic acid sequence of
 CC pParCar 5.2 can be used as part of the recombinant nucleic acid in the
 CC method described above. The compounds identified can be used to treat
 CC diseases or disorders characterized by abnormal calcium homeostasis, e.g.
 CC hyperparathyroidism, osteoporosis and other bone and mineral-related
 CC disorders. They can also be used for the treatment of diseases and
 CC disorders associated with disrupted Ca²⁺ responses, e.g. seizures,
 CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in
 CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative
 CC diseases such as Alzheimer's disease, Huntington's disease and
 CC Parkinson's disease, dementia, muscle tension, depression, and anxiety.
 CC Sequence 1088 AA;

Query Match 18.2%; Score 1063; DB 1; Length 1088;
 Best Local Similarity 31.6%; Pred. No. 4,17e-84;
 Matches 264; Conservative 231; Mismatches 250; Indels 90; Gaps 59;

DB 60 CIRYVFRGFRWLQAMIFAIIEINSSPALLPNTLGRIFDTCNTVSKALEA--TISEYAAQ 117
 QY 3 C-SFNEHGYHFOAMRLGVEEINSTALLPNTLGYCLDYVCSDSANYATLRLVSLPQ 61
 DB 118 NKIDSLNDEFCNGSEHLPSTAVAGATGSGVSTAVNLGLFYIPQVSYASSSRLSNK 177
 QY 62 HHIE-LQ-GDLHHS--PTVLAIVIGPSTNRAATTAALLSPFLV-HISTAASSETLSVK 115
 DB 178 NQFSEFLTIPNDEHQAATAMADIIIEFRMNWGTIAADDYGRPGIEKFEAEERDICI 237
 QY 116 ROYPSFLTIPNDKYQVETWVLLOKFGMTWISLVGSSDDYQGLGVQALENALVRGICI 175
 DB 238 DPFSEISOYDE--EE-IQHVVEVIONSTAKYIVVSSGPDLEPLIKE-IYARNITGKIW 293
 QY 176 AFKDIMP-FSAQVGDERRQCLMRHLAAGATVYVSS--RLARVFEFSVLTNLTKYVW 233
 DB 294 LASEMASSSLIAMPOYFHVVGITGFALKAQIGFREFLKAYPRKSYHNGFAKEFWE 353
 QY 234 VASEMA--L-S--R--HITGVP-GIQ-RIGMVLGV-A-IOK--R-AVP-GL-KAF-E 274
 DB 354 ETEFNGHLOGAGPLPVDTFTLGHESGDRFSGNSSTARPLCTGDENISVETPYIDYTH 413
 QY 275 EAYR-R-ADKE-APRPH---KSGMSCSSNQCRCQAF--M-A--HYMPKILKA---FS- 318
 DB 414 LRISYNYLAVYSIAHALQDIYTCPLPGRGLFTNGSCADIKKVEAMQVILKHLNLFNTNM 473

QY 319 MSSAYNAYRAVYAAVAGHQLHQLGC-AS-EL-----CS-RGRVYPMQLLEQIHKVFLLHK 370
 DB 474 GEQYTPDECGLVAGNYSLIIMWHLSPEDEGSIVFEVGYNNYAKGDELFTNEKILMSGF 553
 QY 371 -DTVAFNDNRPLSSYINIAMDMNGPK-WT-FTVLGS-STWSP-VQ-LTINERKIQWHG- 423
 DB 534 SREDLTVLSVLYQVFPNCSRDCLAGTRKGIIEBEPCCFCEVCECPGGEYSDETDASACN 593
 QY 424 -KNH-----QYPKSVCSDDCEGHQR-VVGFHHCCCECPVCGAGTILNSELRYRCQ 473
 DB 594 KCPDDEMSNENHSCIAKEIEFLSWTEPEG-IAITLFAVIGITLFAVLGVFIKFRNTPI 652
 QY 474 PCGTEEMAPESQCFPRIVFALRREHISVWLLAANTLLILLLG-TAGLFAMHLDTPV 532
 DB 653 VKATNRELSTYLLFSLCCSSSIF-FIGRPQDWTCLRQPARGISVLCISCIYVNTNR 711
 QY 533 VRSAGRLCFMLGSLAAG-SGSLYGFGEPTRPACILRALFALGFTIFLSCITVNSFQ 591
 DB 712 VLVAFE--AKIPTSFHRRKMWGLNQLFLVFLCTPMQIVICVIMLYTAPSPSYRNOLEDE 769
 QY 592 LIITFKSTKVPY-FYIAMVONHAGLFWMISSAQLICLTLWLVYVTPPLPAREYQRFPH 650
 DB 770 IITTCHE-GSL-MALGFLIGYTCLLAICFFFAFKSRKLPENFEAKFTFSMLIFFIV 827
 QY 651 LYMECTETNSLIGFLIAPL--YNGLLISAFACSYLGKDPENYNEAKCYTFSILFNFVS 708
 DB 828 MISFIPYASYR-GKFSAYEVAITLAA-SFGLACIFFNKIYIILKPSRNTIE 880
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2771	100.0	2771	1 PCT-US99-17099-4	Sequence 4, Appl
2	2771	100.0	2771	2 US-09-361-652-4	Sequence 5, Appl
3	2166.8	78.2	2579	1 PCT-US99-17099-5	Sequence 5, Appl
4	2166.8	78.2	2579	2 US-09-361-652-5	Sequence 5, Appl
5	1566.6	56.5	2333	1 PCT-US99-17099-6	Sequence 6, Appl
6	1566.6	56.5	2333	2 US-09-361-652-6	Sequence 6, Appl
7	447.6	16.2	2993	51 US-09-361-631-3	Sequence 3, Appl
8	436	15.7	2532	51 US-09-361-631-4	Sequence 4, Appl
9	395	14.3	1147	54 US-09-471-275-7046	Sequence 7046, Ap
10	392.8	14.2	2010	51 US-09-361-631-8	Sequence 8, Appl
11	350.8	12.7	2466	87 US-60-172-300-1	Sequence 1069, Ap
12	269.2	9.7	571	93 US-60-178-308-1069	Sequence 1069, Ap
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14	252	9.1	558	86 US-60-160-841-23	Sequence 23, Appl
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17	220.6	8.0	412	92 US-09-496-911-9312	Sequence 9312, Ap
18	204.8	7.4	376	92 US-09-489-036-20518	Sequence 20518, A
19	204.8	7.4	382	92 US-09-489-036-23241	Sequence 23241, A


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ALIGNMENTS

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: Sequence 4, Application PC/TUS9917099
: GENERAL INFORMATION:
: APPLICANT: Zuker, Charles S.
: APPLICANT: Adler, Jon Elliot
: APPLICANT: Lindemeyer, Uerger
: APPLICANT: Ryba, Nick
: APPLICANT: Hoon, Mark
: APPLICANT: The Regents of the University of California
: TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
: FILE REFERENCE: 02307E-088610PC
: CURRENT APPLICATION NUMBER: PCT/US99/17099
: EARLIER FILING DATE: 1999-07-27
: EARLIER APPLICATION NUMBER: US 60/094,465
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 4
: LENGTH: 2771
: TYPE: DNA
: ORGANISM: Rattus sp.
: FEATURE:
: OTHER INFORMATION: rat G-protein coupled receptor B3 (GPCR-B3)
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: APPLICANT: Zuker, Charles S.
: APPLICANT: Adler, Jon Elliott
: APPLICANT: Lindemeier, Juergen
: APPLICANT: Ryba, Nick
: APPLICANT: Hoorn, Mark
: APPLICANT: The Regents of the University of California
: TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
: FILE REFERENCE: 02307E-088610DS
: CURRENT APPLICATION NUMBER: US/09/361,652
: CURRENT FILING DATE: 1999-07-27
: EARLIER APPLICATION NUMBER: US 60/094,465
: EARLIER FILING DATE: 1998-07-28
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 2771
: TYPE: DNA
: ORGANISM: Rattus sp.
: FEATURE:
: OTHER INFORMATION: rat G-protein coupled receptor B3 (GPCR-B3)
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RESULT 3
PCT-US99-17099-5
; Sequence 5, Application PC/RUS9917099
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeier, Juergen
; APPLICANT: Ryba, Nick
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; TITLE OF INVENTION: Involved in Sensory Transduction
; FILE REFERENCE: 02307E-088610PC
; CURRENT APPLICATION NUMBER: PCT/US99/17099
; EARLIER FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/094,465
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2579
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: mouse G-protein coupled receptor B3 (GPCR-B3)
PCT-US99-17099-5

Query Match 78.2% Score 2166.8 DB 1: Length 2579;
Best Local Similarity 91.0% Pred. No. 0;
Matches 2316: Conservative 0; Mismatches 222; Indels 6; Gaps 1;

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QY 103 actgctggcttctcagctgcacaaagacagagtcctctccagcgttcaagcttctggg 162
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RESULT 4			
US-09-361-652-5			
Sequence 5, Application US/09361652			
GENERAL INFORMATION:			
APPLICANT: Zuker, Charles S.			
APPLICANT: Adler, Jon Elliot			
APPLICANT: Lindemeyer, Juergen			
APPLICANT: Ryba, Nick			
APPLICANT: Hoon, Mark			
TITLE OF INVENTION: The Regents of the University of California			
TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor			
FILE REFERENCE: 02307E-088610US			
CURRENT FILING DATE: 1999-07-27			
EARLIER APPLICATION NUMBER: US/09/361,652			
EARLIER FILING DATE: 1998-07-28			
NUMBER OF SEQ ID NOS: 8			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 5			
LENGTH: 2579			
TYPE: DNA			
ORGANISM: Mus sp.			
FEATURE:			
OTHER INFORMATION: mouse G-protein coupled receptor B3 (GPCR-B3)			
US-09-361-652-5			
Query Match			
Best Local Similarity 91.0%; Pred. No. 0;			
Matches 2316; Conservative 0; Mismatches 222; Indels 6; Gaps			
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RESULT 5

PCT-US99-17099-6

Sequence 6, Application PC/TUS9917099

GENERAL INFORMATION:

APPLICANT: Zuker, Charles S.

APPLICANT: Adler, Jon Elliot

APPLICANT: Lindemeier, Juergen

APPLICANT: Ryba, Nick

APPLICANT: Hoon, Mark

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor

FILE REFERENCE: 02307E-088610PC

CURRENT APPLICATION NUMBER: PCT/US99/17099

CURRENT FILING DATE: 1999-07-27

EARLIER APPLICATION NUMBER: US 60/094,465

EARLIER FILING DATE: 1998-07-28

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 6

LENGTH: 2333

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: human G-protein coupled receptor (GPCR-B3)

PCT-US99-17099-6

Query Match 56.5%; Score 1566.6; DB 1; Length 2333;
 Best Local Similarity 80.0%; Pred. No. 0;
 Matches 1869; Conservative 0; Mismatches 464; Indels 4; Gaps 2;

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 QY 1023 gtggcgctccagcagaagaacagctcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1082
 Db 778 gtggcgctccagcagaagaagcgtcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 837
 QY 1083 gctgtaacagctgtctccagcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1142
 Db 838 gcaagaagaagggccctcagcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 896
 QY 1143 gtccgggaggtgtccacagcttccagcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1202
 Db 897 tgcagagaatgcaagcttctcagcagacagatgccaagcctcaagccttccatg 956
 QY 1203 agtcgcgcacagatgtatgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1262
 Db 957 agtcgcgcacagatgtatgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1016
 QY 1263 ctggagatgactcttgagatctgttccagagcccaactacacccctggcagcttctcag 1322
 Db 1017 ctggagatgactcttgagatctgttccagagcccaactacacccctggcagcttctcag 1076
 QY 1323 cagatctcaagaagtgatcttctcctacatgagatactgtgtgtgtgtgtgtgtgtgtgtgt 1382
 Db 1077 cagatctcaagaagtgatcttctcctacatgagatactgtgtgtgtgtgtgtgtgtgtgtgt 1136
 QY 1383 gacactcaagttactacagacatcatcgctcgtgacacagatgacatgacatgacatgac 1442
 Db 1137 gatccctcagtgatctataataataatgtcgtgacacagatgacatgacatgacatgac 1196
 QY 1443 gagatcattgtcctgtcctcactgtctccagttcatctgtgacataaataagaacaaatc 1502
 Db 1197 aggtctcctgtctcctcactgtcctcagttcatctgtgacataaataagaacaaatc 1256
 QY 1503 cagtgacagcgggaagaacacacacagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1562
 Db 1257 cagtgacagcgggaagaacacacacagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1316
 QY 1563 gggcacaacaggt 1622
 Db 1317 gggcacaacaggt 1376
 QY 1623 gctgggaccttctcaacatgagtgacatcttccacatctgtgcaagcctgtgtggaacaga 1682
 Db 1377 gctgggaccttctcaacatgagtgacatcttccacatctgtgcaagcctgtgtggaacaga 1436
 QY 1683 tgggaccccaagggagagcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1742
 Db 1437 tgggaccccaagggagagcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1496
 QY 1743 gaaccatctctgt 1802
 Db 1497 gagcaacactctgt 1556
 QY 1803 actgtcgtcgttctgtcctgtgcatcttccacacactgtgtgtgtgtgtgtgtgtgtgtgt 1862
 Db 1557 actgtcgtcgttctgtcctgtgcatcttccacacactgtgtgtgtgtgtgtgtgtgtgtgt 1616

Dh	1751	cgctgcgcacattcgtcatctctcttggaagacatttccaaagccgacattggtgcgtccggcg	1811
Qy	1855	ggggtaagctctgtcttcctccaagctgggttccctgtgtgcggaaagttgcagcttctata	1914
Dh	1811	ggcgccccatgltgtcttcattgtgtgtgcgcctgtgcgttcggatgvtgcccg	1870
Qy	1915	gctctctcggggagcccaaggtgtccgggtgtctgtgtgtgaagccctcttctctcg	1974
Dh	1871	tgatgvgggcccccccacaggttctctctgttcttgcgcgcagggcttcttcaacgltt	1930
Qy	1975	gattgcacattcttcctctctgtcgttgaacatccgcctctcccaactggttaatacttca	2034
Dh	1931	gctctctcgcgtcgtcctctcgtcatcaaggtgcgtcctctccagattgtgtgcttctca	1990
Qy	2035	agtttctcaacaaagtgcaccacattctacagttacgtcgtgggccccaaacagatgtgcagtc	2094
Dh	1991	agatgvcgcaagcgtctgcaagcgcttaccggttcttctgtgtgtgaattgcacaggccctacg	2050
Qy	2095	tattcgtcatctgtcagctcccaaggttccatttg---ctacatcgttccaaatggtctgtaa	2151
Dh	2051	tctctgtgcctctcatcaacgcccgttcaaggtgtgcctctgtgtggcggaacaaatgctgcga	2110
Qy	2152	tggtgacccccagaccacccaaggggaatacaagcgtcctcccccatctggtaattcagagt	2211
Dh	2111	ccaccatacaaccocatgtgcgcgaagccgacccgagatgacccccatataatccctctct	2170
Qy	2212	gcacagaagctcaactctgttaggtcttcgttltgtcttcaaccacacatactctctctcca	2271
Dh	2171	ggcaccttaactaacgcaagcggtactcttccaacccagcatgtgaattgtcgtctgc	2230
Qy	2272	tcaatccttcgtctctgacgttaccctgtgtgaaggaaactgccagaactataatgaagcca	2331
Dh	2231	tgctgggttttcaagttctgtgcgtacgtgtggcaagaaactgtcccaacttacaacggaagcca	2290
Qy	2332	aattgtcaccttcaagcctctctctccaactctgtatccctggatctgcctctcttccaccatgg	2391
Dh	2291	agttcacaccoccctcaagatgaaactcttctcttcaaccctcccaactctccctctgcaggttca	2350
Qy	2392	ccagacattcacagggagagctactctgcctgcgtgtacatgtgtctggcagagctgaaacac	2451
Dh	2351	tgctgtccacagatlgcggtctgtgtacacatcatgtatctctctgttaactgtgccaaact	2410
Qy	2452	tgagcgcgcgcttcaagcggttacttccctccccaagtgtcattgtgattctctgcgtccag	2511
Dh	2411	tctcgtccactcgcgcttgggtgattacttggcccccaaatgtacatgatctcttcttaccgg	2470
Qy	2512	aaccacaataacagaacacttccagcctccatccaggaactacaagagcg	2563
Dh	2471	agcgcaacactcagcttatttaataagatgattcagggtcacaagatgag	2522
RESULT 9			
US-09-471-275-7046			
Sequence 7046, Application US/09471275			
GENERAL INFORMATION:			
APPLICANT: Hyseq, Inc.			
TITLE OF INVENTION: Novel Configs Obtained			
TITLE OF INVENTION: From Various Libraries			
FILE REFERENCE: 782			
CURRENT APPLICATION NUMBER: US/09/471,275			
CURRENT FILING DATE: 1999-12-23			
EARLIER APPLICATION NUMBER: US 09/235,076			
EARLIER FILING DATE: 1999-01-20			
EARLIER APPLICATION NUMBER: US 09/234,611			
EARLIER FILING DATE: 1999-01-22			
EARLIER APPLICATION NUMBER: US 09/240,371			
EARLIER FILING DATE: 1999-01-29			
EARLIER APPLICATION NUMBER: US 09/277,227			
EARLIER FILING DATE: 1999-03-25			
EARLIER APPLICATION NUMBER: US 09/271,490			
EARLIER FILING DATE: 1999-03-18			
EARLIER APPLICATION NUMBER: US 09/293,972			
EARLIER FILING DATE: 1999-04-15			

[illegible]

Db 1532 tctctatgcatcttatacaccggtacccaataatgctatctgtgtaattgtgcatatgctgagcac 1591
QY 2155 ggaaccccccagaccccccaggaataaccagcgtctcccccattgtgtattcttcaggtgca 2214
Db 1592 ggcctcagctccacccccggtacgtaccgagatgaccccaagatacacaattgtctctgta 1651
QY 2215 cagaggtcaactctgttaagctctcgttgcgttcaccacaacaattctctccatca 2274
Db 1652 accccaatacgcgaacacgcgtcgtttcaaacacagccttgagacctgtctctcagtgy 1711
QY 2275 gtacctgtctgcagctacgttggttaaggaactgcgacagaataactaataagaaacaaat 2334
Db 1712 tgggttcatgctctgcctacatagggcaagagctgcaccaactacaatacagggcgaagt 1771
QY 2335 gtgtacctttagcctgtctctccaaacttcgtatccttgatctgcctcttcaaccaagccca 2394
Db 1772 tcaataccctcagctacgtacctctatcttaaccatccgtctccctcgcgaacctcatgt 1831
QY 2395 gcaattaccagggcagctacacgtcgtcggtcaatagtgtcgcaagggttgacaacacatga 2454
Db 1832 ctgctctaacagcgggtgtctgtgtacaccatcggtgacctctgtgtacgtgtgtcaacctcc 1891
QY 2455 gcggcggtctaacgcgttactctctccccaagtgtatgtgattctctgcgcgttccagaac 2514
Db 1892 tggccatcagcctggtgctacttcgcccagaagtgtacatgctctctcttcaaccggagc 1951
QY 2515 tcaataatacagaataacttccagcctccatccagaactacacagcggcgctgctgagc 2570
Db 1952 gcaacacgcgcgcctacttcaacagcatgatacagggttacaacccattgaggaagagac 2007

RESULT 11
US-60-172-600-1
: Sequence 1, Application US/60172600
: GENERAL INFORMATION:
: APPLICANT: Bonazzi, Vivien
: TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
: TITLE OF INVENTION: RECEPTOR, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
: TITLE OF INVENTION: PROTEIN, AND USES THEREOF
: FILE REFERENCE: CLO00178
: CURRENT APPLICATION NUMBER: US/60/172,600
: CURRENT FILING DATE: 1999-12-20
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 2466
: TYPE: DNA
: ORGANISM: HUMAN
: US-60-172-600-1

Query Match 12.7%, Score 350.8; DB 87; Length 2466;
Best Local Similarity 48.0%; Pred. No. 9.6e-80;
Matches 1154; Conservative 0; Mismatches 1217; Indels 33; Gaps 4;

QY 159 gggagctccctcctctgcaggtctgttccctcccatgtgtgactgtctcaggtgtagaac 218
Db 7 ggggactacgtgtcgggggctgttccctcctgagggccgaggaaggtgtgctccgc 66
QY 219 agacctctgttacagtggtgacagggcccgacagcttcaacgagcatggtatcacctc 278
Db 67 agccggaacagccagcagccctgtgtgacacagttctctcaaacggcctgtctctg 126
QY 279 ttcaagcctatgctgctacgttctgaagatataaacactcctcgccctgtccccaac 338
Db 127 gcactgagcatgaaatgctgagtgagatcaacaacaaagtcgattctgtgcccgg 186
QY 339 atcacccgggtatgaggtgtacagcgtgtctcagaatctgcgaactg---tgtatgccc 395
Db 187 ctgctgcctggagctccttctgtatagctgtcggaaacctgtgtgcccataagccc 246
QY 396 accctgaggtgtcttgcctctgcaaggcccgccacatagatatacagaagaacctctgc 455

Db 247 agccctcatgttctcggcgaagcgcagccgcgacacatcgccgctactgacataacag 305
QY 456 aaccactctcccaagggtgtgtgcttcatcgagccttacaacactgtaccagcgttcaact 515
Db 307 cagtaaccagcccggtgtgtctgtgtcgtatctcggtcccaactgtatagatcgcatgtgc 366
QY 516 accgctgctgtgcgggggtcccttccatgagccctgtgtcaacatactgaggaacagctg 575
Db 367 accggcaagttctctcagcttctctctcatggtccagatcagctcagttcgtcagatagag 426
QY 575 gtactcagtgccaaagcgaagtcccgcttctccttgtaacgttccaccgtgacagcggac 635
Db 427 ctgctgagcgcgcggaggaaccttccctctcttccgacacggtgcgaagcagcgtgtg 486
QY 636 caggtgagcgcccaagtgacagctcgtcgaaggttttggtgtggcgtgtgattctgcatt 695
Db 487 cagctgacggcccgcccgcggaactctgtgaaggatctcggtgaactgtgtgtgcccctg 546
QY 696 ggcagctacggtgatttaagggcagactgtgtgtgcaagcgctgagagctgagccgtgccc 755
Db 547 ggcagcgacgagaggtacagcccgacagggccttgagacatctctcgccctgtccggcgca 606
QY 756 cggggcatctgcgtcgccttcaaggacatcggtgcctt-----ctgtcccggtgtggt 809
Db 607 cgggcatctgcatcgccagcagagggcctgtgtgcctgcctgcctgtccggtgactcgcg 666
QY 810 gaaccgagga-gcagagcatgtacagatcgtcgtcagcgccagagacacacggtgtgtg 869
Db 667 ctggggaagggtgcaggaagctctctgacccaagttgaacagagacggtgcaaggtgtgtg 725
QY 870 gtctctctaacccggcagcctgtgtagagttgtcttcaagtgctcgtgtgtgtgccaacctg 929
Db 727 ctgttcgctcctcgtgtcagcagccgcacagcctctcttaactacatataagacagcgttc 786
QY 930 actggaacagtggtgtgtcgtcctcagaaactgtggacatctccacgtatacacaacagcgt 989
Db 787 tgcgccaagtggtgtgtgtgcagcagggcctgctgtacatctgtgacctgtgtcatgtgggtg 846
QY 990 actggtatccaaagcaatggtgagcgtgtcgtgtgtgtgcgcgtccacgaagagcaagttcct 1049
Db 847 cccggcaca-gggccagatgtggacaggtgtgtgtctctccacagagggtgtgccacatgac 906
QY 1050 gggcgtgaagggtttgaagatcttatgttcaagccttgaacagcgtcctccacagcgtgc 1109
Db 907 gagtctcccccagtaagtgtaaagacgacacctgtgcctgtgcacacgacccgctt-ctgtcct 956
QY 1110 ccggaagggtctcgtgtgacgactaacacagctgtgtccggaggtgccacagttcacagact 1169
Db 967 gccctggcgagaggagagcaggtctgtgagagagacgtgtgtggccagcgtgtcccgag 1026
QY 1170 cgtaacatgcccacgcttggagccttctccataggtcccgctccacagaagtgtatgagct 1229
Db 1027 tgtgactgtcatcacagcttcaaaacgtgtgagcgacaggtcaaaatccacaacacagttctct 1086
QY 1230 gttgacgctgtgtgcccacagggcctccacagcgtctcgtgagttactctggaatcgtgtcc 1289
Db 1097 gtccaagcagctgtgtatagcgtgtgcccagggcctgtgcaacaactcttcaattgaacgcc 1146
QY 1290 agagg-----ccagttaccccttgacagcttcttccagcttccacagatcaacaag 1334
Db 1147 tcaagctgtcccccgcagcagaccocctgtgaagccctgcgcagcgtccctcgagaaatgtaacac 1205
QY 1335 gtgaatttctctcatagaaatactgtgtgcatltgtgtgcaacgggggaacctctaggt 1394
Db 1207 ctgaccttccacgtgtggcggtgtccgctgcgtgtgtgcaacacggaacgtgtgacatg 1256
QY 1395 tactacgacatcatcgcctgtgagctgagatgagactgtgacatgtgagatcatgtg 1454
Db 1267 gagtacgaacctggaagctgtgtgtgtgacaggtccag-ggccaggtcttcaagacgtgtggc 1326
QY 1455 tctgctactagtctccagcttcatctgtgacataaataagacaaaatccagctgacagg 1514

[illegible]

```

RESULT 12
US-60-178-308-1069
: Sequence 1069, Application US/60178308
: GENERAL INFORMATION:
: APPLICANT: Bonazzi, Vivien
: TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
: TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
: FILE REFERENCE: CLO00204
: CURRENT APPLICATION NUMBER: US/60/178,308
: CURRENT FILING DATE: 2000-01-27
: NUMBER OF SEQ ID NOS: 3344
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1069
: LENGTH: 571
: TYPE: DNA
: ORGANISM: HUMAN
: US-60-178-308-1069

```

```

Query Match      9.7%; Score 269.2; DB 93; Length 571;
Best Local Similarity 81.1%; Pred. NO. 5.9e-59;
Matches 313; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1647 gacgtcacatctgcagcctctgtgaaacagaagatgagcaccacaagagagacactact 1706
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 186 gacctctacagatgccaacctctgtgaaagaagagatgagcaccctgaggaagcagacc 245
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1707 tgcctccacgacgagctgtgagctctctgtcttgcatgaaccatctcttgtgtcataa 1766
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 246 tgcctcccgccagcatctgtgtgttcttctgtccttcgtagaacacacctcttgggtgcgtcg 305
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1767 gcaagctaacagagcatctgtcgtcgtctgttggagacatcctgacctgttcttgccagat 1826
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 306 gcaagctaacacagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 365
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1837 ttccacacacacctgtagtagaagctcagcctggaggttagcctgtctctccatctgctgttcc 1886
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 366 ctagaacacacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtc 425
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1887 ctgtgtgcgggaagtgtcagctctctatagctctcttcggggagcccaagtgcccgctgc 1946
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 426 ctggcagcagagtagtgcagcctctatgtctctcttcgggaaacccacaagagcctgcgtgc 485
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1947 ttgcttggttcagccccctcttctctcgtgttggttcgcatctctctccctgcgtgcagataac 2006
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 486 ttgcacagccagccctctctgcacctgtgttccatccatctctctgcctgcctgcagatc 545
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2007 cgctcctccacactgctacatcatt 2032
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 546 cgctcatctccactaacatcatcatt 571
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-60-160-202-36
; Sequence 36, Application US/60160202
; GENERAL INFORMATION:
; APPLICANT: BONNAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
; FILE REFERENCE: CLO00114
; CURRENT APPLICATION NUMBER: US/60/160,202
; CURRENT FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 4392
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 558
; TYPE: DNA
; ORGANISM: HUMAN
US-60-160-202-36

```


Query Match	9.1%	Score 252;	DB 86;	Length 558;
Best Local Similarity	76.5%;	Pred. No. 1.6e-54;		
Matches 309;	Conservative 0;	Mismatches 95;	Indels 0;	Gaps 0;

QY	544	tcgccctctgctcagctctctgagccagacagcgctgtgtactcaatctgcacagcgcaatctccgt	603
Db	155	tcccatagatttgctactgtgcgcacagcagcgatgacgctctcagcgtggaagcagcgatctccct	214
QY	604	cttccctctgataccgctcccccagtgacccgagccacaaagtctgaggtctcatgtgtcaactctgc	663
Db	215	cttccctcgagcaaccatccccaatgacaagtattacaagttgagacattgtgtctgtctgc	274
QY	664	agaattcttggtgtggtgtgtgtgatactcgtctcatctgacagctcaagttgattacagtcagctgc	723
Db	275	agaagttctcggtgtgagctctgatactctctgtgttgtagcagcagtgacgactaagtcagctag	334
QY	724	gtgtctcagagcgctctgagagagcctgcgcgtgcgcccgagagcattctctcgtccgctcttaagaga	783
Db	335	gggtgtcagagcaacttgagagaacccacagccacacgtgtcaagggagatctgtctcttaagagaca	394
QY	784	tctgtccctctctctctcccggtgtgtgtaccccgagagatgacagagcatgtatccagacactgc	843
Db	395	tcatgcccctctctgcgcccaagtcggtgcgtatgtagagagattcagctgtccctcatctgcacactgc	454
QY	844	ctcagagccagagacacacgtgtgtgtgtctctctctcaacccgacactgtgtagagttct	903
Db	455	cccagagccgggtccacacgcctgcgtgtgttttctccagcccgacagttgtgcacaggtgtttt	514
QY	904	tcaagttccgtgtgtctctgcagccacatgacatcgacaaagtgtgtgtc	947
Db	515	tctgagttccgtgtgtctgtgaccaaactgtgacatgagttctgtgtgtc	558

```

OY      784  tcgtgcctctctcccggtgtgtgtgacccggagatgcagagcatgacatctg 843
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      395  tcagtcctctctgcccaagtgtggtgataagagatgcagtccctcatgtccacctg 454
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY      844  ctacagcagaacacacacgtgtgtgtgtctctctaacgcgcacccggcctcagaagtctct 903
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      455  cccagcgccggggccacacgtgtgtgtcttcttctccagccgcgcagtgctggccaggtgttct 514
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY      904  tcagctccgtgtgtgtgtgtgcacacctgacctggtcacaagtgtgtgtc 947
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      515  tcgagtcgtgtgtgtgtacccaactgtactgtgcagaagtgtgtgtc 558

RESULT 15
; Sequence 23, Application US/60169842
; GENERAL INFORMATION:
; APPLICANT: Bonazzl, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
; FILE REFERENCE: CLO00162
; CURRENT APPLICATION NUMBER: US/60/169,842
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 5232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Human
US-60-169-842-23

```

[illegible]

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OM nucleic - nucleic search, using sw model

Run on: March 19, 2000, 17:45:41 ; Search time 97.56 Seconds
(without alignments)
3400.480 Million cell updates/sec

Title: US-09-361-652-4

Perfect score: 2771

Sequence: 1 attcaccatcagagctgtgct.....aaaaaaaaaaaaaaaaaaaaa 2771

Scoring table: IDENTITY_NNC

Searched: 214294 seqs, 59861208 residues

Database : Issued_Patents_NA:*

Word size : 0

Number of hits that pass the threshold : 428588

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/5_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PTUS9_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	181.6	6.6	3809	1	US-08-485-588-3	Sequence 3, Appl1
2	181.6	6.6	3809	2	US-08-484-565-3	Sequence 3, Appl1
3	181.6	6.6	3809	3	US-08-480-751-3	Sequence 3, Appl1
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5	181.6	6.6	3809	5	US-08-353-784-3	Sequence 3, Appl1
6	176.4	6.4	5275	1	US-08-485-588-1	Sequence 1, Appl1
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9	176.4	6.4	5275	4	US-08-943-986-1	Sequence 1, Appl1
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11	170.2	6.1	5006	1	US-08-485-588-2	Sequence 2, Appl1
12	170.2	6.1	5006	2	US-08-484-565-2	Sequence 2, Appl1
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16	160.6	5.8	4131	1	US-08-485-588-4	Sequence 4, Appl1
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ALIGNMENTS

RESULT 1
US-08-485-588-3
; Sequence 3, Application US/08485588
; Patent No. 5688938
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: Forrest H. Fuller
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSPRO
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,588
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hebert, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/005


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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 373..3606
OTHER INFORMATION:
US-08-485-588-3

Query Match      6.6%; Score 181.6; DB 1; Length 3809;
Best Local Similarity 49.6%; Pred. No. 3.6e-38;
Matches 522; Conservative 0; Mismatches 524; Indels 6; Gaps 2;

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RESULT 2
US-08-484-565-3
; Sequence 3, Application US/08484565
; Patent No. 5763569
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,565
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: Including application
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:

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APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 373..3606
OTHER INFORMATION:
US-08-480-751-3

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Query Match          6.6%; Score 181.6; DB 3; Length 3809;
Best Local Similarity 49.6%; Pred. No. 3,6e-38;
Matches 522; Conservative 0; Mismatches 524; Indels 6; Gaps 2;

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RESULT 4
US-08-943-986-3
Sequence 3, Application US/08943986
Patent No. 5962314
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,986
FILING DATE: 03-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127

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; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 36,119
; REFERENCE/DOCKET NUMBER: 213/006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5275 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 515..3769
; OTHER INFORMATION:
;
US-08-484-565-1

Query Match          6.4%; Score 176.4; DB 2; Length 5275;
Best Local Similarity 49.0%; Pred. No. 1e-36;
Matches 530; Conservative 0; Mismatches 546; Indels 6; Gaps 2;

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DB 2078 CTTCTCATCATGATGATAAAAAATTCTGTGAGTGTCTCAAGGAGGTGCTTCTCC 2137
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QY 1539 gtgtgtccacgagacgtgtgtgaggagc---cacagggtgtgtgtgtgtccacac 1595
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2138 AACTGCAGTGCAGACTCTCTGTGGCAGGACCAAGAAAGAAATCATTGAGGGGAGCCACC 2197
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1596 tgcgtctttagtgtgtccctgcgaagcttggacatttccaatgagtgtgacttcaac 1655
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2198 TCGTCTTGTAGTGTGTGATGTCGTGATGGGAGTACACAGCAGACAGATGCAAGT 2257
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QY 1656 atctgcagacctgtgaaacagaagaatgggaccccaagagaagactacttcttccca 1715
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QY 1716 cgcagcgtgagatctgtggtgtgcatgaaccatcttctgtgttaataagcagctaac 1775
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DB 2318 AAGGAGATCAGATTTCGTGTGTGACGAGCCCTTCGGGATGCGACGTCACGCTTTTGT 2377
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QY 1776 acgctatgtctgtctgtgtgtgtgactgtgacctgttgcctgtgcaatttcaaca 1835
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DB 2378 GTGCTGGGCAATTTCCTACAGCCTTGCTGTGGCGCTTCATCATGATTCGCAACAG 2437
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QY 1836 ctgttagtgaagtaagctgggggtgaagctgtgtcttcctcatgctgggttccctgtggcc 1895
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DB 2438 CCCATGTCAGGCGCAACCAACCGGAGCTCTCCTATCTCTTCTCTCTCTCTCTCTC 2497
QY 1896 ggaagtgcagctctcatagctctctccgggagagccacagctgcccggctgtgcgt 1955
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DB 2498 TCGTCTCCAGCTCCCTGTTCTTCATCGGGAGCCCAAGACTGGAGTGCGCCCTGCGC 2557
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QY 1956 caagccctcttctctcgtgttgcacattctctctcctcctcctgcaatccgctcttc 2015
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DB 2558 CAGCGGCGCTTGGCATCAGCTTCGTGCTGTGATCTCGTGCATCTCGTGGTGAACCA-- 2616
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DB 2616 -ATCGGTCCTCTCGTGTGTTGAGGCGCAAGATTCACCAAGCTTCACCGGAAAGTGTG 2674
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DB 2675 GGGCTCAACCTGCAAGTTCTGCTGTGTTCTTCTGTGACCTTATGAGATTTGATCTGT 2734
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2136 ctacatgtgttgaatgtgaccccaagaccacacaggaatatcagagcttcccat 2195
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QY 2196 ctggtgatctcgtgagtgacagagtgcaactctgttagcttctgtgttaccacc 2255
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DB 2795 ATCATCTTCATCACCTGCGACAGAGGCTGCTCATGCGCTGGGCTTCTGATGCGCTAC 2854
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2256 aacattctctcctcctacagtaaccttcgtctgagcttacctgtgaagaaactgcagag 2315
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DB 2855 ACCTGCTGTGCGCCGCGCATCTCTTCTTCTTGTGCTTCAAGTCCGGAAAGCTCCAGAG 2914
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DB 2915 AACTCATATGAACCAAGTATCATCACCCTTCAGCATCTCATCTTCTTCATCGCTGAGAC 2974
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QY 2376 gccttctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 2435
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DB 2975 TCTTTATCCCGCGCTACGCGCACTTACGCAAGTGTCTCTCTCGGTGGAGTATC 3034
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QY 2436 gcaaggctgacacacttgaagcggccttgaagcgttacttctctcccaagtgtatgtg 2495
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QY 2556 ac 2557
DB 3155 GC 3156

RESULT 8
US-08-480-751-1
; Sequence 1, Application US/08480751
; Patent No. 5858684
; GENERAL INFORMATION:
; APPLICANT: Edward F. Nemeth
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James E. Garrett, Jr.
; APPLICANT: Forrest H. Fuller
; TITLE OF INVENTION: CALCIDIUM RECEPTOR-ACTIVE
; MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
```



```

STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,986
FILING DATE: 03-OCT-1997
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991

ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 515..3769
OTHER INFORMATION:
US-08-943-986-1

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[illegible]

APPLICANT: Brown, Steven C. Hebert,
 APPLICANT: Bradford C. Van Wagonen, Manuel
 APPLICANT: F. Balandrin, Forrest H. Fuller,
 APPLICANT: Eric G. Delmar, and Scott T. Moe
 TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
 TITLE OF INVENTION: MOLECULES
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: First Interstate World Center
 STREET: Suite 4700
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: FASTSEQ
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/353,784
 FILING DATE: 9 December, 1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA: including application
 PRIOR APPLICATION DATA: described below: 8
 APPLICATION NUMBER: PCT/US/94/12117
 FILING DATE: 21 October, 1994
 APPLICATION NUMBER: U.S. 08/292,827
 FILING DATE: 23 August, 1994
 APPLICATION NUMBER: U.S. 08/141,248
 FILING DATE: 22 October, 1993
 APPLICATION NUMBER: U.S. 08/009,389
 FILING DATE: 23 February, 1993
 APPLICATION NUMBER: U.S. 08/017,127
 FILING DATE: 12 February, 1993
 APPLICATION NUMBER: U.S. 07/993,161
 FILING DATE: 21 August, 1992
 APPLICATION NUMBER: U.S. 07/834,044
 FILING DATE: 11 February, 1992
 APPLICATION NUMBER: U.S. 07/749,451
 FILING DATE: 23 August, 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Heber, Sheldon O.
 REGISTRATION NUMBER: 38,179
 REFERENCE/DOCKET NUMBER: 209/069
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELE: 67-3510
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5275 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 515..3769
 OTHER INFORMATION:
 US-08-353-784-1

	Query Match	Similarity	Score	DB	length
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QY	1539	gttgatcccaacgacacgtctcttgcaaggagc---	caaaaggttggttggtgtcccaaac	1595
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QY	1596	tgtctctttagtgtgtgcccctcgaaagcttgga	cccttctcaacatgattgagttcac	1655
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Db	2498	TGCTTTCACAGCTCCCGTCTTCA	TCCGAGGAGCCCAAGACTGAGACGTGGCGCTGGC	2557
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Db	2616	-ATGGGTCCTCCTGCTGTGTTGAGCGCA	AGATTCCACACAGCTTCCACCGGAAGTG	2674
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QY	2136	ctacatgaggttgtaatgtgagcccaagca	cccaagcaagaaatcacagcgcttcccac	2195
Db	2735	GCCATTGGCTCAATACAGCGCCCCCTG	AGCTACCCGAAACCAAGAGTGGAGACAG	2794
QY	2196	ctggatctctcagttgacagagatcaactct	gtgagcttccgttggtcttccaccac	2255
Db	2795	ATCATCTTCAACACCTGCACGAGGGCT	GTGCTATGGGCTCTGATCGGCTAC	2854
QY	2256	aaactctctctccatcagtaactctgctctg	caagctacctgtgaagaactgtgccag	2315
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QY	2316	aaactataaagcaaaatgtctacacttcag	cgctctcctaactcgtatccagctgac	2375
Db	2915	AACCTTCATGAAGCAAGTATCATCACC	TTTCAGATGCTATCTTCTTCACTGCTGATC	2974
QY	2376	gccttcttccacatgagccagcat	ttaccagggcagctacgctgcgtgagtaatgtg	2435
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QY	2436	gcagaggtgacacacacgagcggcggtctc	aggggttacttctctcccaagtgatgtg	2495
Db	3035	GCATCTGGGCGGCACTTGGCTTGCTG	CTGTATCTTCTTCAACAAGTCTTACATC	3094
QY	2496	attctctgcgcttccagaactcaacaa	ttacagaacattcaagccttccatccagactac	2555
Db	3095	ATCTCTTCAAGCCTTCCCGAACACAT	TCAGAGAGTGCTGCTGACGACCCGCGACAC	3154
QY	2556	ac	2557	
Db	3156	GC	3156	

Db 3095 ATCTCTTCAAGCCTTCCCGGAAACCATTCGAGAGAGTCCGCTGCGACGACCCCGGCACAC 3156


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1  RESULT 12
2  US-08-484-565-2
3  Sequence 2, Application US/08484565
4  Patent No. 5763569
5  GENERAL INFORMATION:
6  APPLICANT: Edward M. Brown
7  APPLICANT: Steven C. Hebert
8  APPLICANT: James E. Garrett, Jr.
9  TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
10 TITLE OF INVENTION: MOLECULES
11 NUMBER OF SEQUENCES: 20
12 CORRESPONDENCE ADDRESSES:
13 ADDRESS: Lyon & Lyon
14 STREET: First Interstate World Center
15 STREET: Suite 4700
16 STREET: 633 West Fifth Street
17 CITY: Los Angeles
18 STATE: California
19 COUNTRY: USA
20 ZIP: 90071
21 COMPUTER READABLE FORM:
22 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
23 COMPUTER: IBM PC compatible
24 OPERATING SYSTEM: PC-DOS/MS-DOS
25 SOFTWARE: FASTSO
26 CURRENT APPLICATION DATA:
27 APPLICATION NUMBER: US/08/484,565
28 FILING DATE: 7 June, 1995
29 CLASSIFICATION: 435
30 PRIOR APPLICATION DATA:
31 PRIOR APPLICATION DATA: including application
32 PRIOR APPLICATION DATA: described below: 9
33 APPLICATION NUMBER: 08/355,784
34 FILING DATE: 9 December, 1994
35 APPLICATION NUMBER: PCT/US/94/12117
36 FILING DATE: 21 October, 1994
37 APPLICATION NUMBER: U.S. 08/292,827
38 FILING DATE: 23 August, 1994
39 APPLICATION NUMBER: U.S. 08/41,248
40 FILING DATE: 22 October, 1993
41 APPLICATION NUMBER: U.S. 08/009,389
42 FILING DATE: 23 February, 1993
43 APPLICATION NUMBER: U.S. 08/017,127
44 FILING DATE: 12 February, 1993
45 APPLICATION NUMBER: U.S. 07/934,161
46 FILING DATE: 21 August, 1992
47 APPLICATION NUMBER: U.S. 07/834,044
48 FILING DATE: 11 February, 1992
49 APPLICATION NUMBER: U.S. 07/749,451
50 FILING DATE: 23 August, 1991
51 ATTORNEY/AGENT INFORMATION:
52 NAME: Heber, Sheldon O.
53 REGISTRATION NUMBER: 38,179
54 REFERENCE/DOCKET NUMBER: 213/006
55 TELECOMMUNICATION INFORMATION:
56 TELEPHONE: (213) 488-1600
57 TELEFAX: (213) 955-0440
58 TELERX: 67-3510
59 INFORMATION FOR SEQ ID NO: 2:
60 SEQUENCE CHARACTERISTICS:
61 LENGTH: 5006 base pairs
62 TYPE: nucleic acid
63 STRANDEDNESS: single
64 TOPOLOGY: linear
65 MOLECULE TYPE: cDNA to mRNA
66 FEATURE:
67 NAME/KEY: CDS
68 LOCATION: 436..3699
69 OTHER INFORMATION:
70 US-08-484-565-2

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Query Match	Similarity	6.1%	Score	170.2	DB 2	Length	5006
Best Local	Similarity	49.5%	Pred	4.1e-35			
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							2:
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QY 1581	gtggtgtcccaacactggttgtttgagtggtgtgccctcggaagctgggaaccttctaac	1640					
Db 2131	GAGGGGGAAGCCACTGCTGTGTTGAGTGTGGAGTCTCTGATGGGAGATATGTGT	2190					
QY 1641	atgaatgagcttcacatctgcacgacctgttgaaacagaagaatgggcaacccaaggaagc	1700					
Db 2191	GAGAGATGGCAAGTGCCTGTATACAAAGTGGCCAGATGACTTGTGTCCATATAGAACAC	2250					
QY 1701	actactgtcttcccaagcaagtgagagttcttgac--tgcatgaacacactctttggtg	1760					
Db 2251	ACCTCCCTCATTTGCCMAAGAAATCAGATTGTGTGTGTGGACGACCCCTTGTGATCGCA	2310					
QY 1761	ctaataagagcttaacagcctatgtgtgtgtcgtcgtgtgtggaacgtcgtgacctgttgc	1820					
Db 2311	CTCACCCCTTTGCCGTGTCTGGGCAATTCTGTGAAGCCTTTGTCTGTGGGTGTATTATC	2370					
QY 1821	tggcaatttcacacacactgtatg--gaagtcagctgggggtatggctgtgtctctcatgtcg	1880					
Db 2371	AAGTCCCAACACACACCATTTGTCAAGGCCAACCAACGAGAGCTCTCTACTCTCTCTC	2430					
QY 1881	ggtctccctggggccgggaagttgacgctctcatagcttcttcggggaaacccaagtgccc	1940					
Db 2431	TTTCCCTGTGTGTGTCTTCAAGCTCCCTGTCTCTCATGGGGAGCCCCAGGACTGG	2490					
QY 1941	ggctgctgtgcgtgtcaacccctcttctctcgggtttgcatctctctcctcctgctg	2000					
Db 2491	ACGTGCCCTCTGGCGACACCGGCTTTGGATTCAGCTCTGTGTGTGTGTGTGTGTGTGT	2550					
QY 2001	acaatcgcctctcccaactgttcaatcattcaagttttctacaaggtgcacatc	2060					
Db 2551	CTGTGGAAMACCAACCGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2607					
QY 2061	tacgttacctgtgcccacaacacatgtgtcaggtctatctgtatgtgtgtgtgtgtgtgt	2120					
Db 2608	CACCGCAAGTGTGTGGGGCTCAACTGTCAATTTCTGTGTGTGTGTGTGTGTGTGTGT	2667					
QY 2121	catgtgtcatctgtctcacaatgtgtgttaatgttgaccccaagacccaacgggaatac	2180					
Db 2668	CAGATTGTATCTGT	2727					
QY 2181	cagcgctcccccaactctgtgtatctgtgaagtcagaaggggttcaactctgttagctctcg	2240					
Db 2728	GAGCTGAGGATGAAATATTTTATTCATCAGTCCAGGAGGCTCTCCATGAGCCCTGGGC	2787					
QY 2241	ttggttttcaccaacaacatctctctctcacaatgaatctatgtgtgtgtgtgtgtgtgt	2300					
Db 2788	TTCTCGATCGGCTACACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2847					
QY 2301	aaggaactgcaagagaactataatgaagccaatgtgtcatccttcaagctgtgctctaac	2360					
Db 2848	CGGAAGCTGCGGAGAACTTCAATTAACCAAGATTCATCACTTACAGATGCTCAATCTTC	2907					
QY 2361	tttgatctctctc--cgctcttcttcaacatgtgcaagca--ttccaggggagcttactgct	2420					
Db 2908	TTTATCGCTGT	2967					
QY 2421	ggcgtaaatgt	2480					
Db 2968	GCCGTAAGAGT	3027					
QY 2481	cccaaggtctatgt--gtatctctgtccgtccagaatcaacaatacaga	2527					
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1      RESULT 3
2      US-08-480-751-2
3      Sequence 2, Application US/08480751
4      Patent No. 5858684
5      GENERAL INFORMATION:
6      APPLICANT: Edward F. Nemeth
7      APPLICANT: Edward M. Brown
8      APPLICANT: Steven C. Hebert
9      APPLICANT: Forrest H. Fuller
10     APPLICANT: James E. Garrett, Jr.
11     TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
12     TITLE OF INVENTION: MOLECULES
13     NUMBER OF SEQUENCES: 20
14     CORRESPONDENCE ADDRESS:
15     ADDRESSEE: Lyon & Lyon
16     STREET: First Interstate World Center
17     STREET: Suite 4700
18     STREET: 633 West Fifth Street
19     CITY: Los Angeles
20     STATE: California
21     COUNTRY: USA
22     ZIP: 90071
23     COMPUTER READABLE FORM:
24     MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
25     COMPUTER: IBM PC compatible
26     OPERATING SYSTEM: PC-DOS/MS-DOS
27     SOFTWARE: FASTSEQ
28     CURRENT APPLICATION DATA:
29     APPLICATION NUMBER: US/08/480,751
30     FILING DATE: 7 June, 1995
31     CLASSIFICATION: 435
32     PRIOR APPLICATION DATA:
33     PRIOR APPLICATION DATA: including application
34     PRIOR APPLICATION DATA: described below: 9
35     APPLICATION NUMBER: 08/353,784
36     FILING DATE: 9 December, 1994
37     APPLICATION NUMBER: PCF/US/94/12117
38     FILING DATE: 21 October, 1994
39     APPLICATION NUMBER: U.S. 08/292,827
40     FILING DATE: 23 August, 1994
41     APPLICATION NUMBER: U.S. 08/141,248
42     FILING DATE: 22 October, 1993
43     APPLICATION NUMBER: U.S. 08/009,389
44     FILING DATE: 23 February, 1993
45     APPLICATION NUMBER: U.S. 08/017,127
46     FILING DATE: 12 February, 1993
47     APPLICATION NUMBER: U.S. 07/934,161
48     FILING DATE: 21 August, 1992
49     APPLICATION NUMBER: U.S. 07/834,044
50     FILING DATE: 11 February, 1993
51     APPLICATION NUMBER: U.S. 07/749,451
52     FILING DATE: 23 August, 1991
53     ATTORNEY/AGENT INFORMATION:
54     NAME: Hebert, Sheldon O.
55     REGISTRATION NUMBER: 38,179
56     REFERENCE/DOCKET NUMBER: 213/004
57     TELECOMMUNICATION INFORMATION:
58     TELEPHONE: (213) 489-1600
59     TELEFAX: (213) 955-0440
60     TELEX: 67-3510
61     INFORMATION FOR SEQ ID NO: 2:
62     SEQUENCE CHARACTERISTICS:
63     LENGTH: 5006 base pairs
64     TYPE: nucleic acid
65     STRANDEDNESS: single
66     TOPOLOGY: linear
67     MOLECULE TYPE: cDNA to mRNA
68     FEATURE:
69     NAME/KEY: CDS
70     LOCATION: 436..3699
71     OTHER INFORMATION:
72     US-08-480-751-2

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				Indels	6;
				Gaps	2
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DB	2668	CAGATTGTATCTGT		2727	
QY	2181	caggtctcccccactgt		2240	
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QY	2421	gcgtgtcaatgt		2480	
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DB	3028	AACCAAGTTCATCATCTTCTTCAAGCATCCGCCCAACCATCATGA	3074		


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14 RESULT
15 US-08-943-986-2
16 Sequence 2, Application US/08943986
17 Patent No. 5962314
18 GENERAL INFORMATION:
19 APPLICANT: Edward M. Brown
20 APPLICANT: Steven C. Hebert
21 APPLICANT: James E. Garrett, Jr.
22 TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
23 TITLE OF INVENTION: MOLECULES
24 NUMBER OF SEQUENCES: 20
25 CORRESPONDENCE ADDRESS:
26 ADDRESSEE: Lyon & Lyon
27 STREET: First Interstate World Center
28 STREET: Suite 4700
29 STREET: 633 West Fifth Street
30 CITY: Los Angeles
31 STATE: California
32 COUNTRY: USA
33 ZIP: 90071
34 COMPUTER READABLE FORM:
35 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
36 COMPUTER: IBM PC compatible
37 OPERATING SYSTEM: PC-DOS/MS-DOS
38 SOFTWARE: FASTSO
39 CURRENT APPLICATION DATA:
40 APPLICATION NUMBER: US/08/943,986
41 FILING DATE: 03-OCT-1997
42 CLASSIFICATION: 530
43 PRIOR APPLICATION DATA:
44 APPLICATION NUMBER: 08/484,565
45 FILING DATE: 7-June-1995
46 APPLICATION NUMBER: 08/353,784
47 FILING DATE: 9 December, 1994
48 APPLICATION NUMBER: PCT/US/94/12117
49 FILING DATE: 21 October, 1994
50 APPLICATION NUMBER: U.S. 08/292,827
51 FILING DATE: 23 August, 1994
52 APPLICATION NUMBER: U.S. 08/141,248
53 FILING DATE: 22 October, 1993
54 APPLICATION NUMBER: U.S. 08/009,389
55 FILING DATE: 23 February, 1993
56 APPLICATION NUMBER: U.S. 08/017,127
57 FILING DATE: 12 February, 1993
58 APPLICATION NUMBER: U.S. 07/934,161
59 FILING DATE: 21 August, 1992
60 APPLICATION NUMBER: U.S. 07/834,044
61 FILING DATE: 11 February, 1992
62 APPLICATION NUMBER: U.S. 07/749,451
63 FILING DATE: 23 August, 1991
64 ATTORNEY/AGENT INFORMATION:
65 NAME: Heber, Sheldon O.
66 REGISTRATION NUMBER: 38,179
67 REFERENCE/DOCKET NUMBER: 213/006
68 TELECOMMUNICATION INFORMATION:
69 TELEPHONE: (213) 486-1600
70 TELEFAX: (213) 955-0440
71 TELEX: 67-3510
72 INFORMATION FOR SEQ ID NO: 2:
73 SEQUENCE CHARACTERISTICS:
74 LENGTH: 5005 base pairs
75 TYPE: nucleic acid
76 STRANDEDNESS: single
77 TOPOLOGY: linear
78 MOLECULE TYPE: cDNA to mRNA
79 FEATURE:
80 NAME/KEY: CDS
81 LOCATION: 435..3699
82 OTHER INFORMATION:
83 US-08-943-986-2

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Query Match	5.1%	Score 170.2	DB 4	Length 5006
Best Local Similarity	49.5%	Pred. No 4.1e-35		
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Db	2071	CAGGTGCCCTTCTCAACTGACAGCGAGACACTCCTGGCAGGGACCAAGAAAGATCAT	2130	
QY	1581	gtgggttcccaacactgctgcttttagtggtgtgccctcgaaagctgggaacctttcaac	1640	
Db	2131	GAGGGGGAGACCACCTGCTGTGTTAGTGTGGAGTGTCTGAAGGGGAGATATGTAT	2190	
QY	1641	atgagtgagcttcaatcctgcagccgctgttgaaacagaagaaatgggcaaccaaagagaagc	1700	
Db	2191	GAGACAGATGCCAGAGCGCTGTACACAAAGTCCCAAGATGACTTGTGTTCCATATGAAACCA	2250	
QY	1701	actactgtcttccacagcaaggtaggaattcttgcttggcatgaaaccaatctcttggtg	1760	
Db	2251	ACCTCTGATGTGCCAAGAGATCCAGATTCTGTGTGGACGAGACCCCTTGGATGCGA	2310	
QY	1761	ctaataagacgtcaaacagcgtatgttgtctgcgtcggtttggagcgtcgscgtgttgcc	1820	
Db	2311	CTACCCCTCTTTGCCGTGTGGGCAATTTTCGACAGCCTTTGTCTGGGTGTGTTATC	2370	
QY	1821	tggcaatttcacacacccctgtagtgagtgacagcttgagggttagctgtgtcttcatactg	1880	
Db	2371	AGTTTCGGCAACACACCCTATGTCAAGGCCAACACACGACAGACTCTCGTACCTCTCTC	2430	
QY	1881	ggcttccctcggcgcccggaagttgcagctctctataagctctcttgaggagaccaggtgcc	1940	
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QY	2301	aaggaaactgccaagaaactataataaagccaatgtgtcaaccttcaagctgtctcacaac	2360	
Db	2848	CGAAGCTGTCCGGAACACTTCATTAAGCGCAAGTTTCATCACTCTTCAAGCATGCTCATCTC	2907	
QY	2361	tctgatactgtatgtgcttcttcaacatgacagcatattacaaggaagctactgctt	2420	
Db	2908	TTCATCTGTGTGATGTCTCTTCATTCACAGCTTATGCGAGCACTATAGGCAAGTTGTCTT	2967	
QY	2421	ggcgtaaatgtcttgcaagggcttgacacaactgaagcggcggtcttaagcgttatctctc	2480	
Db	2968	GCGGTAAAGAGTATTTGCCATCCTGGCAGCGACACTTTGGGTTGCTGTGGCGATCTTCTTC	3027	
QY	2481	cccaagtgtatgtatctctcgccgtccagaactccaacaatacaga 2527		
Db	3028	AACAAGATCTACATCATTTCTTCAAGCATCCCAACACACCATGA 3074		


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Best Local Similarity	49.58;	Pred. No. 4.1e-35;					
Matches 498;	Conservative	0;	Mismatches 503;	Indels	6;	Gaps	2

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OY	1641	atgagtgaagcttcaactctgtccagcctcttgaaacagaagaatgtggacccaagagagac	1700
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Db	2251	ACCTCCCTGCATTTGCCAAGAGATCGAGTTGTGTGTGACGAGACCTTTTGGGATCGCA	2310
OY	1761	ctaatagcagctaacaacgctatgtcgtcgtcgtcgtgtgtggaactgtcgccgttgcc	1820
Db	2311	CTCACCTCTTTCCTCGGCTCGGCGGAGCATTTTCTTGACAGCCTTTGTGCTGGGTGTATTC	2370
OY	1821	tggagatttcacacactgtagtgagtgtaagcttgggggtgaagctgtgcttcctaatgtg	1880
Db	2371	AAGTTCGCAACACACCCATGTCAAGGGCACCAACCGAGAGCTCTCTTACTCTCTCTC	2430
OY	1881	gtttcccttggtagcggaagtgtgcaactctataagctcttcctggaggaaccagtgccc	1940
Db	2431	TTTCTCCCTGCTGCTGCTCTTCCACTCCCGTCTTCTCATGGGGAGACCCCAAGACATGG	2490
OY	1941	gcgtgtctgtcgtcgtcaagcccctctcttctctcgttggttgcaatctctctcgtcgt	2000
Db	2491	ACGTCGCCGCTGTGGCGACGCGGCTTTGGCATCAGTTTGCTCTGATCATATGCATC	2550
OY	2001	acaatccgctcccttccaacgctgcatcacctcctaagttcttcaacaagtgcccaatc	2060
Db	2551	CTGCTGAAMACCAACGCTGTCTCTCTGTGTTTGAAG--CCAGAATCCCAACACGCTTC	2607
OY	2061	taccgtaccgtggcccccaaaaacatagtgtgaagctctatctgcatactgtcagctccag	2120
Db	2608	CACGCGAAGTGGTGGGGGCTCAACACGATTCGATTCGCTGTTCTCTGCACTTCAATG	2667
OY	2121	catctgctcatctgtctacatgctcttg--aatgtgagcccaacgaaccacaagggaataac	2180
Db	2668	CAGATTGTCACTGTGTGATCTGCTGACTGCTACACGGGCCCCCTCAAGTATACGCAACAG	2727
OY	2181	cagagctcccccacatcgtgagatcttcgagtgcaagaagatcaactctgtatgagctctc	2240
Db	2728	GAGCTGAGAGATGATGATCATCTTCACTACGTGCACAGAGGGCTCCCTCATGCTTGCC	2787
OY	2241	ttagcttaccacacacaacatctctctctccatcaatgatactctgtctgagctaac	2300
Db	2788	TTCTGATGGGCTAACACGCTCCGTGCTGGCTGCACATCTGCTTCTTGGCTTCAAGTCC	2847
OY	2301	aagaaactcccaagagaactataatgaagccaaatgtgtactcttaagcctgctctcaac	2360
Db	2848	CGGAGAGTGGCGGAGAACTTCAATGAAGCCAAAGTTATATACCTTAGATGCTCATCTTC	2907
OY	2361	tctgatacccgagatgcctctcttccacacatgagccagcatcttaacaggagagctactg	2420
Db	2908	TTTCTGCTGTGATCTTCTTCTTCACTTCAAGCTTATGCCAGACCTATGGCAAGTTGTCTCT	2967
OY	2421	gcggatcaatgtgtcgtgcaaggcttgacaacacatgagccgagcttcaagcgttactctc	2480
Db	2968	GCGCTAAGGTGATGTGCATCTCGGACGACAGCTTTGGCTTCTGCTGGCTGCATCTTCTTC	3027
OY	2481	cccaagtgtcatgtgattctctgcgtccagaactccaacaatacaga	2527
Db	3028	AACAAATCTACATCATCTTCTTCAAGCTCCATCCGCAACACATCATGA	3074

• Sun Mar 26 09:26:19 2000

us-09-361-652-4.mri

Page 17

Search completed: March 19, 2000, 18:06:40
Job time: 1199 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2000, 18:09:57 ; Search time 185.6 Seconds
(without alignments)
3735.357 Million cell updates/sec

Title: US-09-361-652-4
Perfect score: 2771
Sequence: 1 attcaccatcagacgtgtgct.....aaaaaaaaaaaaaaaaaaaaa 2771

Scoring table: IDENTITY_NUC

Searched: 31185 seqs, 125096042 residues

Database: N_Geneseq_36:*

Word size: 0

Number of hits that pass the threshold: 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	181.6	6.6	3809	1	T61382	Parathyroid calcitri
2	181.6	6.6	3809	1	T95859	Human parathyroid
3	181.6	6.6	3809	1	V26964	Human parathyroid
4	181.6	6.6	3809	1	V82485	Human parathyroid
5	176.4	6.4	5275	1	T95857	Bovine parathyroid
6	176.4	6.4	5275	1	V26962	Bovine parathyroid
7	176.4	6.4	5275	1	V82483	Bovine parathyroid
8	170.2	6.1	5006	1	T61381	Parathyroid calcitri
9	170.2	6.1	5006	1	T95858	Human parathyroid
10	170.2	6.1	5006	1	V26963	Human parathyroid
11	170.2	6.1	5006	1	V82484	Human parathyroid
12	160.6	5.8	4131	1	T95860	Rat kidney cell ca
13	160.6	5.8	4131	1	V26965	Rat kidney calcium
14	160.6	5.8	4131	1	V82486	Rat parathyroid ca
15	154	5.6	4131	1	T89290	Dogfish shark kidn
16	138.2	5.0	3384	1	T86165	Nucleotide sequenc
17	137	4.9	4000	1	T86166	Nucleotide sequenc
18	113	4.1	2148	1	Q73222	BoPCAR 1, bovine p
19	87.4	3.2	2561	1	X05808	Mouse pteromone re
20	86.6	3.1	2821	1	X05812	Mouse pteromone re
21	85	3.1	3080	1	X05801	Mouse pteromone re
22	85	3.1	2550	1	X05840	Mouse pteromone re
23	84	3.0	2907	1	X05803	Mouse pteromone re
24	84	3.0	2409	1	X05842	Mouse pteromone re
25	81.6	2.9	2732	1	X05810	Mouse pteromone re
26	81.6	2.9	2962	1	X05811	Mouse pteromone re
27	78.2	2.8	1644	1	X05856	Rat pteromone rece
28	78.2	2.8	2811	1	X05817	Rat pteromone rece
29	73.6	2.7	2961	1	X05802	Mouse pteromone re
30	73.6	2.7	2434	1	X05841	Mouse pteromone re
31	73.2	2.6	3919	1	O80418	Human mglur3 DNA.
32	73.2	2.6	3410	1	T03887	Human mglur3 DNA.
33	73.2	2.6	3108	1	X05814	Mouse pteromone re
34	73.2	2.6	2412	1	X05853	Mouse pteromone re
35	71	2.6	2618	1	T16710	Metabotropic gluta
36	71	2.6	2619	1	T29408	Human metabotropic
37	71	2.6	2734	1	X05809	Mouse pteromone re
38	71	2.6	2773	1	X05813	Mouse pteromone re
39	70	2.5	3689	1	X05815	Mouse pteromone re

ALIGNMENTS

40	69.2	2.5	1889	1	X05807	Mouse pteromone re
41	69.2	2.5	1889	1	X05846	Mouse pteromone re
42	68.6	2.5	3125	1	X05805	Mouse pteromone re
43	68.6	2.5	2169	1	X05844	Mouse pteromone re
44	67.8	2.4	4085	1	O80419	Human mglur5a cDNA
45	67.8	2.4	4181	1	O80420	Human mglur5b cDNA

RESULT 1
T61382
ID T61382 standard; cDNA to mRNA; 3809 BP.

AC T61382;
DE 22-APR-1997 (first entry)
KW Parathyroid calcium receptor coding sequence clone pRupCAR4.0.
KW Calcium receptor; human parathyroid gland adenoma tumour; pRupCAR1;
KW primary hyperparathyroidism; Xenopus oocyte; alternative splicing;
KW calcium-activated chloride current; agonist; NPS R-467; NPS R-568;
KW variant; untranslated region; alternative polyadenylation; probe;
KW alternative transcription initiation; pRupCAR5.2; pRupCAR4.0;
KW human Car gene; isoform; ss.
OS Homo sapiens.
FH Key
FT cds
FT 373..3609
FT Location/Qualifiers
FT /*tag= a
FT /product= Calcium receptor
FT /note= "Pages 94-95 are missing from the specification,
sequence information was obtained from the EPO"

MO9612697-A2.
PD 02-MAY-1996.
PF 23-OCT-1995; U13704.
PR 21-OCT-1994; WO-U12117.
PR 08-DEC-1994; US-353784.
PI (NPS-) NPS PHARM INC.
PI Balandrin MF, Delmar EG, Moe ST, Nemeth EF, Van Wagenen BC,
DR WPI; 96-230520/23.
DR P-PDB; M1889.

PT New di-arylalkyl amine cpds. useful for modulating inorganic ion
PT receptor activities - esp. for modulating effect of extracellular
PT calcium on cell surface calcium receptors, useful for treating e.g.
PT hyperparathyroidism, Paget's disease or osteoporosis
PS Example 1: Page 93-100; 231pp; English.
CC The sequences given in T61381-82 encode functional calcium receptors.
CC These sequences were isolated from human parathyroid gland adenoma
CC tumour using pRupCAR1 as a hybridisation probe. mRNA was isolated from
CC a 39 year old caucasian male diagnosed with primary hyperparathyroidism
CC and two clones of approx. 5 and 4 kb were identified. These cDNA's were
CC injected into Xenopus oocytes which were assayed for the presence of
CC functional calcium receptors. Both clone types gave rise to functional
CC calcium receptors as assessed by the stimulation of calcium-activated
CC chloride currents upon addition of appropriate calcium receptor agonists,
CC e.g. NPS R-467 and NPS R-568. Sequence analysis of the two cDNA clones
CC indicated the existence of at least two sequence variants differing in
CC the 3' untranslated region and which may result from alternative
CC polyadenylation. Sequence variation also exists in the 5' end of the
CC inserts. These sequence differences may have arisen due to alternative
CC transcription initiation and/or splicing. Three additional sites of
CC sequence variation occur within the coding regions of cDNA clones
CC pRupCAR5.2 and pRupCAR4.0 demonstrating that they encode distinct
CC proteins. Sequence analysis of the human Car gene indicates that the
CC additional 30 bp in clone pRupCAR5.2 as compared to pRupCAR4.0, results
CC from alternative mRNA splicing. This alternative splicing is predicted
CC to insert 10 additional amino acids into the Car protein encoded by
CC pRupCAR5.2 between residues 536 and 537 of the protein encoded by
CC pRupCAR4.0. In addition pRupCAR4.0 encodes Gln at position 925 and Gly
CC at position 990, whereas pRupCAR5.2 encodes Arg at both equivalent
CC positions. The human Car gene encodes for Gln and Arg respectively at
CC these positions. These two receptor isoforms may be functionally and/or
CC pharmacologically distinct.
SQ Sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T;

Query Match	6.68;	Score 181.6;	DB 1;	Length 3809;
Best Local Similarity	49.68;	Pred. No. 4.1e-35;		
Matches 522;	Conservative	0;	Mismatches 524;	Indels 6;
				Gaps 2;

QY	1479	ctggacaaataaagacaaaataacacagctgacagggaaagaacaaatcaggtgctgctgctgca	1578
Db	1933	CTCTTTCATCAACGAGGAGAAAATCTCTGTGGAGTGGGTTTCCAGGGAGAGTGCCCTTCTCC	1992
QY	1539	gtgtgtacacacagagctgtctgtgcagaggcaac--caagaggtgtgtgtgtgtgtgtgtgtgt	1595
Db	1993	AACTCGACGGAGACTGCTGTGCAGGGAGACCAGAAAGGATCATTTGAGGGGAGGCCACCC	2052
QY	1596	tgctgcctttgagtggt	1655
Db	2053	TGCTGCTTTAGAGTGTGGAGTGTCTGTGAGGGGAGTAAGTGAAGAGACAGATCCAGT	2112
QY	1656	atctgcacagcctttgtgaaacagaagaatgtggaccccaagagagagcaactgtgtgtgtgtgt	1715
Db	2113	GCCGTATCAACAGTGCCCAAGATGACTTCTGTGTCCAAAGAAACACACCTCTGCTATTGCC	2172
QY	1716	cgaacagtgagagttctgtgcttgtgcattgaaccatctcttgtgtgtataagcagctaac	1775
Db	2173	AAGAGATATCAGATTCTGTGTGTGAAGAGAGCCCTTGGATGTGCACCTACCTCTTTTGGC	2232
QY	1776	agcgtattgt	1835
Db	2233	GTGTGTGGGCAATTTCCGACAGACGCTTTGTGTGGGTGTGTATTAAGTTCGGACACCA	2292
QY	1836	cctgtatgtgagtgtaagctgtgggttaagcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	1895
Db	2293	CCCATGTCAAGGGCACCAACGAGAGCTCTCTACTCTCTCTTCTCTCTCTCTCTCTCTCTCT	2352
QY	1896	ggaaagttgcagctctctatagctctcttcctgcgggagccacagtgccggtgtgtgtgtgtgt	1955
Db	2353	TGCTTTCACAGCTCCCGTTCCTTATCCGGGAGAGCCCAAGATGGAGCTGCGCGCTGTGCG	2412
QY	1956	cagcgcctcttttctctcgcgggtgtgtgcacctctctctctctgtgtgtgtgtgtgtgtgtgt	2015
Db	2413	CAGCGGCGCTTTGGCATCACTCTGTGTCTGTGATCTATGATCTCTGTGTGTAACCAAC	2472
QY	2016	caactgtgtcatcattctcaagctttcttaccagaagtggtccacacttaccgttaccgtgtgtgt	2075
Db	2473	CGTGTCTCTCGTGGTGTGAG--GCCAAGATCCACACAGCTTCCACGCAAGAGTGGG	2529
QY	2076	caaaacatgtgtgcaggtctatctgtcatctgtcatgttcaggtctcaaggtctcatgtctcatgt	2135
Db	2530	GGGCTCAACCTGCAGTTCCTGTGGTGTTCCTCTGTGCACCTTCATCAATTTGATCTGT	2589
QY	2136	ctcacatgtgtcttaatgtgtgaccaccaagccacacaggaataaccagcttctcccat	2195
Db	2590	GTGATCTGGGTCTACACCGCGGCCCTCTCAAGCTACCGCAACBAGBAGCTGGAGATGAG	2649
QY	2196	ctgtgtatctctgagtgacagagtgcaagtgcaactgtatagcttctgtgtgtgtgtgtgtgtgt	2255
Db	2650	ATCATCTTTCATACGTCGACGAGGGGCTCCCTCATAGGCCCTGGGCTTCTGATGTGGCTAC	2709
QY	2256	aaactctctctccatcagtaagtaactctcgtctcgtcagctactactgtgtgaaagaaatgcagag	2315
Db	2710	ACCTGCTGTGTGCTGCCATCTCTCTTCTTGTGCTTCAATCCCGGAACCTGTGCGGAG	2769
QY	2316	aaactataatgaacaaatgtgtcaccttcacgtctgtcctcaacttgatctgtctgtgtgtgt	2375
Db	2770	AACCTCAATGAAGCCAAAGTTCATCACCTTCACAGATGCTATCTTTTATGTGTGTGTGATC	2829
QY	2376	gccttcttccacatggtgcagcaatttaccagggcaggtactcgtcgtgtgtgtgtgtgtgtgtgt	2435
Db	2830	TCTCTTCACTTCCAGCCATATGCCACACACTATGCAAGATTGTCTGTGCGGTGAGGTGATT	2889
QY	2436	gcagaggtgtgcacacatcgtgagcggcgtcttcacggttacttctctcccaatgtctatgtgt	2495
Db	2880	GCCATCTGTGGACAGCTTTGGCTGTGTGCGGTGTGATCTTTTCAACAAATCTCATATC	2949

QY 2496 attctctgcgcgtccagaactcaacatacaga 2527
 ||||| | ||| | ||| | ||
 Db 2950 ATTCTTCAAGCCATCCCGCAACACCATCGA 2981

Query Match	Best Local Similarity	Matches	522: Conservative	0: Mismatches	524: Indels	6: Gaps
1479	ctgagcataaataagacacaaatccagtcggcagggagaagaacatcaggtgctgtgca	1538	1993	CTCTTCAATCAACGAGAGAAAATCTCTGTGAGTGGGCTCTCCAGGAGAGTGCCTTCTCC	1992	
QY	1539	gtgtgtacacagcagtcgtctgacagggac--cacaggtgtgtgtgtgtgtgtccacac	1595	1993	AACATGACACCGAGACTGCTGCGACAGGACACGAAAGGATCATTTGAGGGGAGCCACAC	2052
QY	1596	tgt	1655	2053	TGCTGCTTTGAGTGTGTGAGATGTCTGATGGGGAGTATGATGAGACAGCATGCCACT	2112
QY	1656	atcttcacagccttggagacagagaagatgggacaccccaagagagagactactgttccca	1715	2113	GCTGTATTAACAGTGGCCGACGATGACTTCTGTGTTCCATGTAGGAAACACACCTCTGCAATGGC	2172
QY	1716	cgcacagtgagatcttctgt	1775			

[illegible]

	PR	11-FEB-1992:	US-834044.	
	PR	21-AUG-1992:	US-934161.	
	PR	12-FEB-1993:	US-017127.	
	PR	23-FEB-1993:	US-009389.	
	PR	22-OCT-1993:	US-141248.	
	PR	19-AUG-1994:	US-292827.	
	PR	21-OCT-1994:	WO-012117.	
	PR	08-DEC-1994:	US-353784.	
	PA	(BGHM) BRIGHAM & WOMENS HOSPITAL.		
	PA	(NPSP-) NPS PHARM INC.		
	PI	Brown EM, Garrett JE, Hebert SC;		
	DR	MPJ: 98-347412/30.		
	DR	P-PDSB; W54846.		
	PT	Calcium receptor polypeptide(s) - useful for drug screening or		
	PT	antibody production		
	PS	Example 27: Fig 49: 174pp: English.		
	CC	The human parathyroid calcium receptor gene encodes a 1078 amino acid		
	CC	protein. The tissue from which the receptor and receptors from bovine		
	CC	parathyroid and rat kidney are derived, respond to changes, and control		
	CC	changes, in calcium ion concentration, e.g. parathyroid hormone regulates		
	CC	Ca2+ homeostasis in blood and extracellular fluid, and kidney function		
	CC	alters through changes in Ca2+ levels in juxtaglomerular and proximal		
	CC	tubule cells in the kidney. The purified receptors (produced		
	CC	recombinantly) can be used to screen for compounds that modulate calcium		
	CC	receptor activity, especially those that can be used to treat diseases		
	CC	associated with the receptors in these tissues. They can also be used		
	CC	to raise antibodies for use in detection assays.		
SQ	Sequence	3809 BP; 910 A; 1071 C; 979 G; 849 T;		
	Query Match	6.6%; Score 181.6; DB 1; Length 3809;		
	Best Local Similarity	49.6%; Pred. No. 4,le-35;		
	Matches 522; Conservative	0; Mismatches 524; Indels	6; Gaps	2
QY	1479	ctggacataatagaagcaaaatccacgtygcaccggygaagaacaatcaggtgccgtgtca	1538	
Db	1933	ctcttcattcacagaggagaaaatccgttgactgggttctccaggagagtccctttccc	1992	
QY	1539	gtggtaccacggaacctctggcagaagac--cacagggttgtgtgtgttccaccac	1595	
Db	1993	aactgcagcgcgaactgcctggcagsgaccagaaaggatcatitgaaggsgagaccac	2052	
QY	1596	tgcgtcttgagtggtctccctcgcaagcttggaaccttctcaaatagtgaacttaac	1655	
Db	2053	tgctgctttgagtggtgagtgctcctgatgggagcgtatgatatgacacagatgscagt	2112	
QY	1656	atctgcacagctctgtcgacaagaagaatgagacccaagagagacactactgtctcca	1715	
Db	2113	gccctgtaacagagccccaatgacttctgtgtccaatgagAACACACTCCTGATTTGCC	2172	
QY	1716	cgcacagtgtagctctgtgcttgacatgaaccaactctcttggtgtctaataagagctaac	1775	
Db	2233	gtgtgtggcattttcctgacacagcctttgtgctgggtgtgttatcagatttcggaacaca	2292	
QY	1776	acgctatctgcgtgtcgtctgtgtggaactgtgccttgctgccttgatcttacaca	1835	
Db	2173	AAGGAGATCGAGTGTTCGTGCTGGACGGACCCTTTGGGATCGCACTCACCTCTTTGCC	2232	
QY	1836	cctgtagtagaggtcagcctggtgggtatgagctgtctctcatgctgtggttccctgtgccc	1895	
Db	2293	CCCATTGTCAAAGGCCACCAACGAGAGCTCTCTAACCCTCCTCTCTCTCTCTGC	2352	
QY	1896	ggaagtgcagcgtctcatagctctctctggggggcccaagcgtgcccaggtgtgtctcgt	1955	
Db	2353	TGCTTTCACAGCTCCTCTGTTCTTCATCGGGGA6CCCACAGAGTGAGAGCTGCGCCTTCGC	2412	
QY	1956	cagccccctcttctctcgtggttccacactctctctctcctcgtgaacaatccgtctctc	2015	
Db	2413	CAGCGGCGCTTTGGCATACAGCTTCGCGCTCTGCATCTATGCACTCTTGTAATAAACCAAC	2472	
QY	2016	caactgtcatcatcttcaagttttctaaccaaggtgccacaattcaacgttacctggccc	2075	
Db	2473	CGTGCTCCTCTGGTGTGTTAG--GCCAAGAATCCCCACACACTTTCACCGCAAGTGTGG	2529	

QY	2076	caaacacatgctgaagctctatctccatctgcatgacgtcccaagctcatctgctatctgt	2135
Db	2530	GGGCTCACTGCAGTTCCTCGTGGTTTTCCTGCACTTATGACATGTTATCTCTGT	2589
QY	2136	ctcacatgactgttaatgctgagaccaccaagccaccagaagaaataccagcgcttcccac	2195
Db	2590	GTGATCTGGCTCTACACCGGGCCCCCTCAAGCTACCGCAACCAAGAGAGCTGGAGATAG	2649
QY	2196	ctggctgctctcgagctgcaaaagggccaactcctgtatgcttccgtcttgcgttccaccac	2255
Db	2650	ATCATCTTCAATCAAGTCCACGAGGGCTCCCTCATGGCCCTGGGTCCTGTATCGCTAC	2709
QY	2256	aacatctccctccatcactgataactctgctctgctgacgttaccgtgtaagaaatgccagag	2315
Db	2710	ACCTGCTGGTGGGTGCATCTCTCTCTCTCTTTCCTTTCCTTAATCCCGAAGTGGCGGAG	2769
QY	2316	aactaataatgaagcaaaatgctgtaaccttcacgtccacgtctccctcaactctgtaacctgta	2375
Db	2770	AACCTCATATGAAGCAAGTTCATCACTTCCTCAGATGCTCATCTTCTCATCGTCTGATAC	2829
QY	2376	gacctcttcacatgagccagcattaccagggcagagcttaccctctcggcggttaatgctgt	2435
Db	2830	TCCCTTCTCCAGCCTATGCCACACACCTTAGGCAGATTGTCTTGCCGTAGAGGTGATT	2889
QY	2436	gcagaggtctgacacacactgagcgcggtcttcacagcggttactctccccaagtctgctg	2495
Db	2890	GCCATCTGTGGCAGACACACTTGGCTGTGGGTGGGTGATCTTCTTCAACAAAGATCTTACATC	2949
QY	2496	attctctgcgcgttcagacacccaatactagca	2527
Db	2950	ATTCTCTTCAAGCATCCGCAACACCATCGA	2981

AC	ID	VS2485	standard; cDNA to mRNA; 3809 BP.
DT	19-MAR-1999	(first entry)	
DE	Human parathyroid calcium receptor PhupCar 4.0 encoding cDNA.		
KW	Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;		
KW	calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;		
KW	spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;		
KW	neonatal distress; neurodegenerative disease; Alzheimer's disease;		
KW	Huntington's disease; Parkinson's disease; dementia; muscle tension;		
KW	depression; anxiety; ss.		
OS	Homo sapiens.		
FN	Key	Location/Qualifiers	
FT	CDS	373..3609	
FT		/tag= a	
PN	US5856684-A.		
PD	12-JAN-1999.		
PF	07-JUN-1995; 480751.		
PR	07-JUN-1995; US-480751.		
PR	23-AUG-1991; US-749451.		
PR	11-FEB-1992; US-834044.		
PR	21-AUG-1992; US-934161.		
PR	12-FEB-1993; US-017127.		
PR	23-FEB-1993; US-009389.		
PR	22-OCT-1993; US-141248.		
PR	19-AUG-1994; US-282827.		
PR	21-OCT-1994; WO-012117.		
PR	08-DEC-1994; US-353784.		
PA	(BGM) BRIGHAM & WOMEN'S HOSPITAL.		
PA	(NPSP-) NPS PHARM INC.		
PI	Balandin MF, Brown EM, Del Mar EG, Garrett JE,		
PI	Hebert SC, Nemeth EF, Van Wagenen BC;		
DR	WPI; 99-119871/10.		
DR	P-PSDB; W89565.		
PT	Screening for calcium receptor-active compounds - by recombinant		
PT	expression of nucleic acid encoding calcium receptor and determining		
PT	the effect of compounds on calcium receptor activity		
US	Claim 1; Fig 49; 176pp; Engl15h		

A method has been developed of screening for a compound able to affect one or more activities of a calcium receptor (CR) comprising: (A) contacting a recombinant cell with a test compound, where the recombinant cell comprises a recombinant nucleic acid expressing the CR, provided that the cell does not have functional CR expression from endogenous nucleic acid; (B) determining the ability of the test compound to affect one or more activities of the calcium receptor; and (C) comparing the ability with the ability of the test compound to affect the one or more CR activities in a cell not comprising the recombinant nucleic acid. The present sequence encodes human parathyroid CR, designated a pHPaCR 4.0. The nucleic acid sequence of pHPaCR 4.0 can be used as part of the recombinant nucleic acid in the method described above. The compounds identified can be used to treat diseases or disorders characterised by abnormal calcium homeostasis, e.g. hyperparathyroidism, osteoporosis and other bone and mineral-related disorders. They can also be used for the treatment of diseases and disorders associated with disrupted Ca2+ responses, e.g. seizures, stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in cardiac arrest or neonatal distress, epilepsy, neurodegenerative diseases such as Alzheimer's disease, Huntington's disease and Parkinson's disease, dementia, muscle tension, depression, and anxiety. Sequence 3809 BP, 910 A; 1071 C; 979 G; 849 T.

Query Match	6.6%;	Score 181.6;	DB 1;	Length 3809;
Best Local Similarity	49.6%;	Pred. No. 4.1e-35;		
Matches 522;	Conservative 0;	Mismatches 524;	Indels 6;	Gaps 2;

QY	1479	ctgagacataataagaacaaatccagctggcaccgggaagaacaacatcaagctgcgtgtca	1538
Db	1333	CTCTTCATCAACAGGAGGAAATCCCTGTGGATGGGTTCTCCAGGAGGTCCCTTCTCC	1992
QY	1539	gtgtgtacacaggaactgtctggccaaggac--caagagtggtgtgtgtgtcccaacc	1595
Db	1593	AACTCGACGCCGAGACACTGCTGGAGGAGCACAGAAAGGATCATGAGGGGAGCCACCC	2052
QY	1596	tgtcgtcttbaagtggtgtgcccgcgaagctgggaaccttccaaatagagtgagcttcac	1655
Db	2053	TGCTGCTTTAGTGTGTGGAGTGTCTCTGATGGGAGGTATTAGTATGATACAGATGCCAGT	2112
QY	1656	atctgcacagccttgttgaaacagaagaatlyggacccaagagagagacactgtgtccca	1715
Db	2113	GCTGTACACAGTGGCCCAATGACTCTGTGTCATATGAAACACACACTCTGCATTGGCC	2172
QY	1716	cgcagcgttgagcttcttggctcttgcgatgaaacacactctcttgggtctaatagcagctaac	1775
Db	2173	AAGGAGATCAGATTCTGTGCTGGACGGAGGCCCTTTGGAGTGCATCACCTCTTTGCC	2232
QY	1776	acgctatgtcgtcgtcgtctgtgttgggaactgcgtgcacgttctgtccatcttcaaca	1835
Db	2233	GTGCTGGGCAATTTCCTGACAGCCCTTTGTGCGGGTGTGTTATCAATTCGGACACACA	2292
QY	1836	ccctgtagtgaggtcagcgtcgtgggtagagctcgtgtctctccatcagctgtggtttccctgtggcc	1895
Db	2293	CCCATATGTCAAGGCCACACACGAGAGCCTCTCACTCTCTCTCTCTCTCTCTCTCTGCG	2352
QY	1896	ggaagttgcagcctctatagctctcttcggggagaccagcgtgcgcggctgtgttcgctgct	1955
Db	2353	TGCTTCTCCAGCTCCCTGTTCTTCATCGGGAGGCCACAGACTGAGACGTGCCGCTCGCC	2412
QY	1956	cagccccccttctctcgtgggttgcacatctctctctctcctcgtcgtgacatccgctcttc	2015
Db	2413	CAGCGGCGCTTTGGCATCAGCTTCGAGCTCTGCATCTCATGTGATCCTGTGTAACAAAC	2472
QY	2016	caactggtatcatctcttaagtttctcaacaaagtgcgcccaactctaacgtaacctggcc	2075
Db	2473	CGTGTCTCTCTGGTGTGTTAG--GCCAAGATCCCCACACTTCCACACCGGAAGTGGTG	2529
QY	2076	caaaacacatgctcaggtctatctgtcaattgtcagcctccagtcacattgtctatcgt	2135
Db	2530	GGGCTCAACCTGCAAGTTCCTGCTGTGTTTCCCTCTGACACTTCATGACAGATTGTATCTGT	2589
QY	2136	ctcacatggtcttgtaatgttgaaacccaagaccacacaggaataaccagcgtctccccat	2195

D	b	2590	GTGATCTGGCTCTACACGGCGCCCCCCTCTACAGTACCGACACAGAGAGCTGAGAGATGAG	2649
Q	y	2196	ctgagatctctcgaagtgacagagatcaactctgtaggctctcgtgttcacccac	2255
D	b	2650	ATCATCTTCATACAGTCTGCCACGAGGGGCTCCCTCATGGCCCTGGGCTTCCTGATCGGCTAC	2709
Q	y	2256	aacatctctctccatcaagtactctcgtctgtagtactctggtgaagaactgcgaag	2315
D	b	2710	ACTGCTGCTGGTGGCATCTCTCTCTCTTTTGCTTCAAGTCCCGGAGAGCTGCGGAG	2769
Q	y	2316	aactataatgaagccaatctgtcacctcaagcctctcctaactctgtacccgagtc	2375
D	b	2770	AACITTCATGAGCGCAAGTTCATCACCTTTCATGAGATGCTCATCTCTCATGCTCGATC	2829
Q	y	2376	gccttctccacatgagccacattaccagagcagctacgcctgcggtcaatgtctg	2435
D	b	2830	TCCITTCATTCAGAGCTATGGCACACACCTATGAGCAATTTGCTCTGCGCTAAGAGTGA	2889
Q	y	2436	gcgaagcgttcgacacacatgcagcgcgagcttcgaagcggttactctctcccaagtcagt	2495
D	b	2890	GCCATCTCTGGCAGCCACACTTTGGCTTGCTGCTGCGCTGATCTTCTTCAACAGATCTTACATC	2949
Q	y	2496	attctctgcctccagagaactcaacaalacaga	2527
D	b	2950	ATTCTTTCAGGCATATCCCGCACACACATGA	2981
RESULT	5			
FT	FT	195857	195857	
ID	AC	T95857	standard: cDNA to mRNA; 5275 BP.	
DT	AC	T95857		
DE	08-MAY-1998	(first entry)		
KM	Bovine parathyroid cell calcium receptor 1 (BOPCAR 1) cDNA.			
KW	Bovine parathyroid cell calcium receptor 1; BOPCAR 1;			
KW	calcium homeostasis; hyperparathyroidism; osteoporosis; ss.			
OS	Bos sp.			
FM	Key	Location/Qualifiers		
FT	CDS	515..3772		
FT		/*tag= a		
FT		/product= parathyroid_cell_calcium_receptor_1		
PN	US5688938-A.			
PD	18-NOV-1997.			
PF	07-JUN-1995; US-485588.			
PR	07-JUN-1995; US-485588.			
PR	23-AUG-1991; US-749451.			
PR	11-FEB-1992; US-834041.			
PR	21-AUG-1992; US-934161.			
PR	12-FEB-1993; US-017127.			
PR	23-FEB-1993; US-009389.			
PR	22-OCT-1993; US-141248.			
PR	19-AUG-1994; US-292827.			
PR	21-OCT-1994; WO-012117.			
PR	08-DEC-1994; US-353784.			
PA	(BGM) BRIGHAM & WOMENS HOSPITAL.			
PA	(NPSD-) NPS PHARM INC.			
PI	Brown EM, Fuller FH, Garrett JE, Hebert SC;			
DR	WPI: 98-008040/01.			
DR	P-P-SDB: W38272.			
PT	DNA encoding calcium receptor polypeptide(s) - useful for			
PT	therapeutic purposes, e.g. hyperparathyroidism and osteoporosis			
PS	Claim 1: Columns 107-116; 174pp; English.			
CC	The present sequence encodes bovine parathyroid cell calcium			
CC	receptor 1 (BOPCAR 1).			
CC	The specification includes details of molecules that can modulate			
CC	one or more inorganic ion receptor activities, and antibodies and			
CC	antibody fragments targeted to inorganic ion receptor proteins. The			
CC	proteins, nucleic acids and antibodies may be used to treat			
CC	disorders by modulating one or more inorganic ion receptor			
CC	activities, preferably disorders of calcium homeostasis, e.g.			
CC	hyperparathyroidism and osteoporosis.			
CC	Sequence 5275 BP: 1277 A: 1476 C: 1315 G: 1207 T;			

Query March	6.4%	Score 176.4	DB 1	Length 5275
Best Local Similarity	49.0%	Pred. No. 8.9e-34		
Matches 530	Conservative	0	Mismatches 545	Indels 6
				Gaps
QY 1479	ctggacaataaataagacaataatccagtggcagcggaagaacaatacaggtgcgtgtgca	1538		
DB 2078	CTCTTCATCATGATGATGATAAAATTTCTGTGTGAGTGATCTCAAGGAGAGGTGCTTTCTCC	2137		
QY 1559	gtgtgtacacagcactgtctcgggaaggcaac---caagagtgtgtgtgtgtgtgtcccaac	1599		
DB 2138	AACGCAAGTCGAGAGCTCCGCGGAGGAGACAGAAAAGATCATTTAGGAGGAGGCCACG	2197		
QY 1596	tgtcgttttaagtgtgtgccttcgacgtcgagacctttccaacatgagtgaattcac	1555		
DB 2258	GCCGTGATATAGTGCCCTGTATGATCTTCTTGTCCTAATGAAACACATCTTCGATCGCC	2317		
QY 1716	cgaacggtagagtcttggtttgacatggaaacacatctcttggtgctatagcagctac	1775		
DB 2318	AAGGATATCGAGTTTCTGTGTGTGACCGAGCCCTTGGATGTGACATACGCTCTTTCT	2377		
QY 1776	acgcatagtctgtcgtcgtcgtgtggaaagtgcgttttgcctggacatttcaaca	1835		
DB 2378	GTGCTGGGCAATTTCCACAGAGCTTCGTGTGTGGGCTTTCATCAAGTCCGGACAAAG	2437		
QY 1836	ccgtatgtgggttcaagcttgggggttaagcgtctctctcaatgctgtgttccctgtgtgc	1895		
DB 2438	CCCATGCTCAAGGCAACCAACCGGAGGCTCTCTATCTCTTCTCTTCTCTCTCTCTCTG	2497		
QY 1896	ggaagtgtgaagcttcaagctctctcgtcgsgagagccacagctgcgcgagctgtgtgt	1955		
DB 2498	TGCTTTCACAGTCCCGTCTCTCATTCGGGGAGCCCAAGATGGACGTGCGGCTTGCG	2557		
QY 1956	cagccctcttctctctcgtgggttgcacatctctctcctcgtcgtgaacatccgtctctc	2015		
DB 2558	CAGCGGCGCTTTGGATCATACACTTCGTGCTCTGATCTCTGATCTCTGATCTCTGATCTCTG	2615		
QY 2016	caactgtctcgtcttcaagatttctacaaagtgagcgaacttaccgaacttaccgaactgagcc	2075		
DB 2616	-ATGGGTCCTCTCGTGTGTTAGAGGCCAAGATTTCCACAGCTTCCACCGGAGATGGTGG	2674		
QY 2076	caaaacacatggtgcaggtctatctgcgtatgttcaggtccacaggtccatgttcgtctgt	2135		
DB 2676	GGGCTCAAGCTGAGTTCCGTGCTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2734		
QY 2136	ctcaaatgcttctaatgtgtgagcccaagcaacccaagsgaataccagagcttccccat	2195		
DB 2736	GCCATTTGGCTCAATACAGAGGCCCTCGAGCTACGCGCAACAGAGACTGGAGAGCAG	2794		
QY 2196	ctgtgtatctcgtcagtcscacagagaggtcaactcgttagcgtctcgttggcttcaacc	2255		
DB 2796	ATCATCTTCAATACGTCGCAAGAGGCTGCGTCAATGAGGCTTCTCTATCGGCTAC	2854		
QY 2256	aacattctctctccatcagtaactctgtctcgaagtacactggttaaggaactgccaag	2315		
DB 2856	ACCTGCTGTGTGCGCCCACT	2914		
QY 2316	aactatataaagcaaaagtgtgacacttcacgcgtctcctaacttgtatccgtgtc	2375		
DB 2916	AACCTCATATAAACCAAGTTCATCACACTTTCACATGCTCTATCTTCTTATGCTGTGGATC	2974		
QY 2376	gacctcttcaacatgscagcaatttaccaggggagctacactgctcgtcggttcaatgtgtg	2435		
DB 2976	TCTTTCATCCCGCGCTACGCGACACTTACGCGAAGTTGTGTCTGTGCGGTGGAGTGATC	3034		
QY 2436	gcagagctgacacacactgaagcggtcagcgttaccgttactctctcccaagtgtatgtg	2495		
DB 3036	GCAATCTCGCGGCGACGCTTGTGCTGTGCGGCTGTATCTTCTTCAACAGAGTCTACTC	3094		


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Qy 2496 attctgcgcgtccagaactcaacatacagaacattcagagctccatccagactac 2555
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Db 3095 ATCCTCTTCAAGCCTTCCCGGAACACCATCGAGAGTGGCTGACAGACGGCGGACAC 3154

Qy 2556 ac 2557
Db 3155 GC 3156

RESULT 6
V26962
ID V26962 standard; cDNA to mRNA; 5275 BP.
AC V26962;
DT 01-SEP-1998 (first entry)
DE Bovine parathyroid calcium receptor 1 gene 5Kb fragment.
KW ss; calcium ion concentration; parathyroid hormone; homeostasis;
    kidney; calcium receptor; detection.
OS Bos sp.
FH Key Location/Qualifiers
FT CDS 515..3772
    /tag= a
    /product= "BOPCAR 1 5kb fragment"
PN US763569-A.
PD 09-JUN-1998.
PF 07-JUN-1995; 484565.
PR 07-JUN-1995; US-484565.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-017127.
PR 23-FEB-1993; US-009389.
PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PR (BCHM ) BRIGHAM & WOMENS HOSPITAL.
PA (NPSF-) NPS PHARM INC.
PI Brown EM, Garrett JE, Hebert SC;
DR WPI: 98-347412/30.
DR P-PSDB: W54844.
PT Calcium receptor poly:peptide(s) - useful for drug screening or
    antibody production
PS Example 25; Fig 47; 174pp; English.
CC The bovine parathyroid calcium receptor gene encodes a 1085 amino acid
    protein. The tissue from which this receptor and receptors from human
    parathyroid and rat kidney are derived, respond to changes, and control
    changes, in calcium ion concentration, e.g. parathyroid hormone regulates
    Ca2+ homeostasis in blood and extracellular fluid, and kidney function
    alters through changes in Ca2+ levels in juxtaglomerular and proximal
    tubule cells in the kidney. The purified receptors (produced
    recombinantly) can be used to screen for compounds that modulate calcium
    receptor activity, especially those that can be used to treat diseases
    associated with the receptors in these tissues. They can also be used
    to raise antibodies for use in detection assays.
SQ Sequence 5275 BP; 1277 A; 1475 C; 1316 G; 1207 T;

Query Match 6.4%; Score 176.4; DB 1; Length 5275;
Best Local Similarity 49.0%; Pred. No. 8.9e-34;
Matches 530; Conservative 0; Mismatches 346; Indels 6; Gaps 2;

Qy 1479 ctgacataaataaacaacatcagtcgacggaagaacatcagtcgtgtgtca 1538
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Db 2078 CTCTTCATCATGATGAAAAAATTTCTGTGAGTGTATCTCAAGGAGGTGCTTCTCC 2137

Qy 1539 gtgtgtacacaggtctgtctgcagggcac--cacaggtgtgtgtgtgtccaccac 1595
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Db 2138 AACTGCAATCGAGACTGCTGTGGCAGGACCAAGAAAGCATATGAGGGAGGCCCCACC 2197

Qy 1596 tgcctcttgagtggtgtgtcccggaagcttccttcaaatatgagtgttcaac 1655
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2198 TGTCTCTTGAATGTGTGAATGTCTCTGATGGGAGTACAGCGACAGACAGATCAAGT 2257

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Qy 1656 attcgcagccttctgtgaacagaaatgggcaaccaggagagcaacttctccca 1715
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Db 2258 GCCGTGTATAGTGTCCCTGATGACTTGTGGTCAATAGAAACACACACTTCTGTGATGCC 2317

Qy 1716 cgcaggtgaaattcttggcttggcatgaaccatctcttgtgttaataagcagtaac 1775
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2318 AAGGAGATCGAGTTCGTGTGGACCGAGCCCTTCGGAGATCGCACACAGCTCTTGTCT 2377

Qy 1776 acgctattgctgctgctgctgctgtggagctgtgctgttgcgtgcatattcaaca 1835
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Db 2378 GTGCTGGGCAATTTTCTTCACAGCCTTGTGCTGGGCGCTTCATCAAGTTCCGCAACAG 2437

Qy 1836 cctttagtgaagtcagctggggtgagctgtgtcttcccaatgtcgtgtgtgtgtgccc 1895
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Db 2438 CCATGCGTAAGGCGCACCAACCGGAGCTGCTCATCTCTCTCTCTCTCTCTCTCTCTCTG 2497

Qy 1896 ggaagttgcagctctatagcttcttcggggagcccaagtggtccgggtgtgtgtgt 1955
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2498 TGTCTTCACACTCCCTGTTCTTCATGGGGAGGCCAGAGACTGGAGTGGCGGCTGCGC 2557

Qy 1956 cagccccccttctctcgtggttgcacatcttccctcctcgtcgtgacaatccgtcttc 2015
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2558 CAGCGGCGCTTTGGCATACAGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2616

Qy 2016 caactgtgcatcatctcaagttcttcaacaaggtgccacatctacacgttaccgtggcc 2075
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Db 2616 -ATGGGTCCTCGTGTGTGAGCGCCAGATGCCACAGACTCCACGGAAAGTGGTG 2674

Qy 2076 caaaacatgtgtcaggtctatctgtcatgttcagctcccaagtcattgtcatctgt 2135
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Db 2675 GGGGTCAACCGCATCTCTGCTGTGTCTTCTCTGACACTTCATGACGATGTGTATCTGT 2734

Qy 2136 ctcaatggtctgtgaatgtgagcccaacagcaaggaataacagagcttcccccac 2195
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Db 2735 GCCATTGGCTCAATACAGCGCCCTCGAGCTACCGCAACAGAGCTCCAGGAAGAGAG 2794

Qy 2196 ctgtgtatctcgaatgcacagaagtaactctgtaggtctcctgtgtgtgttccaccac 2255
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2795 ATCATCTTCATCACCTGCGACAGAGGCTCGCTCATGGCGGTGCTCTCGATGGCGCTAC 2854

Qy 2256 aacattcccttcacacagtaacttgcctgtgcagcttgcagctgtgttaaggaactccagag 2315
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Db 2855 ACCGTCTTGCTGGCGGCGCATCTGCTTCTTCTCCCTTCAAGTCCGGAAGCTCCAGAG 2914

Qy 2316 aacataatgaagaatgtgtacattcagctgtcctcccaactcgtatcgtatgc 2375
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2915 AACTTCATATGAGCGCAATTCATACCTTACGATCGCTCATCTTCTCATGTGTGATC 2974

Qy 2376 gcttcttcacacatgtgccaatttaccaggtcagactcgtcgtggtatgtgtcgtg 2435
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Db 2975 TCTTTCAATCCCGGCTACGCGACAGCACTTACGCAAGTTGCTGCTGCGGTGAGAGTATC 3034

Qy 2436 gcaaggtcgtacacacagcagagtggtggttcaagtggttacttcccccagtgatgtg 2495
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3035 GCCATCTCGGGGGCGACGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGATC 3094

Qy 2496 attctgcgcgtccagaactcaacatacagaacattcagagctccatccagactac 2555
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Db 3095 ATCCTCTTCAAGCCTTCCCGGAACACCATCGAGAGTGGCTGACAGACGGCGGACAC 3154

Qy 2556 ac 2557
Db 3155 GC 3156

RESULT 7
V82483
ID V82483 standard; cDNA to mRNA; 5275 BP.
AC V82483;
DT 19-MAR-1999 (first entry)
DE Bovine parathyroid calcium receptor BOPCAR 1 encoding cDNA.
KW parathyroid calcium receptor; inorganic ion receptor; osteoporosis;
    calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;

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PR 22-OCT-1993; US-141248 .
 PR 19-AUG-1994; US-292827 .
 PR 21-OCT-1994; WO-012117 .
 PR 08-DEC-1994; US-353784 .
 PA (BGM) BRIGHAM & WOMENS HOSPITAL .
 PA (NPSP-) NPS PHARM INC .
 PI Brown EM, Fuller FH, Garrett JE, Hebert SC;
 DR WPI: 98-008040/01 .
 DR P-PsDE: w38273 .
 PT DNA encoding calcium receptor polypeptide(s) - useful for
 PT therapeutic purposes, e.g. hyperparathyroidism and osteoporosis
 PS Claim 15: Columns 117-126; 17pp; English .
 CC The present sequence encodes human parathyroid cell calcium
 CC receptor 5.2 (HmPCar 5.2)
 CC The specification includes details of molecules that can modulate
 CC one or more inorganic ion receptor activities, and antibodies and
 CC antibody fragments targeted to inorganic ion receptor proteins. The
 CC proteins, nucleic acids and antibodies may be used to treat
 CC disorders by modulating one or more inorganic ion receptor
 CC activities, preferably disorders of calcium homeostasis, e.g.
 CC hyperparathyroidism and osteoporosis.
 CC Sequence 5006 bp: 1227 A; 1378 C; 1219 G; 1182 T;
 QQ

Query Match	6.18;	Score 170.2;	DB 1;	Length 5006;
Best Local Similarity	49.58;	Pred. No. 2.9e-32;		
Matches 498; Conservative	0;	Mismatches 503;	Indels 6;	Gaps 2;

OY	1524	caagcgctctgtgtaagtggtgtacccagcagctcttcgcaggagccac---caagagtgagttc	1580
Db	2071	caagtgcccttctccaaactgcacgacccgacactcctctggcagggagaccagaaaggatcatt	2130
OY	1581	gtcgggtctcccaacacatctgcgtcttgatgtgtgcctctggaaagcttggaccttctcaac	1640
Db	2131	gaggggagagccaccactgccttgctttcagtggtgtgagatgctccgataggagagatatagat	2190
OY	1641	atgagtgtgacttcaatctgcgcagcctctgtgaaacagaagaatgggcaccccaagsgaac	1700
Db	2191	gagacagatgcccagtgccctcgtacaaagttcccaatgactttggccaatagaaccac	2250
OY	1701	actactctctcccaacgcacaggttggaagtcctgtgacttggcagaacccaactctctgtg	1760
Db	2251	acctcttgatgtgcacaaagagatgcagatttcgtgtgtagcagagagcccttggatgcga	2310
OY	1761	ctaataagcagctaacacgctatctgctgtcgtcgtgtgtggagctgcgtctgtgc	1820
Db	2311	ctcaccccttctggccgtgtggcagattttctcgcagacgctttgtgctgggtgtgattac	2370
OY	1821	tggcatttccaaacacctgtatgtgagtgtagtggsgtgagctgtgcctctccatagctg	1880
Db	2371	aagttcccgacacacacocctatttcaaagggccaccacgaagagcttcttaacctctcttc	2430
OY	1881	ggtctccctgtgtgcgcggaagtgtcagcctctctataagactcttctcggggagccacggtgc	1940
Db	2431	ttctccctgctgtgctgtcttctcagactccctgattctcatgtggggagagccacgagactgg	2490
OY	1941	gcgtcctgtcgtgcgtcagagccctcttctctcgggtttgcacatctctctctccgcg	2000
Db	2491	acgttcgcgcctgtggcagccggccttttggcattacgcttgcctctgcattctcattccatc	2550
OY	2001	acaacgcgctctccccaactgtcacaatcacttcaagttcttctaaccaagtgcccacatc	2060
Db	2551	ctgggtgaaaacacacccgtctcctcctcgtggtttgag---ccaagatcccaacacacttc	2607
OY	2061	tacgtaacctggagcccaaaaaccaaagtgtagtctatctcgtcatatgtccagctccagctc	2120
Db	2608	caaccccaagtggtgggggctctcaacctgcagttcctgcctgttttctctgcacacttccag	2667
OY	2121	catctgtcatctgtctccacatgagctgttaagtgtgagcccaagaccacccaagsgaatc	2180
Db	2668	cagatttgtatctgtgtgattcttggtctctacacggcccccctctcaagactaccgcaaccag	2727
OY	2181	caagccttccccaactgtgtgattcttcgagtgcacagaagtgtaactctgtlaagcttctctg	2240

Db	2728	GAGCTGGAGGATAGATTCATCTTCATCCAGCTGCACAGAGGCTCCCTCATGAGCCCTGGGC	2787
Qy	2241	ttgagcttccaccacaacatctctctctccatcagtaaccccttcctcagcgttaacctgagt	2300
Db	2788	TTCCGTGATCGGCTACACCTCCGCTGGCTGGCCATCTGTTTCTTTTGCCCTCAAGATC	2847
Qy	2301	aaggaactccgaagaagactataatgaagccaatgtcactctagcctctcctcaac	2360
Db	2848	CGGAGGCTGGCGGAGCACTTCATGAAAGCAAGTTCATACCTTGAGATGCTATCTTC	2907
Qy	2361	ttcgatcctcgaatccgacctcttcacacatggcagaatctaacaggcagcatcactgct	2420
Db	2968	TTTACTGCTTGGATCTCCTTCATTCACGCCATAGCCAGACCTAAGGCAAGTTGTCTCT	2967
Qy	2421	gcgagtcacatgtctggaagggctgaccacaactgaagcgtgcgagcttaacggttaactctc	2480
Db	2968	GCCCTAAGAGTGATGGCATCTCGCAGCCACACTTTGGCTTCTGGCTGCATCTTCTTC	3027
Qy	2481	ccgaagtgcatatgtaattctctgcgctccagaactcaaaataacga	2527
Db	3028	AACCAAGATTCATCATCTCTCTTCAAGCCATCCCGCAACATATGA	3074

RESULT 10
V26963
ID V26963 standard; cDNA to mRNA; 5006 BP.

Query Match	6.1%	Score 170.2	DB 1	Length 5006
DT	01-SEP-1998	(first entry)		
DE	Human parathyroid calcium receptor 5.2 gene 5kb fragment.			
KW	ss; calcium ion concentration; parathyroid hormone; homeostasis;			
KW	kidney; calcium receptor; detection.			
OS	Homo sapiens.			
FT	Key	Location/Qualifiers		
FT	CDS	436..3702	/*tag= a	
FT		/product= "pHupCar 5.2 5kb fragment"		
PN	US5763568-A.			
PD	09-JUN-1998.			
PF	07-JUN-1995; 484565.			
PR	07-JUN-1995; US-484565.			
PR	23-AUG-1991; US-749451.			
PR	11-FEB-1992; US-836044.			
PR	21-AUG-1992; US-934161.			
PR	12-FEB-1993; US-071127.			
PR	23-FEB-1993; US-009389.			
PR	22-OCT-1993; US-141248.			
PR	19-AUG-1994; US-292827.			
PR	21-OCT-1994; WO-012117.			
PR	08-DEC-1994; US-353784.			
PA	(BGHM) BRIGHAM & WOMENS HOSPITAL.			
PA	(NPSP-) NPS PHARM INC.			
PI	Brown EM, Garrett JE, Hebert SC;			
PI	WPI; 98-347412/30.			
DR	P-BSDS: W54845.			
PT	Calcium receptor poly:peptide(s) - useful for drug screening or			
PT	antibody production			
PS	Example 27; Fig 48; 174pp; English.			
CC	The Human parathyroid calcium receptor gene encodes a 1088 amino acid			
CC	protein. The tissue from which this receptor and receptors from bovine			
CC	parathyroid and rat kidney are derived, respond to changes, and control			
CC	changes, in calcium ion concentration, e.g. parathyroid hormone regula			
CC	Ca2+ homeostasis in blood and extracellular fluid, and kidney function			
CC	alters through changes in Ca2+ levels in juxtaomemular and proximal			
CC	tubule cells in the kidney. The purified receptors (produced			
CC	recombinantly) can be used to screen for compounds that modulate calca			
CC	receptor activity, especially those that can be used to treat diseases			
CC	associated with the receptors in these tissues. They can also be used			
CC	to raise antibodies for use in detection assays.			
SO	Sequence 5006 BP; 1228 A; 1376 C; 1220 G; 1182 T;			

Db 2614 CAGCTGCTTTGGCATACGCTTTGCTGCTATCTGTCATCTTGGTGAAGACCAAT 2673
Qy 2016 caactgcatcatcttcaagttcttcaacaagtgccacatctacacgtacccg 2075
Db 2674 CGCGTCCCTGCTGATTGTA---AGCAAGATACCCACAGGTTCCACCGGAAGGTTGG 2730
Qy 2076 caaaccatggtgacggttctatctgcatctgcaagtcacagtcacgttctatctgt 2135
Db 2731 GGGCTCAACCTGACATTCCTGCTGTTTCCCTGACCTTCATCAGATCTCTCATCTGC 2790
Qy 2136 ctacatggtctgtatgtgagccacagaccacaggaatatacagctctcccat 2195
Db 2791 ATCATCTGGCTTACACGGCGCCGCCCTCTTACCTACCCGACCAATGAGCTGGAAGACGA 2850
Qy 2196 ctggtgattctcagtgacacaggttcaactctgtagctctctctgtgtcttccaccc 2255
Db 2851 ATCATCTTATCATCGTCGCATGAGGGCTCATCATGACACTTGGCTCCCTGATCGGCTAT 2910
Qy 2256 aacattctctctcactcaagtcactctgtctgacagctacacgtggttaaggaactgcagag 2315
Db 2911 ACCTCCCTGCTGGCTGACATCTGCTTCTTCTTGGCTTCACTCAAGGAACTTACCAAG 2970
Qy 2316 aactaatgaagcaaatgtgtcaacttcaagctctcctcaacttgaactctgagtc 2375
Db 2971 AACTTCAAGCAAGCCAAAGTTCAATACCTTACAGATGCTCATCTTCTTCTGATC 3030
Qy 2376 gctcttccatcaccatggtgacagcttcaagaggaactacactctgctggtcaatgtctg 2435
Db 3031 TCGTTTCATTCAGCTTANGCCAGACCTACGCAAGTTGTGTGCGGTAAAGTGAATC 3090
Qy 2436 gcaaggtgacacacactgaagcggtctcagcgttactctctcccaagtgctatgtg 2495
Db 3091 GCCATTTTGGCAGCGCTTGGCTTACTAGCCTCATCTTCTTCAACAAGGCTTACATTT 3150
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Db 3151 ATCTCTTCAAGCTTCCCGAAGACCAATGAGGAGTCCGCTCCAGCAC 3201

RESULT 13
V26965
ID V26965 standard: cDNA to mRNA; 4131 BP.
AC V26965:
DT 01-SEP-1998 (first entry)
DE Rat kidney calcium receptor 3A gene 4Kb fragment.
KW ss: calcium ion concentration; parathyroid hormone; homeostasis;
OS kidney: calcium receptor; detection.
FH key
FT Location/Qualifiers
FT 574..3813
FT CDS /product= "PRAKAR 3A 4Kb fragment"
PD US7635569-A.
PE 09-JUN-1998
PF 07-JUN-1985; 484565.
PR 23-AUG-1995; US-484565.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-017127.
PR 23-FEB-1993; US-009389.
PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (NPSp-) NPS PHARM INC.
PI Brown EM, Garrett JE, Hebert SC;
DR P-PSDB; W54847.
PT Calcium receptor poly:peptide(s) - useful for drug screening or
PS antibody production
Example 30; Fig 50; 17app; English.

CC The rat kidney calcium receptor gene encodes a 1079 amino acid protein.
CC The tissue from which this receptor and receptors from bovine parathyroid
CC and rat kidney are derived, respond to changes, and control changes, in
CC calcium ion concentration, e.g. parathyroid hormone regulates Ca2+
CC homeostasis in blood and extracellular fluid, and kidney function alters
CC through changes in Ca2+ levels in juxtaglomerular and proximal tubule
CC cells in the kidney. The purified receptors (produced
CC recombinantly) can be used to screen for compounds that modulate calcium
CC receptor activity, especially those that can be used to treat diseases
CC associated with the receptors in these tissues. They can also be used
CC to raise antibodies for use in detection assays.
SQ Sequence 4131 BP; 988 A; 1170 C; 1052 G; 921 T;

Query Match 5.8%; Score 160.6; DB 1; Length 4131;
Best Local Similarity 48.2%; Pred. No. 6e-30;
Matches 516; Conservative 0; Mismatches 549; Indels 6; Gaps 2;

Qy 1479 ctgacataaataagacaaaatcagtgacagcaggaagaatacagtgctgtgtca 1538
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Db 2194 AATTGCAAGCCGGGACTGTCAAGGACCAAGAAAGGGAATCATCAGAGGAGAGCCAC 2253
Qy 1596 tgcgtcttgatgt 1655
Db 2254 TGCGCTTTTGTGATGT 2313
Qy 1656 atctgcaagcctgttgacagaagaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1715
Db 2314 GCGTGTGACAGATGCCGAGATGATCTGTGTCATGAGAACACACTTCTTGATGCGC 2373
Qy 1716 cgcacggt 1775
Db 2374 AAGGAGATGTGATGT 2433
Qy 1776 acgctatgt 1835
Db 2434 GTGCTGGGCAATTTCTCGACCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2493
Qy 1836 cctgtagtgagtgatgt 1895
Db 2494 CCRATGCGAAGGCGACCAACCGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2553
Qy 1896 ggaagtgacgctctctatgtctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1955
Db 2554 TGCTTCTCAGCTCTTGT 2613
Qy 1956 cagccctcttctctcgt 2015
Db 2614 CAGCTGCTTCCGACATGACGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2673
Qy 2016 caactgcatcatcttcaagttcttcaacaagtgccacatctacacgttcaactggtg 2075
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Qy 2076 caaaccatggtgacggttctatctgcatctgcaagtcacagtcacgttctatctgt 2135
Db 2731 GGGCTCAACCTGACATTCCTGCTGTTTCCCTGACCTTCATCAGATCTCTCATCTGC 2790
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Qy 2196 ctggtgattctcagtgacacaggttcaactctgtagctctctctgtgtgtcttccaccc 2255
Db 2851 ATCATCTTATCATCGTCGCATGAGGGCTCATCATGACACTTGGCTCCCTGATCGGCTAT 2910
Qy 2256 aacattctctctcactcaagtcactctgtctgacagctacacgtggttaaggaactgcagag 2315
Db 2911 ACCTCCCTGCTGGCTGACATCTGCTTCTTCTTGGCTTCAAGTCCAGGAGTTACCAAG 2970

Oy	2316	aaataatagagccaatagtgtcacttagcttgcttctctaacttgcatacttgcatactgac	2375
Db	2971	AACTTCAAGGAGGCAAGTTCATTACCTTAGCAATGCTATCTTTCATCTGTGGATC	3030
Oy	2376	gcctcttcacacatgagccagcatcttaccagagagcactgcctgcggatcgtgcg	2435
Db	3031	TCCTTCATTCAGGCTATGCGAGACCTACGGCAAGTTTCTCTCCGCGAAGGTGATC	3090
Oy	2436	gcagagctgaccacacatgagcgcgcgttcaagcgttactctctcccagaagtcatg	2495
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Oy	2496	attctctgcgttcagaactcaacaataacagacactttagcctccatc	2546
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ID	V82486	standard: cDNA to MRNA: 4131 BP.	
AC	V82486:		
DC	19-MAR-1999	(first entry)	
DE	Rat parathyroid calcium receptor prakcar 3A encoding cDNA.		
KW	Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;		
KW	calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;		
KW	spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;		
KW	neonatal distress; neurodegenerative disease; Alzheimer's disease;		
KW	Huntington's disease; Parkinson's disease; dementia; muscle tension;		
OS	Rattus sp.		
FH			
FT	Key	Location/Qualifiers	
ET	CDS	574..3813	
FI		/*tag= a	
PN	US5858684-A.		
PD	12-JAN-1999.		
PF	07-JUN-1995.	480751.	
PR	07-JUN-1995.	US-480751.	
PR	23-AUG-1991.	US-749451.	
PR	11-FEB-1992.	US-834044.	
PR	21-AUG-1992.	US-934161.	
PR	12-FEB-1993.	US-011721.	
PR	23-FEB-1993.	US-009389.	
PR	22-OCT-1993.	US-141248.	
PR	19-AUG-1994.	US-292827.	
PR	21-OCT-1994.	WO-012117.	
PR	08-DEC-1994.	US-353784.	
PA	(BGM) BRIGHAM & WOMEN'S HOSPITAL.		
PA	(NPSP-) NPS PHARM INC.		
PI	Balandin MF, Brown EM, Del Mar EG, Garrett JE,		
PI	Hebert SC, Nemeth EF, Van Wagonen BC;		
DR	WPI: 99-119871/10.		
DR	P-PSDB: W89565.		
PT	Screening for calcium receptor-active compounds - by recombinant		
PT	expression of nucleic acid encoding calcium receptor and determining		
PT	the effect of compounds on calcium receptor activity		
PS	Claim 1: Fig 50: 176pp: English.		
CC	A method has been developed of screening for a compound able to affect		
CC	one or more activities of a calcium receptor (CR) comprises: (A)		
CC	contacting a recombinant cell with a test compound, where the		
CC	recombinant cell comprises a recombinant nucleic acid expressing the		
CC	CR, provided that the cell does not have functional CR expression from		
CC	endogenous nucleic acid; (B) determining the ability of the test		
CC	compound to affect one or more activities of the calcium receptor; and		
CC	(C) comparing the ability with the ability of the test compound to		
CC	affect the one or more CR activities in a cell not comprising the		
CC	recombinant nucleic acid. The present sequence encodes rat		
CC	parathyroid CR, designated a PRAKCAR 3A. The nucleic acid sequence of		
CC	PRAKCAR 3A can be used as part of the recombinant nucleic acid in the		
CC	method described above. The compounds identified can be used to treat		
CC	diseases or disorders characterised by abnormal calcium homeostasis, e.g.		
CC	hyperparathyroidism, osteoporosis and other bone and mineral-related		
CC	disorders. They can also be used for the treatment of diseases and		

Query Match	Best Local Similarity	5.8%	Score 160.6	DB 1	Length 4131
Matches 516	Conservative	0	Mismatches 549	Indels	6
Gaps	2				
CC disorders associated with disrupted Ca2+ responses, e.g. seizures, stroke, spinal cord injury, hypoxia-induced nerve cell damage such as cardiac arrest or neonatal distress, epilepsy, neurodegenerative diseases such as Alzheimer's disease, Huntington's disease and Parkinson's disease, dementia, muscle tension, depression, and anxiety.	1539	gtgttaccacgagctatctctgcaagggacacacagggcgtgtgt--gggttccaccac	1595		
SO Sequence 4131 BP; 988 A: 1170 C: 1052 G: 921 T;	1596	tactctttgaagtgatgtgccccgcgaagctggagacctttccaatagtagcttaac	1655		
	2254	tgtctctttgaatgtgtgtgagatgtcttcatgagagctacagtgagagacagatccgagt	2313		
	1656	atctgcagcccttctggaaacagaagaatgaggaccccaaggagagactactgtctcca	1715		
	2314	gcctttgacaaatgccccggatgacttctggttccatagaaacacacactttctgcattgcc	2373		
	1716	cgcaaggaggagttcttggtcttgcatgaaccacactctttggtgtatataagcgtaac	1775		
	2374	amgagattgattttcttggcgtgacccagccgctttggaattgccttcaactcttcttcgcg	2433		
	1776	agccatctgctgctgctggttgtagaactgtgcctgtttgacctgcatcttccaca	1835		
	2434	gttcgtggcgatttttcttctatccacccttttgcgggtgtgtttcatcaaatccgaatac	2493		
	1836	cctgtagtgaagtcagctgtgggtagtgctgtgtctctcaatgtgtgttccctgtggcc	1895		
	2494	cttatctgtccaaagccacacacaggaactgttccrtaactcttcttccactactctgac	2553		
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	2554	tgccttccagctcttctgtttcttatttggggagcccaagactggacgtgcgccttgca	2613		
	1956	caagccctctttctctcgggtgttcacatctccctcctgcctgaacatccgccttc	2015		
	2614	cagcctgcttttggcattacgcttttgcctgtctatctgttcattttgtgtaaagccaat	2673		
	2016	caactgtgcatcatcttcaagtttcttcaagaagtgcccaacttaccgttaacctgggcc	2075		
	2574	cgcgttcccttgatmttga--agccaaagataccacacagcttccacgggaagtggtgg	2730		
	2076	caaaacatgtgtgcagcctcatctgcatctgtcagctcccaagttccatttgtcatctgt	2135		
	2731	ggcgcaacctgcacattctctgtgtgttttctcttcacaccttcatcacaattctctatccgc	2790		
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	2196	ctgtgattctcagtagtgacaaggttcaactgttagccttccgtgttgcttttccacac	2255		
	2851	atcattcttcatcagctgcattgaggccctacatcagcactttgggtccctatcggcgtat	2910		
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 19, 2000, 00:19:26 ; Search time 3521.68 Seconds
(without alignments)
-2389.150 Million cell updates/sec

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Perfect score: 2771
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Scoring table: IDENTITY_NUC

Searched: 821193 seqs, -1518192014 residues

Database: GenEmbl.*

Word size: 0

Number of hits that pass the threshold: 1642386

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50: gb_pl3:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2520	90.2	2520	12	AF127389	AF127389 Rattus no
2	447.6	16.2	2529	12	AF127390	AF127390 Rattus no
3	185.8	6.7	270	13	G09859	G09859 human STS C
4	181.6	6.6	3809	5	AR012624	AR012624 Sequence
5	181.6	6.6	3809	5	AR028467	AR028467 Sequence
6	181.6	6.6	3809	5	I75053	I75053 Sequence 3
7	181.6	6.6	3361	9	HUMCASR	D50355 Human mRNA
8	181.6	6.6	3783	10	HSU20759	U20759 Human parat
9	181.6	6.5	3234	10	S83175	S83175 CaSR-calcitri
10	180	6.5	3234	9	HSPCAR1	X81086 H. sapiens
11	176.4	6.4	5249	3	S67307	S67307 Ca(2+)-sens
12	176.4	6.4	5275	5	AR012622	AR012622 Sequence
13	176.4	6.4	5275	5	AR028465	AR028465 Sequence
14	176.4	6.4	5275	5	I75051	I75051 Sequence 1
15	172.4	6.2	4319	12	AF110179	AF110179 Mus muscu
16	170.2	6.1	5006	5	AR012623	AR012623 Sequence
17	170.2	6.1	5006	5	AR028466	AR028466 Sequence
18	170.2	6.1	5006	5	I75052	I75052 Sequence 2
19	170.2	6.1	5009	10	HSU20760	U20760 Human extra
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21	169.8	6.1	4550	12	AF110178	AF110178 Mus muscu
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23	160.0	5.8	4131	5	AR012625	AR012625 Sequence
24	160.0	5.8	4131	5	AR028468	AR028468 Sequence
25	160.5	5.8	4131	5	I75054	I75054 Sequence 4
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27	160.6	5.8	3761	12	RNJ20289	U20289 Rattus norv
28	154	5.6	3106	10	HSFPR301	U45324 Human Krupp
29	133.2	4.8	798	40	S81755	S81755 calcium rec
30	114.4	4.1	2815	4	AF083081	AF083081 Carassius
31	113	4.1	2148	5	A73577	A73577 Sequence 1
32	107.6	3.9	4981	4	AB008859	AB008859 Fugu rubr
33	107.2	3.9	761	12	AB027140	AB027140 Mus muscu
34	105.2	3.8	2568	12	AF053985	AF053985 Mus muscu
35	98.8	3.6	2785	4	AF083080	AF083080 Carassius
36	98.4	3.6	4781	4	AB008860	AB008860 Fugu rubr
37	98.2	3.5	4743	4	AB008862	AB008862 Fugu rubr
38	90.2	3.3	3506	4	AB008857	AB008857 Fugu rubr
39	90.2	3.3	2739	12	AF053986	AF053986 Mus muscu
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41	88	3.2	1927	4	AB009044	AB009044 Fugu rubr
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ALIGNMENTS

RESULT 1
AF127389 AF127389 2520 bp mRNA ROD 04-MAR-1999
LOCUS Rattus norvegicus putative taste receptor TRL mRNA, partial cds.
DEFINITION
ACCESSION AF127389
VERSION AF127389.1 GI:4337085
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE
1 (bases 1 to 2520)

AUTHORS Hoon, M.A., Adler, E., Lindemeyer, J., Batley, J.F., Ryba, N.J. and Zuker, C.S.
 TITLE Putative mammalian taste receptors: a class of taste-specific GPCRs with distinct topographic selectivity
 JOURNAL Cell 96 (4), 541-551 (1999)
 MEDLINE 99159821
 REFERENCE 2 (bases 1 to 2520)
 AUTHORS Hoon, M.A., Adler, E., Lindemeyer, J., Batley, J.F., Ryba, N.J.P. and Zuker, C.S.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-1999) Taste and Smell Unit, NIDCR, 10 Center Drive MSC 1188, Bethesda, MD 20892-1188, USA
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 IVSSVTHLLICLTMVLMWTRPTREYQRFHLVILFETEVNSVGFLLAFHNLILIS
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 Query Match 90.9%; Score 2520; DB 12; Length 2520;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2520; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 361 CAAGGGCCCCGACATAGAGATACAGAAAGACCTTCGCAACCATCTCCAAAGTGGTG 420
 Qy 477 gctctacatggccttgacaacactgacacgctgtctactacgctgcttgcgtgcttcc 536
 Db 421 GCCTTATCGGGCTTGACAACTAGACACAGCTGTACTACCGCTGCTTGTGGTCTT 480
 Qy 537 ttccatgccccctgtgcaactatgagcaagcagctgtgactcagttgcaacgcaag 596
 Db 481 TTCCTGATGCCCTCGTACACTATGAGCAAGCAGCGTGTACTACATGCGCAAGCGCAG 540
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 Qy 657 ctctgtagaggttttgggtgtgtgatatctgctcatcttgacagctacagttgagtg 716
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 Db 661 CAGCTGGGTGTGACAGGGCTGGAAGAGCTGGCGGTGCCCGGGGCAATCGTGCCTTC 720
 Qy 777 aaggacatgtgctctctctctgccccgggtgtgtgacccggagatgacagatgagtg 836
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 Qy 897 ggtctctcagctcgt 956
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Db	1501	CTGGAGGGGACACACAGGTGGTGTGGGTCCACCACTGGTGGTTGAGTGTGGCC	1560
OY	1617	tgcgaagctgtgaccttccacaatgagtgagcttcacatctgcacagctgttgaaaca	1676
Db	1561	TGGCACTGGGAACTTTCTCMATGAGTACGACTTCACATCTGCCAGCCTGTGGAAACA	1620
OY	1677	gaagaatgagcaacccaagagagacactatgtctccacagacaggtgagatcttgact	1736
Db	1621	GAAGAATGGGACCCCAAGAGAGAGACTACTCTCTCCACGACGGTGGAGTCTTGACT	1680
OY	1737	tggataaacccatctctttgtgtcctaataagagcgtcaaacagctcttctgtgtgtg	1796
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OY	1797	gttggaactgtctgagccggttttgctgtggcatcttccacaacccgtgatgaggtcaactgtg	1856
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OY	1857	ggtgagctgtgtcttcccaatgctgtggtttccctgtgtgtgtgtgtgtgtgtgtgtgtgt	1916
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Db	1861	TTCTTTGGGAGACCCACAGGAGGCCGGGTGTCTGTCTGTACACCCCTCTTTCTGTGGG	1920
OY	1977	cttgacatcttcctctctctctctgtccgtgacaatcgcctctccatcaactgtgtcatcatcacaag	2036
Db	1921	TTTGCAATCTTCTCTCTCTCTGTGTAACATCGCTCTCTTCCATCGTATCATCTTCAAG	1980
OY	2037	ttttctaccaaggtgtcccaaatcttcaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2096
Db	1961	TTTTCTACCAAGGTGCCACATCTTCACTGACGTGGGCCCAAAACCATGTGTGACAGTCTA	2040
OY	2097	cttgcatctgtgcaactcctcagaggtccaatcttccatctgtctgtcacaatgtgtgtgtgtgtgt	2156
Db	2041	TTTGCATTTGTGACGCTCACGGTTCATTTCCTATCTGTCTACATGGCTGTATATGTGG	2100
OY	2157	accccaagaccacacagagaataaccagagcgttccccaatctgtgtatctcgaatgtcacaca	2216
Db	2101	ACCCACAGACCCACACAGGAATACAGAGCGTTTCCCACTCTGTATCTCGATGTGACACACA	2160
OY	2217	gaggtcaactgtgaggtcttccgt	2276
Db	2161	GAGGTCAACTCTGTGAGGCTTCTGTGGCTTTCACCAACAACTTCTCTCTCACTCACTG	2220
OY	2277	accttgcgtcagactcctccgttgaaagaaactgccagaaactataatgaagcacaagt	2336
Db	2221	ACCTTGCCTCACTACCTGCTGGGTAAAGAACTGCCAGAACTATATATGAAGCCAAATGT	2280
OY	2337	gtcacctcagcctgtcctcctcaactcttgtatctccgtgatcgtcttcaaccaatgtgccac	2396
Db	2281	GTCACCTTCAGCCGCTGCTCTCAACTTCGTATCTCTGATGTGCTTTCACCATGTGCCAGC	2340
OY	2397	atttacaagggagagactacacgcgtctgtgttaatgctgtgtgtgtgtgtgtgtgtgtgtgtgt	2456
Db	2341	ATTTACCAAGGGACACTACCTGCTCGGGGTAAATGTCTGTGGAGGGCTGACCACTGTAGC	2400
OY	2457	ggcgactcttcagcggttactcctccccaagtgtctatgtatctctgcgcgttccagaactc	2516
Db	2401	GGCGGCTTACGGGTTACTTCTCTCCCAAGTGCTATGTATTTCTGTGGCGTGTCAAAATC	2460
OY	2517	aacaatatagaacacttcaagcctccatccacagagctacagaagcgctgtcgagcaatcc	2576
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RESULT	2		
AF127390	AF127390	2529 bp	MRNA
LOCUS			ROD
			04-MAR-1999

DEFINITION	Rattus norvegicus putative taste receptor TR2 mRNA, partial cds.
ACCESSION	AF127390
VERSION	AF127390.1 GI:4337087
KEYWORDS	.
SOURCE	Norway rat.
ORGANISM	Rattus norvegicus
REFERENCE	Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 2529)
AUTHORS	Hoon/M.A., Adler/E., Lindemeier/J., Battey,J.F., Ryba,N.J. and Zuker,C.S.
TITLE	Putative mammalian taste receptors: a class of taste-specific GPCRs with distinct topographic selectivity
JOURNAL	Cell 96 (4), 541-551 (1999)
MEDLINE	99159821
REFERENCE	2 (bases 1 to 2529)
AUTHORS	Hoon,M.A., Adler,E., Lindemeier,J., Battey,J.F., Ryba,N.J.P. and Zuker,C.S.
TITLE	Direct Substitution
JOURNAL	Submitted (10-FEB-1999) Taste and Smell Unit, NIDCR, 10 Center Drive MSC 1188, Bethesda, MD 20892-1188, USA
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	1..>2529
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	/codon_start=1
	/product="putative taste receptor TR2"
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Best Local Similarity	51.6%; Pred. No. 1.4e-93;
Matches 1266; Conservative	0; Mismatches 1144; Indels 42; Gaps 9;
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DB	83 CTGATTTCACCTGGCGGGAGACTACCTCTTGCGTGGCGCTCTTTACCCTCCATGCCAACG 142
OY	202 gtctgcaggtagagaca--cagaacctgtgtgacaaagtltgtacagggccagactca 258
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OY	255 aeggccaaigctcacaccctcttccaagccaaigcgtttcacgttgtgaagaataaacact 318
DB	203 AGGTTTGAGGCTACAACTCATGACAGGCCATGCGCTTGCTGTGAGAGAAGATCAACAACACT 262
OY	319 cctcgscactgcttcaccaacaacaccctggsgtatcaactctlacagcttgctagaat 378
DB	263 GTAGCTCCCTGACTACCGGGCGTGGCTCGGGCTACGAGATGTGGATCTCTGTTAACCTCT 322
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DB 323 CCAACAATATCCACCTGGGGCTTACTTCTGCGACAGAGC---ACAGACTCTCTGCCCA 379
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DB 1931 GCTTCTCATCTGTCTATCTGT 1990
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ACCESSION	AR012624		04-DEC-1998
VERSION	AR012624.1	GI:3970614	
KEYWORDS			
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ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 3809)		
TITLE	Brown,E.W., Hebert,S.C. and Garrett,J.E. Jr.		
JOURNAL	Calcium receptor-active molecules		
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ORIGIN			849 +

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OY	2436	gcagagctgacacacatgtagcgcggtcttcaagcgttatctcctcccacgtcatgtg	2495
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RESULT	5
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DEFINITION	Sequence 3 from patent US 5858684.
ACCESSION	AR028467
VERSION	AR028467.1 GI:5940440
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 3809)
TITLE	Nemeth,E.F., Brown,E.M., Hebert,S.C., Garrett,J.E. Jr., Van Wageningen,B.C., Balandrin,M.F. and Del Mar,E.G. Method of screening calcium receptor-active molecules Patent: US 5858684-A 3 12-JAN-1999;
JOURNAL	Location/Qualifiers
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Query Match	6.6%; Score 181.6; DB 5; Length 3809;
Best Local Similarity	49.6%; Pred.No.6,4e-32;
Matches 522: Conservative	0; Mismatches 524; Indels 6; Gaps 2

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ACCESSION	I75053	
VERSION	I75053.1	GI:301194
KEYWORDS	.	
SOURCE	Unknown.	
ORGANISM	Unknown.	
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REFERENCE	1 (bases 1 to 3809)
AUTHORS	Brown, F.M., Fuller, F.H., Hebert, S.C. and Garrett, J.E. Jr.
TITLE	Calcium receptor-active molecules
JOURNAL	Patent: US 5688938-A 3 18-NOV-1997;
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LOCUS				PRI
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ACCESSION		D50855		
VERSION		D50855.1		GI:904209
KEYWORDS		Ca-sensing receptor.		
SOURCE		Homo sapiens kidney cdna to mRNA.		
ORGANISM		Homo sapiens		
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AUTHORS		Eutheria; Primates; Carnivora; Canidae; Felidae; Felis; Felis		
TITLE		1 (bases 1 to 3361)		
JOURNAL		Aida, K., Kohshi, S., Tawata, M. and Ohsawa, T.		
MEDLINE		Molecular cloning of a putative Ca(2+)-sensing receptor cDNA from		
REFERENCE		human kidney		
AUTHORS		Biochem. Biophys. Res. Commun. 214 (2), 524-529 (1995)		
TITLE		2 (bases 1 to 3361)		
JOURNAL		Aida, K.		
MEDLINE		Direct Submission		
REFERENCE		Submitted (02-JUN-1995) to the DDBJ/EMBL/Genbank databases. Kaoru		
AUTHORS		Aida, Yamanashi Medical University, The Third Department of		
TITLE		Internal Medicine; 1110 Shimokoto, Yamaho, Yamanashi 409-38, Japan		
JOURNAL		(E-mail: kaide@eres.yamanashi-med.ac.jp, Tel:0552-73-1111(ex.2318),		
FEATURES		Fax:0552-73-7108)		
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		ECDPGEYSDETDAACKCPDDFMSNENHTSCAKTEIPLSMPEKGIITLIVAGIT		
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 DEFINITION Sequence 1 from patent US 5763569.
 ACCESSION AR012622
 VERSION AR012622.1 GI:3970612
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS Brown, E.M., Hebert, S.C. and Garrett, J.E. Jr.
 TITLE Calcium receptor-active molecules
 JOURNAL Patent: US 5763569-A 1 09-JUN-1998;
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LOCUS AR028465
DEFINITION Sequence 1 from patent US 5858684.
ACCESSION AR028465
VERSION AR028465.1 GI:5940438
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5275)
AUTHORS Nemeth,E.F., Brown,E.M., Hebert,S.C., Garrett,J.F. Jr., Van
Wagenen,B.C., Balandrin,M.F. and Del Mar,E.G.
TITLE Method of screening calcium receptor-active molecules
JOURNAL Patent: US 5858684-A 1 12-JAN-1999;
FEATURES
Location/Qualifiers
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BASE COUNT 1277 a 1475 c 1315 g 1207 t
ORIGIN
Query Match 5.4% Score 176.4; DB 5; Length 5275;
Best Local Similarity 49.0% Pred. No. 1e-30;
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DEFINITION Sequence 1 from patent US 5688938.
ACCESSION I75051
VERSION I75051.1 GI:3011192
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5275)
AUTHORS Brown,E.H., Fuller,F.H., Hebert,S.C. and Garrett,J.F. Jr.
TITLE Calcium receptor-active molecules
JOURNAL Patent: US 5688938-A 1 18-NOV-1997;
FEATURES
Location/Qualifiers

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ACCESSION	AF110179				
VERSION	AF110179.1				
KEYWORDS	GI:4731164				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 4319)				
TITLE	Oda,Y., Tu,C.-L., Mauro,T. and Bikle,D.				
JOURNAL	The calcium-sensing receptor and its alternatively-spliced form in murine epidermal differentiation				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 4319)				
TITLE	Oda,Y., Tu,C.-L., Mauro,T. and Bikle,D.				
JOURNAL	Direct Submission				
FEATURES	Submitted (10-NOV-1998) 190 Dermatology, VA Medical Center - San Francisco, 4150 Clement Street, San Francisco, CA 94121, USA				
source	1..4319				
gene	/organism="Mus musculus"				
CDS	/strain="C57BL/6"				
	/db_xref="taxon:10090"				
	1..4319				
	/gene="Cacr"				
	525..3533				
	/note="G protein-coupled membrane receptor; inactive splice variant lacking exon 5; expression correlated with calcium-stimulated differentiation in keratinocytes"				
	/codon_start=1				
	/product="calcium-sensing receptor"				
	/protein_id="AND28372.1"				
	/db_xref="GI:4731165"				
	/translation="MAWFQYCLALALTWHSSAYGPDQAROKGDIILGGLPIHFHGAAKDOLKSPRESVCIRYNFRGFRLQAMFALEINSFALLPNTLTGLRIFEDICYSKALEATLIEVAONKIDSLNDEFCSSISSTIAYVAGTSGYSTAVNMLDLTYPOVYASSRLSLNKNOPKSFRTIPNDHONAMADIEFRMWWGTIADDDGPGICFPRPEAEPEDICIDSELSISQSDDEETIOOVYONSTAKAVIYVSGDDPELIKTYARNITGRIWLASEMASSSLINAPETFRHYGGTIEGGLKAGDIPERFEEQVHPKRSVHNGFAKEWETPNCHLDGAGPLVDTFVRSHEGGNRULNSTAFPLCTGGENINSVEPYMGVEHLRIYSNYLAVYSIAHALDDIYTLGRLFTNGSCDIKTEAGMVPFNSRDCOAGTRGKIGEGHTCCPECVECPDGETSGEDASACRCPDPMENENYTCIAKIEFLIAMEPEGIALTEFAVGIFLEAVLGVAFKFNFTPDKAMRELSTLLFLSLCCFSSAFPIEGPODMOTRLOPAPGASIVLCISCIIVKNINVLTPBEAKPTIFFRHKWGMNDLOPLVLTCTFPMIYCIIMLYTAPSSVSRMNEIDILITFHSGSLMAUGSLIGITCLLAAGICFFAFRSKRLPENFNKRTTISMLIFPTWISFIPVASTYGRKFSVAEVAIALAASFGLLAFENKYYILIFKSNRTIEVNSATAHAFKVARATLIRPNISRRSSSLGGSTGSPSSISKSNSEDRFPDQPEROKOOPALALCOOCCOQPLTLPPOOQOOPQPCRCOKYTFGSGVTFSLSDEPOKNAHAMNSKRSRLEAKSNDTLNRHALLPQCAEADSMTIQETGLGPMVGDHQPLEESRNSKPSALVYTSRSFYISGCGSSYNTNTHS"				
BASE COUNT	1046 a	1235 g	1058 g	980 t	
ORIGIN					


```
Db 2714 TACCTTACGATGCTCATCTTCTTCATGCTGTGATCTCCTTCATTCACGCTATGCCAG 2773
QY 2399 ttaccagggcagcctaccctgcctgggtcaatgctgcaaggctgaaccaactgaagcg 2458
Db 2774 CACCTACGGCAAGTTGTCTCTGCGGTGAGGTGATCGCATCCTGCGAGCCAGCTTTGG 2833
QY 2459 cggctcagcggttactcctccccaagtgtatgtatctctgcccgtccagaactcaa 2518
Db 2834 CTGTAGCCCTGCATCTTCTTCAACAAGTCTACATCATCTCCTTCAAGCCTTCACGGA 2893
QY 2519 caatacagaacacttcaaggcctcca 2544
Db 2894 CACCATCGAGGAGGTGCGCTCCAGCA 2919
```

Search completed: March 19, 2000, 01:20:07
Job time: 3641 sec

RESULT 2
AL562167/c
LOCUS AL562167 298 bp mRNA EST 25-MAR-1999
DEFINITION vw33d10.x1 Strataegene mouse heart (#937316) Mus musculus cDNA clone
IMAGE:1260595 3' similar to SW:ICASR_HUMAN P41180 EXTRACELLULAR
CALCIUM-SENSING RECEPTOR PRECURSOR ;, mRNA sequence.
ACCESSION AL562167
VERSION
KEYWORDS
SOURCE EST.
ORGANISM house mouse.
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 298)
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Sailer,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
TITLE The Mashu-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
COMMENT On Mar 10, 1998 this sequence version replaced gi:2948814.

Email: mouseest@watscn.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE consortium (info@image.llnl.gov) for further information.
MGI:66347
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
High quality sequence stop: 286.

FEATURES	location/Qualifiers
source	1. .298

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/organism="Mus musculus"
/strain="NIH/Swiss"
/db_xref="taxon:10090"
/clone IMAGE:126055"
/clone_id="Stratagene mouse heart (#937316)"
/sex="pooled"
/tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: heart; Vector: pBluescript SK-; Site:1:
EcoRI; Site:2: XhoI; Cloned unidirectionally. Primer
Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts.
Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5'
adaptor sequence: 5' CATTCGCACGAG 3' -3' adaptor
sequence: 5' CTCGACGTTTTTTTTTTTTTTTTT 3'"

```

Query Match	11.4%	Score 294.8	DB 48	Length 298
Best Local Similarity	99.3%	Pred. No. 1.3e-68		
Matches 296	0	Mismatches 2	Indels 0	Gaps 0

Qy	506	ccccgcgtcaactatctgagcgacgacgctgctctctcagctggaagcgcaagttccctcc	565
Dp	298	ccacaggtcacactatgagcgcgagcgtgtatctctcaatgtgggaagcccaattctccctcc	239
Qy	566	tcttgcgcacacatcccacgagataaagtaacagttgtaagctcaatgcgcgtctgtcag	625
Dp	238	ttcttgcgcacacatcccacgagataaagtaacagttgtaagctcaatgcgcgtctgtcag	179
Qy	626	agcttcgcgtcgtctgtatctcgtctgttgcgcgtatgtgtactacgagcaagctggc	683
Dp	178	agcttcgcgtcgtctgtatctcgtctgttgcgcgtatgtgtactacgagcaagctggc	119

Oy 686 gtacagagcgctcgagagagctgagccacaccacacagggagctctgcgcttcaagagactg 745
 Db 118 GTACAGCGCGCTGAGAGACTTGGACCTTCACCTCCACGAGGACTTCTGCTGGCTTCAGAGAGCTG 59
 Oy 746 gtgctctcttcgcgccacagcgcggtgaccccaagaagatgacgcgcatgatgcgcgctcgg 803
 Db 58 GTGCTCTCTCTCGGCCCAAGCGCGGTGACCCCAAGGATGACGGCCAGAGAGCTGCGCTGTGG 1

[illegible]

REFERENCE 1 (bases 1 to 562)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Dec 20, 1995 this sequence version replaced gi:1130951.

Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:1130951.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LINT; contact the
IMAE Consortium (info@mae.lint.gov) for further information.
Seq primer: 400P from Gibco
High quality sequence stop: 468.

FEATURES	Location/Qualifiers
source	1. .562

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2357578"
/clone_1ib=" Soares.NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: Pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following BAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NBHSF pool 1: 309384-310919, 323308-325893 Soares Nb2MF pool 1: 145032-147335, 147720-148303, 148872-149255, 15002 - 150407, 151176-152327 Soares Nb2MF8_9W pool 1: 758280-760583, 772104-774407 Soares NbHFA pool 1: 304776-306311, 320136-322823, 325280-32663 Soares NBHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bencton Soares and M. Fatima Bonaldo."

```

BASE COUNT	116 a	161 c	167 g	117 t	1 others
ORIGIN					

Query Match	10.8%	Score 279.2	DB 51	Length 562
Best Local Similarly	83.2%	Pred. No. 3e-54		
Matches 317	Conservative	0	Mismatches 64	Indels 0
				Gaps 0

Oy	2159	gtatcttccttaagtcacaaaggagcacaactcgcgtagcttcccgagcttgacacacac	2218
Dd	562	GTATGCTTAAAGTCACAAAGACCACCTCCNBSGCTTATACTGGCTTCTCTTACAAT	503
Oy	2219	atctctctctocacagcacctttgtctcgaagtaccctggtaagaacctccgagaac	2278
Dd	502	GGCCTCCTCCATCATAGTGGCTTTTGCTCGTAGTACTGGTAAGAAGACTTGCCAAGAAC	443

[illegible]

RESULT	4
A1A15100/c	
LOCUS	A1A15100 421 bp mRNA EST 09-FEB-1999
DEFINITION	mb98601.x1 Soares mouse p3MMF19.5 Mus musculus cDNA clone
CALCULUM-SENSING RECEPTOR PRECURSOR ;;	similar to SW/CASR RAT P48442 EXTRACELLULAR RNA sequence.

ACCESSION	AI415100	GI:4258604
VERSION	AI415100.1	
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE
AUTHORS
1 (bases 1 to 421)
Marr, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.
Eukaryota; Metazoa; Chordata; Crinata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE Underwood, R., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
 Person, B., Swaller, T., Gibbons, M., Paped, D., Harvey, N., Schurk,
 Rittner, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., Mcconn,
 Waterston, R. and Wilson, R.
 The WashU NCI Mouse EST Project 1999
 JOURNAL Unpublished (1999)
 COMMENT On Apr 21, 1998 this sequence version replaced g1:3073000.

Contact: Marra M/Mashu-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel.: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LINDL ; contact the
IMAGE Consortium (info@image.lindl.gov) for further information.
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 373.

FEATURES

source

```

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:337441"
/clone_lib="Soares mouse p3N9F19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/notes="Vector: p77R3 (Pharmacia) with a modified
polylinker. Site 1: Not I; site 2: Eco RI; 1st strand cDNA
was primed with a Not I oligo(dT) primer; 15'
TGATCCCAATCTGAAGGGAGGCGCCGCAATTTTTTTTTTTT 3'1,
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p77R3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento

```

Soares and M. Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

Query Match	10.5%	Score 270.2;	DB 46;	Length 421;
Best Local Similarity	98.9%;	Pred. No. 6.5e-62;		
Matches 272; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0

QY 2276 aactataacgaagccaatgtgtcaacttcagcctgcctcccaacttcgtatcctggtc 2335

DB 421 AACAAACGAGGCCAAAGTGTGTCACCTTCAGCCCTGCTCCCTCCACTTGTGTAACCTGGATC 362

Db 361 GCTTCTCACCATGTCCAGCATTTACCGAGGACGCTACCTACCGCGGCTAATGTGCTG 302

2396 gcaggcgctgccaactctgagtgcgcgcttcagcgcgctttccctccctaagtctaagt 2455

Db 301 GCAGGCTGGCCACTCTGATGCGGGCTTCAGCGGCTATTCCCTCCCTAAATGCTACGTG 242

Db 241 ATCTCTGGCCGTCGAACACTCAACAACACAGAACACTTTCAGGCTCCATCCAGGACTAC 182

QY 2516 acgagggcgtgcgcgcactaactgagggcgtcgcgc 2550

Db 181 ACGAGGCGCTGCGGCACCTACTGATCCGCTGGGGC 147

RESULT	5
AA853967/c	
LOCUS	
DEFINITION	AA853967 496 bp mRNA
	aj51d10.s1 Soares:testis_NRT Homo sapiens cDNA clone IMAGE:133986666
	EST 31-DEC-1998

ACCESSION	AA853967	RECEPTOR PRECURSOR ; mRNA sequence.
VERSION	AA853967.1	3 similar to SW:CAPS_RAT P48442 EXTRACELLULAR CALCIUM-SENSING
KEYWORDS	EST.	
SOURCE	human.	

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS	1 (Bases 1 to 496)
TITLE	NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap .
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT	Unpublished (1997)
COMMENT	On Jan 14, 1998 this sequence version replaced g1:1797381.

Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert.Strausberg@nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CCAB clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNM at:
www-bio.lnl.gov/bbrp/image/image.html

Possible reversed clone: similarity on wrong strand
Insert Length: 878 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 223.

```

FEATURES
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    location/Qualifiers
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      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:133865"
      /clone_1lb="Soares_testis_NBT"
      /sex="male"
      /lab_host="DH10B"

```


/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5', TGTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 102 a 145 c 148 g 100 t 1 others

ORIGIN

Query Match 7.9%; Score 204.4; DB:39; Length 496;
Best Local Similarity 81.5%; Pred. No. 3.3e-44;
Matches 260; Conservative 0; Mismatches 57; Indels 2; Gaps 2;

QY 2221 cctctctccatcagcaacttctgtctgagctactcgtgtaagagatccggaacta 2280
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 494 CCTCTTCCCATCAGATGCGCTTCCCTGCAGCTACTGGTAAAGACTTGCCAGAACTA 435
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2281 taacgaagccaatggtcactctcagcctgcctccacttcgtatcctgagcttt 2340
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 434 CAAGGAGGCCAAATGTCTACCTTCAGCCTGCTTCAATTCGTCTGATCGCCTT 375
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2341 cttaacatgtccagatcttccacgggagagctactaccgagcgaatgctgagcgg 2400
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 374 CTTCACCGCGGCTCTACGAGGCAAGTA-ANCTTTCGGCGCAATGATGCG-IG 317
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2401 gctgcccactgagtgagcagctcagcagcgtatctctccctaatactcagatctct 2460
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 316 GCTAGACGACCTGAGCAGCGGCTTGGTGGATTTTCTGCTAAGTCTACGATATCT 257
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2461 ctgcgctccaaactcaacacagaaacttcaaggcctccatccaggaactacagag 2520
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 256 CTGCCGCCACAGCTCAACAGACAGACTTCAGCGCTCCATTCAGGACTACAGCAG 197
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2521 ggcgtggcagctactcgtta 2539
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 196 GCGCTGCGGCTCCACCTTA 178
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
LOCUS W18663 247 bp mRNA EST 10-SEP-1996
DEFINITION m986d01.t1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
IMAGE:337441 5', mRNA sequence.
ACCESSION W18663
VERSION W18663.1 GI:1294371
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 247)
Geisel,S., Kucaba,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Teisling,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
On May 9, 1995 this sequence version replaced gi:802427.
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:218841
Seq primer: mob. REGA-ET
High quality sequence stop: 225.
Location/Qualifiers

FEATURES
source
1. 247
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:337441"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

BASE COUNT 44 a 89 c 42 g 72 t

ORIGIN

Query Match 7.5%; Score 192.2; DB:26; Length 247;
Best Local Similarity 98.5%; Pred. No. 4e-41;
Matches 194; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1904 tgcgtgcgtcgaagccctcttctctcgggttccatcttccctcctcgtctgaca 1963
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 46 TTCTTGTGCTCAGCGCCCTTTTCTCTCGGTTTGCAATTTCTCTCTGTCTGACA 105
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1964 atccgctctcttcacatggtcatcatctcaagtcttccacaaaggtaccacattctac 2023
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 106 ATCCGCTCCTTCACAGTGCATCATCTTCAAGTTTCTACCAAGTACCAATCTAC 165
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2024 cagactggggcccaaacatagtgccgggaatctctcatctgcaagctccaggtccat 2083
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 165 CACACTTGGGCCCAAAACAGTGGCGGAATTCTGTCATTTGACGCTCCACGGTCCAT 225
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2084 ttgttcctc-gtctcac 2100
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 226 TTGTTCTCTGTCTCAC 242
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
LOCUS AA937218/c 464 bp mRNA EST 09-JUN-1998
DEFINITION OK13f08.s1 Soares_NSF_F8_9W_OT_PA_2-S1 Homo sapiens cDNA clone
IMAGE:1507719 3 similar to SW:CA5R_HUMAN P41180 EXTRACELLULAR
CALCIUM-SENSING RECEPTOR PRECURSOR; mRNA sequence.
ACCESSION AA937218
VERSION AA937218.1 GI:3095329
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 464)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2150441.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1252 Std Error: 0.00

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE	99380589
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L

Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPO1-11. For BAC library availability, please contact Pieter de Jong (pieterdejong@med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering/bac.htm>) or from Research Genetics (info@resgen.com). BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 714 row: F column: 8
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 514.

```

FEATURES
  source
    Location/Qualifiers
      1..514
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="Plate714 Col=8 Row=F"
        /clone_lib="RPCr-11 Human Male BAC Library"
        /sex="male"
        /note="Vector: pBACe3.6; Genomic sequence of BAC ends
122 a 123 c 124 g 104 t 1 others
BASE COUNT
ORIGIN

```

Query Match:	2.9%	Score 74.4:	DB 105:	Length 514:
Best Local Similarity:	63.7%	Pred. No. 2.7e+09:		
Matches 128:	Conservative 0:	Mismatches 72:	Indels 1:	Gaps 1:

QY 1408 catggtctctgcgccactgtctctcagtttcacatcagacataataagacaaaaatccagtg 1467

QY 1468 gcaacgggaagaacaatcagtgccctgtctcagtggtgtaccaggagactgtctcgaaggca 1527

309 GCCCCTCCTGGCTTACAGGTCATAGCTCTGTGTGTCACGCMACATGCTCTGAAAGGCA 310
 DU
 1528 GCACAGTTGTGTCATGTGATCCCAACCAC-TGCTGCTTCAGATGACATGCCCTGTAACTG 1529
 QY

Db 309 CCAGCAGTGTGTAACGGGTTCCATCACATGCTGCTTGTGATGTGTGCCCTGTGGGCTG 250

Db 249 GGACCTTCCTCATCAAGAGTG 229

RESULT	10
AV278654	
LOCUS	AV278654 260 bp mRNA EST 05-NOV-1999
DEFINITION	AV278654 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4933403B08 3', RNA sequence.
ACCESSION	AV278654
VERSION	AV278654.1 GI:6266691
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE
AUTHORS

1 (bases 1 to 260)
Kono, H., Aikawa, K., Akhira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Iwano, M., Kadoya, K., Kagawa, I., Kai, C., Kawai, Y., Kikuchi, N., Kojima, Y., Koya, S., Kusakaue, M.,

Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
 Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K.,
 Shibata,Y., Shigemoto,Y., Shikata,T., Sugabe,Y., Sugihara,Y.,
 Suzuki,H., Suzuki,H., Takahashi,F., Tano,M., Tomihara,Y.,
 Tsunoda,Y., Uchihiki,A., Watanabe,S., Yamamura,T., Yasunishi,A.,
 Yokota,Y., Yoshiki,A., Yoshino,M., Yamatsu,M., and Hayashizaki,Y.
 RIKEN KOSEI ESIS (Konno,H., et al.)
 Unpublished (1999)
 On Mar 10, 1998 this sequence version replaced g1:2948605.
 JOURNAL COMMENT

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp
URL: <http://genome.rtc.riken.go.jp/>
Sasaki, N., Izawa, M., Watanabe, M., Ozawa, K., Tanaka, T., Yoneda, Y.,
Matsunari, S., Carninci, P., Muramatsu, M., Okazaki, Y., and
Hayashizaki, Y.
Transcriptional sequencing: A method for DNA sequencing using RNase
polymerase. *Proc. Natl. Acad. Sci. U.S.A.* 95 (7), 3455-3460 (1998).
Itoh, M., Kitsumori, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
Okazaki, Y., and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. *Genome Res.* 9 (5), 463-470 (1999)
Carninci, P., and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303,
19-44 (1999)

FEATURES	Location/Qualifiers
source	1. .260

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="493403308"
/clone_lib="RIKEN full-length enriched, adult male testis
(DH10B)"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Site.1: SalI; Site.2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAAGAGAGAGAGATCCACAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAAGAGAGAGATCTCGAGTAAATTAATATGCCCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I. Cloning sites, 5' end: SalI, 3' end: BamHI."

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Query Match	2.9%	Score 74.2	DB 71	Length 260
Best Local Similarity	71.9%	Pred. No. 2e-09		
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b	2	tgttttttccctacatccraccctgattttatacccttccctgattttttttacatttaacg	61

[illegible]

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ORIGIN					
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Best Local Similarity	54.0%;	Pred. No. 3.3e-06;			
Matches 129;	Conservative 0;	Mismatches 110;	Indels 0;	Gaps 0;	
Qy	437	gcactcattggcgctcgtataacactgtaccacgcgtctacacactgtctcctgttgagcct	496		
Db	206	GCATTCCTGGGAGAAACACTACTCTGAGCTATCATTCATTCGCTATGCGCAAGCTCCTCAGGCTC	265		
Qy	497	tttcctgatgccccctgttaagctataagagcgagacagcgtgatctcctaagtggggaagcgcaag	556		
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Db	326	TACCGCTCTTCATTCATTCGCTGCTGATTTCCAGATATGCTGTACACAGGCTCAGCGCTGCTCAAG	385		
Qy	617	ctgctgcagagccttcgcgttggtgtgaatctgcctcgtctgttgccagctatgtgtactacgg	675		
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LOCUS	FR0044379	619 bp	DNA	GSS	22-Oct-1999
DEFINITION	Fugu rubripes GSS sequence, clone 184F17aE5, genomic survey				
ACCESSION	AL131871				
VERSION	AL131871.1	GI:5113817			
KEYWORDS	GSS; genome survey sequence.				
SOURCE	Fugu rubripes.				
ORGANISM	Fugu rubripes				
REFERENCE	Elgar, G., Clark, M.S., Smith, S., Meek, S., Warner, S., Edwards, Y.J.K., Umranta, Y., Williams, G. and Brenner, S.				
AUTHORS	Umranta, Y., Williams, G. and Brenner, S.				
TITLE	Direct Submission				
JOURNAL	Submitted (11-Oct-1999) MRC Human Genome Mapping Project Resource				
COMMENT	Centre, Hinxton, Cambridge, CB10 1SB. UK Email: biolhelp@mp.mrc.ac.uk				
Y-clone: pBluescript II KS					
PRIMER: KS					
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sequence.					
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QY	2335	tatcttgagcgtctcttcacacagtcacagattacacagggcagcgtaccacccggg	2384
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Db	166	TGGAAATCTTTGCCATTTTGGCCTCCACAGTTTGGACTCATCTGTGCAATTTTGGCTCCA	225
QY	2445	aatgtcagcgtgattctctgcgcgttcagaaactcaacaacacagaaacct	2493
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LOCUS	AL040113	732 bp	EST
DEFINITION	DKFZP434C2213.F1 434 (synonym: htes3) Homo sapiens cDNA clone		29-SEP-1999
ACCESSION	AL040113		
VERSION	AL040113.2	GI:5935280	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 732)		
TITLE	Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.		
JOURNAL	EST (Koehler, et al.)		
COMMENT	Unpublished (1999)		
	On Jul 7, 1999, this sequence version replaced gi:5409080.		
	Contact: Koehler K		
	MIPS		
	Am Klopferpitz 18a D-82152 Martinsried, Germany		
	This is the 5' sequence of the clone insert		
	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de		
	Sequenced by BMFZ within the cDNA sequencing consortium of the German Genome Project.		
	No sl sequence available.		
	This clone is available at the RZPD in Berlin.		
	Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMAN; Email: clone@rzpd.de.		
FEATURES			
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QY	1829	tccccaagcgtggtgttcccttggttacctcgggaattgcagaccttcaagctcttcgggaag	1888
Db	79	TACATCTGCTGGTGGGTGGTGTCTCTCTGCTACTGATGCAATGACCTTATCTATTGGCAAG	138
QY	1889	cccaagtgagcccgagcgtctgcgtgcagagccctcttcctcggggttgcaatttc	1948
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[illegible]

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RESULT 14
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LOCUS
DEFINITION
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t120c10.x1 NCI-CGAP_Kid11 Homo sapiens CDNA clone IMAGE:2131025 3'
SIMILAR to SW:GCSR_HUMAN P41180 EXTRACTED FROM CALCIUM-SENSING
RECEPTOR PRECURSOR ; , mRNA sequence.
ACCESSION
AI434785
VERSION
AI434785.1 GI:4298607
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 602)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Mar 7, 1998 this sequence version replaced gi:3121344.
COMMENT
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdnp/image/image.html
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RESULT 2
US-08-484-565-3
; Sequence 3, Application US/08484565
; Patent No. 5763569
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,565
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9

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; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hebert, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ. ID NO. 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3809 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 373..3606
; OTHER INFORMATION:
; US-08-484-565-3

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 Qy 1667 tgccttcacagcagctgt 1726
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 Qy 1787 cttaacagcagctgt 1846
 Db 2284 CGCACACACCATTTGTCAAGGCGCAACAGAGAGCTTCTTACCTCTCTCTTCTTC 2343
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 Qy 1907 ttgt 1966
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RESULT 3

US-08-480-751-3
 ; Sequence 3, Application US/08480751

; Patent No. 5858684

; GENERAL INFORMATION:

; APPLICANT: Edward F. Nemeth

; APPLICANT: Edward M. Brown

; APPLICANT: Steven C. Hebert

; APPLICANT: Forrest H. Fuller

; APPLICANT: James E. Garrett, Jr.


```

? TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
? TITLE OF INVENTION: MOLECULES
? NUMBER OF SEQUENCES: 20
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Lyon & Lyon
? STREET: First Interstate World Center
? STREET: Suite 4700
? STREET: 633 West Fifth Street
? CITY: Los Angeles
? STATE: California
? COUNTRY: USA
? ZIP: 90071
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: FASTSEQ
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/480,751
? FILING DATE: 7 June, 1995
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? PRIOR APPLICATION DATA: including application
? PRIOR APPLICATION DATA: described below: 9
? APPLICATION NUMBER: 08/353,784
? FILING DATE: 9 December, 1994
? APPLICATION NUMBER: PCT/US/94/12117
? FILING DATE: 21 October, 1994
? APPLICATION NUMBER: U.S. 08/292,827
? FILING DATE: 23 August, 1994
? APPLICATION NUMBER: U.S. 08/141,248
? FILING DATE: 22 October, 1993
? APPLICATION NUMBER: U.S. 08/009,389
? FILING DATE: 23 February, 1993
? APPLICATION NUMBER: U.S. 08/017,127
? FILING DATE: 12 February, 1993
? APPLICATION NUMBER: U.S. 07/934,161
? FILING DATE: 21 August, 1992
? APPLICATION NUMBER: U.S. 07/834,044
? FILING DATE: 11 February, 1992
? APPLICATION NUMBER: U.S. 07/749,451
? FILING DATE: 23 August, 1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Heber, Sheldon O.
? REGISTRATION NUMBER: 38,179
? REFERENCE/DOCKET NUMBER: 213/004
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (213) 489-1600
? TELEFAX: (213) 955-0440
? TELEX: 67-3510
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 3809 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: CDNA to mRNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 373..3606
? OTHER INFORMATION:
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? US-08-480-751-3

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Query Match 6.4% Score 166.2 DB: 3 Length 3809;
Best Local Similarity 46.3% Pred. No. 1.9e+37;
Matches 1130: Conservative 0; Mismatches 1143; Indels 168; Gaps 11;

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RESULT 4
US-08-943-986-3
Sequence 3, Application US/08943986
Patent No. 5962314
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,986
FILING DATE: 03-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:


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Db 2881 GAGGTGATTTGCCATCTTGCAAGCCAGCTTGTGCTGCTGCGCTGCTTCTTCAACAG 2940
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Db 2941 ATCTACATCATCTTCTTCAAGCCATCCCGCAACACATCA 2981

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RESULT 5
US-08-353-784-3
Sequence 3, Application US/08353784
Patent No. 6011068

GENERAL INFORMATION:

APPLICANT: Edward F. Nemeth, Edward M.
APPLICANT: Brown, Steven C. Hebert,
APPLICANT: Bradford C. Van Wagonen, Manuel
APPLICANT: F. Balandrin, Forrest H. Fuller,
APPLICANT: Eric G. Delmar, and Scott T. Moe
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,784
FILING DATE: 9 December, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 8
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827

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? FILING DATE: 23 August, 1994
? APPLICATION NUMBER: U.S. 08/141,248
? FILING DATE: 22 October, 1993
? APPLICATION NUMBER: U.S. 08/009,389
? FILING DATE: 23 February, 1993
? APPLICATION NUMBER: U.S. 08/017,127
? FILING DATE: 12 February, 1993
? APPLICATION NUMBER: U.S. 07/934,161
? FILING DATE: 21 August, 1992
? APPLICATION NUMBER: U.S. 07/834,044
? FILING DATE: 11 February, 1992
? APPLICATION NUMBER: U.S. 07/749,451
? FILING DATE: 23 August, 1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Heber, Sheldon O.
? REGISTRATION NUMBER: 38,179
? REFERENCE/DOCKET NUMBER: 209/069
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (213) 489-1600
? TELEFAX: (213) 955-0440
? TELEX: 67-3510
? INFORMATION FOR SEQ. ID NO. 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 3809 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 373..3606
? OTHER INFORMATION:
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? US-08-353-784-3

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Query Match 6.4%; Score 166.2; DB 5; Length 3809;
Best Local Similarity 46.3%; Pred. No. 1.9e-37;
Matches 1130; Conservative 0; Mismatches 1143; Indels 168; Gaps 11;

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Qy 1667 tgccttcaagcagcgtgtgagttcttgggtgtgcatgaaaccaatctcttgtgtgtat 1726
Dh 2164 TGCATTGCCAAGAGATCGAGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2223
Qy 1727 gcagctaacagcgtatgt 1786
Dh 2224 CTTTGTGCGGT 2283
Qy 1787 ctccacagcgt 1846
Dh 2284 CGCAACACACCCATTGTCAAGGCGCACCAACGAGAGCTCTTCACTCTCTCTCTCTCC 2343
Qy 1847 tigtgtcgtgaggtgtgcagcctctcaagcttcttgggaagcccaagtggtgtgtgt 1906
Dh 2344 CTGCTGTGCTGTCTTCTCAAGCTCTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCT 2403
Qy 1907 tigtgtcgtcagcgcctctcttctctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1966
Dh 2404 CGCTGCGCGCAGCGGCGCTTTGGCATCAGCTTGCTGTGTGTGTGTGTGTGTGTGTGT 2463
Qy 1967 cgtctcttccaaactgtgtcatctcaagtcttctcacaaggtaccacatctacac 2026
Dh 2464 AAACCAACCGTGTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2520
Qy 2027 actgtgtcccaazacacatgt 2085
Dh 2521 AAGTGTGGGGGCTCAACCTCGACATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2580
Qy 2087 ttcctctgtctcagctgt 2146
Dh 2581 GTCATGT 2640
Qy 2147 tcccccaatcgt 2206
Dh 2641 GAGAGATGAGATCATCTTCACTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2700
Qy 2207 ttcgacacaaactcctctctccatcaagcactgtgtgtgtgtgtgtgtgtgtgtgtgt 2266
Dh 2701 ATGCGCTACACCTGCTGT 2760
Qy 2267 ctgcgagaaactataaagcagaagcagaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2326
Dh 2761 CTGCGGAGAGACTTCATATGAAGCAAGTTCATCACCCTTAGCATGCTCATCTTCTCATC 2820
Qy 2327 tccgt 2386
Dh 2821 GTCTGATCTCTTCAATTCAGGCTATGCGACAGCACTATGCGAAGTGTGTGTGTGT 2880
Qy 2387 aatgt 2446
Dh 2881 GAGGTATTTGCCATCTGTGCGACGCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2940
Qy 2447 tgt 2487
Dh 2941 ATCTACATCATTTCTTCAAGCATCCCGCAACACATGCA 2981

RESULT 6
US-08-485-588-1
: Sequence 1, Application US/08485588
: Patent No. 5688938
: GENERAL INFORMATION:
: APPLICANT: Edward M. Brown
: APPLICANT: Steven C. Hebert
: APPLICANT: Forrest H. Fuller
: APPLICANT: James E. Garet, Jr.
: TITLE OF INVENTION: MOLECULES
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: First Interstate World Center


```

STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSO

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 515..3765
OTHER INFORMATION:
US-08-485-588-1

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Query Match 6.1%; Score 157.2; DB 1; Length 5275;
Best Local Similarity 46.0%; Pred. No. 8e-35;
Matches 1136; Conservative 0; Mismatches 1168; Indels 168; Gaps 11;

QY 382 gacagc-----caactagacatgcagagagatcttcgcaaccaactctccaagtgct 435
DB 874 AATTGACTCTTTGAACTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 933
QY 436 ggcacatcttgagcctgataaacaatgcagcgtgtaccactgtctcctcgaagcc 495
DB 934 CGCAGTGTGGGAGCTACAGCTGCGGCTCCGATCCACAGCAGTGGCCAACTCTGGGCT 993
QY 496 ttctcgatgcccctgtgacatgagcagcagcgtgacccatgagtggaagcgaca 555
DB 994 CTCTACATCCCGAGCTGACGATGCTCTCTCCAGCAGCTCTCCAGCAGCAGATCA 1053
QY 556 gtcccgctctcttcgcacacatcccccagcagataagtaagcaggtggaatgatg 615
DB 1054 ATTCAGTCTCTCTCTCCGACCATACCAATGATGATGATGATGATGATGATGATGAT 1113
QY 616 gctgctgcagagcttcgctggtgtgatactcgtctgctgctgagcactatgtaag 675
DB 1114 CATCATCGAGTACTTCCGCTGGAACGTGGGTCACAAATTCAGCTGACGATGACTAT 1173
QY 676 gcaagctggcgtgacagcgtgagagctggtccactccagcagcgtgctgctgct 735
DB 1174 CCGCCAGGAGATCGAAGATTTGAGAGGAGCTGAGAGAGGAGATCTGATGACTT 1233
QY 736 caagagcgtggtgctctctcgcgccagcgggtgagcccaagatgcaagcgtatgct 795
DB 1234 CACGCA-----GCTCATCTCCCAATACCTGATGAGAAAAGATTCACAGAGTGGTGA 1287
QY 796 ggcctgctgcagagcagcagcagcagcagcagcagcagcagcagcagcagcagc 855
DB 1288 GGTGATCCAGAAATCCACCCGCAAAAGTCTGCTCTCCAGCGGCTCCAGCTGGA 1347
QY 856 aggtcttcacagctggtggtgctgctgctgctgctgctgctgctgctgctgctg 915
DB 1348 ACCCTCATCAAGAGATGCTCGGCGCAATATCACAGCAGAGATCTGCTGCGCAGCA 1407
QY 916 agactggccatctccagctacatcaccaatgctccggatgctcagggatctgagcgt 975
DB 1408 GGCCTGGGCGAGCTCTCCCTGATGCTATGCCCCGAGTATTCATGCTGAGGCGC 1467
QY 976 gctggggtggtgcacatcagcagcagcagcagcagcagcagcagcagcagcagc 1024
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DB 1588 CTCGACCTGCAAGAGAGGTGTAAGGCCCCATTTACCGGTGACACCTCTCGAGGTCA 1647
QY 1125 cgaacatggaacatgccgagcgtgagcgttccatcagcagcgtgagcagcgtg 1170
DB 1648 CGAAGAAGAGGTGCGAGGTAAAGCAACATCCACTGCTTCCGACCTGTGCACTGG 1707
QY 1170 -----c 1170
DB 1708 GAGAGGAACATTCAGAGTGTGAGACTCTTACATGATTTTACACATTTTACGATATC 1767
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DB 1768 CTCAACAGCTACTTACGCGGTCTACATTCCTGCTGCTGCTGCTGCTGCTGCTGCT 1827
QY 1231 tacctctgga-----cgtgacagagcagcagcagcagcagcagcagcagcagc 1266
DB 1828 CATACCTGGAGAGGCTCTTACCAACAGCTTCTGCGGAGATATCAACAAAGTTGAAC 1887
QY 1267 ctgagcgtctctgacagcagcagcagcagcagcagcagcagcagcagcagcagc 1323
DB 1888 TTGGCAGGTCTGAACACCTGCGGCACTTAATTTTACCAACATATGAGGAGCAAGT 1947

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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 515..3769
OTHER INFORMATION:
US-08-484-565-1

Query Match 6 1%; Score 157.2; DB 2; Length 5275;
Best Local Similarity 46.0%; Pred. No. 8e-35;
Matches 1136; Conservative 0; Mismatches 1168; Indels 168; Gaps 11;

QY 205 gctcgaagcttcaacagcagctgcatcacccttcccaagccatcggttaccgttga 264
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QY 265 ggaagataaacaactcacaagctctgtctcccaacatcacccttgggtatgnaactgtatga 324
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QY 325 cgtgtg---ctcagagcttcccaatgtctatgtcacccttggaggtgtcccgcccaagaag 381
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QY 382 gacagc-----cacctagagaatgagagagatcttcgaacactctcccaagttgt 435
DB 874 aattgaccttttgaaccttgatgatttgcacactgctcagacacatccctctacact 933
QY 436 ggcactcaattgtgctgataaacaactgtacacagctgtacacactgtgcctctgagccc 495
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QY 616 gctgtctcagaagctcgtgctggtgtgatactcgtcgtgttggaactatgtgtactcag 675
DB 1114 catcatcgactgacttctccgagaaactgggtgggacacatttgcagctgagatgactatg 1173
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QY 1125 cgaacttgaaacatcccgagcttggagccttccatgagcgtg----- 1170
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QY 1324 agcatctgatacgaagggagccctctagattatgacatcactgcctgtgagtgaa 1383
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DB 2368 gcttcttggctgt 2427
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QY 1846 ctgtgtacgt 1905
DB 2488 cctgctgt 2547
QY 1906 ctgt 1965
DB 2548 ccgctgt 2607
QY 1966 ccgctgt 2025
DB 2608 gaaaac---caatcggt 2664


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QY 2026 cacttgagcccaaacatggtgcggaatatctgcatctgacgtccacggctccatt 2085
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Db 2665 GAGGTGGTGGGGGCTCAACTGCAAGTTCCTGGTGGTCTCTCTGCACTTATGCGAT 2724
QY 2086 gtccctctgctcaagtggtcttcaatgctgaagcccaaggcccaaggagtaacagcg 2145
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2725 TGTATCTGTGGCATTTGGCTCAATACAGCGCCCCCTCGAGCTACCGCAACGACGAGCT 2784
QY 2146 ctcccccacatcgtgagttcttgatgacagaggtcaactcgtggtgcttcctgtagcg 2205
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Db 2785 GAGGAGACGAGATATCTTATACCTTGCCACAGGGGTCCCTATGCGCTGGGCTTCTT 2844
QY 2206 ttccgacaacaacatccctctccatcagcaccttctgctcagcttaactggtgaagga 2265
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Db 2845 GATCGGCTACACCTGCTGGTGGCGGCGCATCTGTTCTTTTGGCCTTCAAGTCCCGAA 2304
QY 2266 actgcgcggaactataaagaagccaaatgttcaaccttcaagctgctcctcaactcgt 2325
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Db 2905 GCTGCCAGAACTTCAATGACCAAGTTCATCACCCTTCAGCATGCTCATCTTCTCAT 2964
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Db 3025 GAGAGGTGATGGCATCTGCGGCGGCGCAAGCTTGGCTTGTCTGTGCTTATCTTCAACAA 3084
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Db 3085 GGCTTACATCTCTCTTCAAGCTTCCCGAAACACCATCGAGAGGTGCGCTGACGAC 3144
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Db 3145 CCGCGCACACGC 3156

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RESULT 8

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US-08-480-751-1
; Sequence 1, Application US/08480751
; Patent No. 5858684
; GENERAL INFORMATION:
; APPLICANT: Edward F. Nemeth
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: Forrest H. Fuller
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIDIUM RECEPTOR-ACTIVE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,751
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784

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; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 2: October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5275 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 515..3769
; OTHER INFORMATION:
US-08-480-751-1

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Query Match 6.1%; Score 157.2; DB 3; Length 5275;

Best Local Similarity 46.0%; Pred. No. 8e-35; Matches 1136; Conservative 0; Mismatches 1168; Indels 168; Gaps 11;

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Db 874 AATTGACTCTTTAACTTGATGATGATTCTGCAACTCTCTAGAGACATATCCCTCTACAT 933
QY 436 ggaactcatgtggccatgaacactgacacagcgtgtcaccaactgtgacctgtgagcc 495
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Db 934 CGCAGTGGTGGAGCTACAGGCTCGGCGCATCTCCACAGCAGTGGCCACACTGTGGGGCT 993
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Db 1114 CATCATCGAGTACTCCGCTGGAACTGGGTGGGACAAATTGCAGCTGACATGACTATGG 1173
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RESULT 9
 US-08-943-986-1
 ; Sequence 1, Application US/08943986
 ; Patent No. 5962314
 ; GENERAL INFORMATION:
 ; APPLICANT: Edward M. Brown
 ; APPLICANT: Steven C. Hebert

APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,986
FILING DATE: 03-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/006
TELECOMMUNICATION INFORMATION:
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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 515..3769
OTHER INFORMATION:
US-08-943-986-1

Query Match 6.1%; Score 157.2; DB 4; Length 5275;
Best Local Similarity 46.0%; Pred. No. 8e-35;
Matches 1136; Conservative 0; Mismatches 1168; Indels 168; Gaps 11;

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RESULT 10
 US-08-353-784-1
 ; Sequence 1, Application US/08353784
 ; Patent No. 6011068
 ; GENERAL INFORMATION:
 ; APPLICANT: Edward F. Nemeth, Edward M.
 ; APPLICANT: Brown, Steven C. Hebert,
 ; APPLICANT: Bradford C. Van Wageningen, Manuel
 ; APPLICANT: F. Balandrin, Forrest H. Fuller,
 ; APPLICANT: Eric G. Delmar, and Scott T. Moe
 ; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: First Interstate World Center
 ; STREET: Suite 4700
 ; STREET: 633 West Fifth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: FASTSEQ
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/353,784
 ; FILING DATE: 9 December, 1994
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; PRIOR APPLICATION DATA: including application
 ; PRIOR APPLICATION NUMBER: described below: 8
 ; APPLICATION NUMBER: PCT/US/94/12117
 ; FILING DATE: 21 October, 1994
 ; APPLICATION NUMBER: U.S. 08/292,827
 ; FILING DATE: 23 August, 1994
 ; APPLICATION NUMBER: U.S. 08/141,248
 ; FILING DATE: 22 October, 1993
 ; APPLICATION NUMBER: U.S. 08/009,389
 ; FILING DATE: 23 February, 1993
 ; APPLICATION NUMBER: U.S. 08/017,127
 ; FILING DATE: 12 February, 1993
 ; APPLICATION NUMBER: U.S. 07/993,161
 ; FILING DATE: 21 August, 1992
 ; APPLICATION NUMBER: U.S. 07/834,044
 ; FILING DATE: 11 February, 1992
 ; APPLICATION NUMBER: U.S. 07/749,451
 ; FILING DATE: 23 August, 1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Heber, Sheldon O.
 ; REGISTRATION NUMBER: 38,179
 ; REFERENCE/DOCKET NUMBER: 209/069


```

: TELECOMMUNICATION INFORMATION
: TELEPHONE: (213) 489-1600
:
: TELEFAX: (213) 955-0440
:
: TELEX: 67-3510
:
: INFORMATION FOR SEQ ID NO: 1:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 5275 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: MOLECULE TYPE: cDNA to mRNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 515..3769
:
: OTHER INFORMATION:
:
: US-08-353-784-I

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QY	2146	cttcccccatactgtgtattctttgagtgacagaggtcaactctgttggcttctgtgac	2205
Db	2785	GGAGAGAGAGATCATCTTCACTACCTGCCACGAGGGCTGCTCAAGGCCCTGGCTTCT	2844
QY	2206	tttcgcacacaaacatccctctctccatcagcaccttgtctcgaagttacgttggtaaga	2265
Db	2845	GATGGCTACACCTGCTTGTGCTGGCGCCGCAATCTCTTCTTGCCCTTAAGTCCCGGAA	2904
QY	2266	actgcggaggaactacatacagaagccaatgtgtccacttccagcctgtctctcaattgt	2325
Db	2905	GCTTCCACAGAACTTCATATAAGCCAAATTCAACACTTTCAGATAGCTCATTTTAT	2964
QY	2326	atctctgatactcttcttcaacatgtccagcatlttaccagggcaagttaccacccggt	2385
Db	2965	CGTGTGATCTCTTTCATCCCGGCTNAGCGCACTTACGGCAAGTTGTTCTGCGCT	3024
QY	2386	caatgtcgtgcagaggtctgcacatctgagtggtgcggttcagcggtattctctccaa	2445
Db	3025	GGAGGTATGGCCATCTCTGGCGGCGCAAGCTTTGGCTTGTGCGCTGATCTTCAACA	3084
QY	2446	atgtgagtgtatctctgcgcgtccagaactccaacacacagaacatttcagctctcat	2505
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RESULT	11		
	US-08-485-588-2		
	Sequence 2, Application US/08485588		
	Patent No. 5688938		
	GENERAL INFORMATION:		
	APPLICANT: Edward M. Brown		
	APPLICANT: Steven C. Hebert		
	APPLICANT: Forrest R. Fuller		
	APPLICANT: James E. Garrett, Jr.		
	TITLE OF INVENTION: CALCION RECEPTOR-ACTIVE		
	TITLE OF INVENTION: MOLECULES		
	NUMBER OF SEQUENCES: 20		
	CORRESPONDENCE ADDRESS:		
	ADDRESSEE: Lyon & Lyon		
	STREET: First Interstate World Center		
	STREET: Suite 4700		
	STREET: 633 West Fifth Street		
	CITY: Los Angeles		
	STATE: California		
	COUNTRY: USA		
	ZIP: 90071		
	COMPUTER READABLE FORM:		
	MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage		
	COMPUTER: IBM PC compatible		
	OPERATING SYSTEM: PC-DOS/MS-DOS		
	SOFTWARE: FASTSEQ		
	CURRENT APPLICATION DATA:		
	APPLICATION NUMBER: US/08/485, 588		

1 FILING DATE: 7 June, 1995
 2 CLASSIFICATION: 435
 3 PRIOR APPLICATION DATA: including application
 4 PRIOR APPLICATION DATA: described below: 9
 5 APPLICATION NUMBER: 08/353,784
 6 FILING DATE: 9 December, 1994
 7 APPLICATION NUMBER: PCT/US/94/12117
 8 FILING DATE: 21 October, 1994
 9 APPLICATION NUMBER: U.S. 08/292,827
 10 FILING DATE: 23 August, 1994
 11 APPLICATION NUMBER: U.S. 08/141,248
 12 FILING DATE: 22 October, 1993
 13 APPLICATION NUMBER: U.S. 08/009,389
 14 FILING DATE: 23 February, 1993
 15 APPLICATION NUMBER: U.S. 08/017,127
 16 FILING DATE: 12 February, 1993
 17 APPLICATION NUMBER: U.S. 07/934,161
 18 FILING DATE: 21 August, 1992
 19 APPLICATION NUMBER: U.S. 07/894,044
 20 FILING DATE: 11 February, 1992
 21 APPLICATION NUMBER: U.S. 07/749,451
 22 FILING DATE: 23 August, 1991
 23 ATTORNEY/AGENT INFORMATION:
 24 NAME: Heber, Sheldon O.
 25 REGISTRATION NUMBER: 38,179
 26 REFERENCE/DOCKET NUMBER: 213/005
 27 TELECOMMUNICATION INFORMATION:
 28 TELEPHONE: (213) 489-1600
 29 TELEFAX: (213) 955-0440
 30 TELE: 67-3510
 31 INFORMATION FOR SEQ ID NO: 2:
 32 SEQUENCE CHARACTERISTICS:
 33 LENGTH: 5006 base pairs
 34 TYPE: nucleic acid
 35 STRANDEDNESS: single
 36 TOPOLOGY: linear
 37 MOLECULE TYPE: cDNA to mRNA
 38 FEATURE:
 39 NAME/KEY: CDS
 40 LOCATION: 436..3699
 41 OTHER INFORMATION:
 42 US-08-485-588-2

Query Match	5.9%	Score 152.6	DB 1	Length 5006
Best Local Similarity	48.4%	Pred. No. 1.6e-33		
Matches 487	Conservative 0	Mid. matches 514	Indels 6	Gaps 2
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QY 1601	acgaatgagcttcacacactgcacagctctgtgtgaacagaagaatgggccccctgaagggagac	1660		
Db 2191				
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QY 1661	tcaagctctcttcacagcaacgctgttgagttcttgggtgtgacatgaaaccaatctcttggty	1720		
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QY 1721	ctattagcagctaaacagctattgctgctgctgctgattggagacgtcgtgctgtttgcc	1780		
Db 2311				
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QY 1781	tggcgcttcacacagcctgtgttgagagtcacgtcgtgggttagagctgtgtctctcaatcg	1840		
Db 2371				
	AAGTCCCAACACACCATTGTCAAGGCCAACCAACGAGAGACTCTCCATCTCTCTCC	2430		

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2000, 18:57:59 : Search time 185.6 seconds
(without alignments)
3476.538 Million cell updates/sec

Title: US-09-361-652-5
Perfect score: 2579
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Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36:*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	166.2	6.4	3809	1	T61382	Parathyroid calcinu
2	166.2	6.4	3809	1	T95859	Human parathyroid
3	166.2	6.4	3809	1	V26964	Human parathyroid
4	166.2	6.4	3809	1	V82485	Human parathyroid
5	157.2	6.1	5275	1	T95857	Bovine parathyroid
6	157.2	6.1	5275	1	V25962	Bovine parathyroid
7	157.2	6.1	5275	1	V82483	Bovine parathyroid
8	152.6	5.9	5006	1	T61381	Parathyroid calcinu
9	152.6	5.9	5006	1	T95858	Human parathyroid
10	152.6	5.9	5006	1	V26963	Human parathyroid
11	152.6	5.9	5006	1	V82484	Human parathyroid
12	151	5.9	4000	1	T86186	Nucleotide sequenc
13	150.8	5.8	4131	1	T89290	Dogfish shark kidn
14	138.2	5.4	4131	1	T95860	Rat kidney cell ca
15	138.2	5.4	4131	1	V25965	Rat kidney calcium
16	138.2	5.4	4131	1	V82486	Rat parathyroid ca
17	127	4.9	3384	1	T86185	Nucleotide sequenc
18	125.4	4.9	2148	1	Q73222	BOPCAR 1, bovine p
19	82.2	3.2	3919	1	Q80418	Human mglur3 DNA.
20	82.2	3.2	3410	1	T03887	Human mglur3 DNA.
21	73.8	2.9	2732	1	X05810	Mouse pheromone re
22	73.8	2.9	2962	1	X05811	Mouse pheromone re
23	72.6	2.8	2907	1	X05803	Mouse pheromone re
24	71.4	2.8	2409	1	X05842	Mouse pheromone re
25	71.4	2.8	2561	1	X05808	Mouse pheromone re
26	70.8	2.7	2618	1	T16710	Metabotropic gluta
27	70.8	2.7	2519	1	T29408	Human metabotropic
28	70.8	2.7	2821	1	X05813	Mouse pheromone re
29	70.8	2.7	2773	1	X05813	Mouse pheromone re
30	69.2	2.7	3080	1	X05801	Mouse pheromone re
31	69.2	2.7	2550	1	X05840	Mouse pheromone re
32	65.8	2.6	1889	1	X05806	Mouse pheromone re
33	65.8	2.6	1889	1	X05845	Mouse pheromone re
34	65.6	2.5	2394	1	X05863	Mouse pheromone re
35	65.6	2.5	3359	1	X05824	Rat pheromone rece
36	65.2	2.5	3108	1	X05814	Mouse pheromone re
37	65.2	2.5	2412	1	X05853	Mouse pheromone re
38	64.8	2.5	2085	1	X05864	Rat pheromone rece
39	64.8	2.5	3012	1	X05825	Rat pheromone rece

40	64.4	2.5	2304	1	X05857	Rat pheromone rece
41	64.4	2.5	3584	1	X05818	Rat pheromone rece
42	64.2	2.5	2961	1	X05802	Mouse pheromone re
43	64.2	2.5	1889	1	X05807	Mouse pheromone re
44	64.2	2.5	2424	1	X05841	Mouse pheromone re
45	64.2	2.5	1889	1	X05846	Mouse pheromone re

ALIGNMENTS

RESULT 1
T61382
ID T61382 standard; cDNA to mRNA; 3809 BP.

AC 22-APR-1997 (first entry)
DE Parathyroid calcium receptor coding sequence clone pHPuCAR4.0.
KW Calcium receptor; human parathyroid gland adenoma tumour; pBOPCAR1;
KW primary hyperparathyroidism; Xenopus oocyte; alternative splicing;
KW calcium-activated chloride current; agonist; NPS R-467; NPS R-568;
KW variant; untranslated region; alternative polyadenylation; probe;
KW alternative transcription initiation; pHPuCAR5.2; pHPuCAR4.0;
KW human Car gene; isoform; ss.
OS Homo sapiens.
FH Key
FT cds
FT Location/Qualifiers
FT 373..3609
FT /*tag= a
FT /product= Calcium receptor
FT /note= "Pages 94-95 are missing from the specification,
FT sequence information was obtained from the Epo"

PD 09-01-1997-A2.
PF 23-OCT-1995; U13704.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (NPSP-) NPS PHARM INC.
PI Balandin MF, Delmar EG, Moe ST, Nemeth EF, Van Wagenen BC;
DR WPI: 96-23050/23.
DR P-PSDB: W11889.
PT New di:arylalkyl amine cpds. useful for modulating inorganic ion
PT receptor activities - esp. for modulating effect of extracellular
PT calcium on cell surface calcium receptors, useful for treating e.g.
PT hyperparathyroidism, Paget's disease or osteoporosis
PS Example 1, Page 93-100/231pp. English.
CC The sequences given in T61381-82 encode functional calcium receptors.
CC These sequences were isolated from human parathyroid gland adenoma
CC tumour using pBOPCAR1 as a hybridisation probe. mRNA was isolated from
CC a 39 year old caucasian male diagnosed with primary hyperparathyroidism
CC and two clones of approx. 5 and 4 kb were identified. These cDNAs were
CC injected into Xenopus oocytes which were assayed for the presence of
CC functional calcium receptors. Both clone types gave rise to functional
CC chloride currents upon addition of appropriate calcium receptor agonists,
CC e.g. NPS R-467 and NPS R-568. Sequence analysis of the two cDNA clones
CC indicated the existence of at least two sequence variants differing in
CC the 3' untranslated region and which may result from alternative
CC polyadenylation. Sequence variation also exists in the 5' end of the
CC inserts. These sequence differences may have arisen due to alternative
CC transcription initiation and/or splicing. Three additional sites of
CC sequence variation occur within the coding regions of cDNA clones
CC pHPuCAR5.2 and pHPuCAR4.0 demonstrating that they encode distinct
CC proteins. Sequence analysis of the human Car gene indicates that the
CC additional 30 bp in clone pHPuCAR5.2 as compared to pHPuCAR4.0, results
CC from alternative mRNA splicing. This alternative splicing is predicted
CC to insert 12 additional amino acids into the Car protein encoded by
CC pHPuCAR5.2 between residues 536 and 537 of the protein encoded by
CC pHPuCAR4.0. In addition pHPuCAR4.0 encodes Gln at position 925 and Gly
CC at position 990, whereas pHPuCAR5.2 encodes Arg at both equivalent
CC positions. The human Car gene encodes for Gln and Arg respectively at
CC these positions. These two receptor isoforms may be functionally and/or
CC pharmacologically distinct.
SQ Sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T;

Query Match 6.4%; Score 166.2; DB 1; Length 3809;
Best Local Similarity 46.3%; Pred. No. 1.6e-33;
Matches 1130; Conservative 0; Mismatches 1143; Indels 168; Gaps 11;

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DB 610 GAGATTAACACACGCCACGCTTCTTCCCACTTGACGCTGGGATACAGGATATTTGAC 669
QY 326 gctgcagacgttcacaaatgctc---atgcacccctggaggtgcgccacga--- 379
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QY 379 --aggagacagccacatagatagacagagatcttcgcaacacacccctccaaagtgtg 436
DB 730 ATTGATCTTTGAACCTTGATGAGTTCTGCAACTGCTCAGAGCACAATTCCTCTACGATT 789
QY 437 gcaactatggcctgataacacacagcctgtaacacactgctgcctcgtcagccct 496
DB 790 GCTGTGGTGGAGCACTGCTCAGCGCTCTCCACGGCAGTGGCAAACTGCTGGGCTC 849
QY 497 ttctcgtacccctgctcagcctatgagcgagcagcgtgatacctcagtgagagcgcaag 556
DB 850 TTCTACATTCGCCAGTCACTTATGCTCTCCACAGACACTCCCTCAACAACAAATCA 909
QY 557 ttcccgctctctcgtgcacacacacccacagatagacacaggtgagatcagtcgag 616
DB 910 TTCAAGGCTTCTCCCAACCATCCCAATGATGAGCAGCGGCACTGCTGCTGAGCAG 969
QY 617 ctgctgagagagcctcggcgtgctgatacctcgtcgttgacgtctggtgactaagg 676
DB 970 ATCATCAGATATTTCCCTGCACTGGGTGGCAAAATGCACTGATGAGACTATAGGG 1029
QY 677 cagctggcgctacagagcgctgagagagctgacacacacagcgcatcgtcgtcgtc 736
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DB 1144 GTGATTTAAATTCACAGGCCAAAGTATGCTGTTTCTCCAGTGGCCAGATCTTGAG 1203
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DB 1204 CCCCCTATCAAGGAGATTTGTCGCGCAATATCAAGGAGCAAGATCTGGTGGCAAGGAG 1263
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DB 1264 GCGTGGGCGACGCTCCCTGATGCGCATGCTCAGTACTTCACTGATGCTGGGCGACCC 1323
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DB 1324 ATTGGATTCGCTCTGAAGGCTGGGCAATCCAGGCTTCGCGGAATTCCTGAAGAGGTC 1383
QY 1024 -----tgaagagctctatctcagcagcagtgatg----- 1052
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Db 2941 ACTTACATCATCTCTTCAAGCCATCCCGACACCATCA 2981

RESULT 2
ID 795859
AC T95859: standard; cDNA to mRNA; 3809 BP.
DT 08-MAY-1998 (first entry)
DE Human parathyroid cell calcium receptor 4.0 (HuPCar 4.0) cDNA.
KW Human parathyroid cell calcium receptor 4.0; HuPCar 4.0;
KW calcium homeostasis; hyperparathyroidism; osteoporosis; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 373..3809
FT /tag= a
FT /product= parathyroid_cell_calcium_receptor_4.0
PN US5688938-A.
PD 18-NOV-1997.
PF 07-JUN-1995; 485588.
PR 07-JUN-1995; US-485588.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-017127.
PR 23-FEB-1993; US-009389.
PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (BGHM) BRIGHAM & WOMEN'S HOSPITAL.
PA (NESP) NPS PHARM INC.
PI Brown EM, Fuller FH, Garrett JE, Hebert SC;
PI WPI; 98-008040/01.
DR P-PEDB; W38274.
PT DNA encoding calcium receptor polypeptide(s) - useful for
PT therapeutic purposes, e.g. hyperparathyroidism and osteoporosis
PT Claim 15; Columns 125-134; 174bp; English.
CC The present sequence encodes human parathyroid cell calcium
CC receptor 4.0 (HuPCar 4.0).
CC The specification includes details of molecules that can modulate
CC one or more inorganic ion receptor activities, and antibodies and
CC antibody fragments targeted to inorganic ion receptor proteins. The
CC proteins, nucleic acids and antibodies may be used to treat
CC disorders by modulating one or more inorganic ion receptor
CC activities, preferably disorders of calcium homeostasis, e.g.
CC hyperparathyroidism and osteoporosis.
SQ Sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T;
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Query Match 6.4%; Score 166.2; DB 1; Length 3809;
Best Local Similarity 46.3%; Pred. No. 1.6e-33;
Matches 1130; Conservative 0; Mismatches 1143; Indels 168; Gaps 11;
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Db 670 ACTTGCAACACCGTTTCTTAAGGCTTTGGAAGCACACCCCTAGTTTGTGCTCAAAAACAA 729
QY 379 --agggacggccaccctaaagatgacagagaatcttcgaacacacccccaagtgtg 436
Db 730 ATTGATTTCTTGAACCTTATAGATTCTCAACTGCTCAGACACGATTCCTCTACGATT 789
QY 437 gcactcatgagcctgataaacactgacacgctgtacacactgcctgcctgtgaagcct 496
Db 790 GCGTGTGTGGAGCAACTGGCTCAGGCGTCTCCAGCGCAGTGGCAAAATTCGTGGGGCTC 849
QY 497 ttctgaatgccctggctcagctatgagcgagcagcgtgatcctcagtgaggcgcgaag 556
Db 850 TTCTACATTCGCCAAGGTCAAGTATGCTCTCCAGCAGACTCCTCAGCAACAAGATCAA 909
QY 557 ttcccgctctcttgccgcacatcccccagcgttaagctacagagtggaaatcatagtgag 616
Db 910 TTCAAGTCTTTCTCCGACCAATCCCAATGATGAGCACACGACCACTCCATGGCAGAC 969
QY 617 cgcctcagaagcttcgcctgagctcgtgatcctgcctgttgagcagctatgttactacg 675
Db 970 ATCATGAGATATTTCGCTGGAACTGTGTGGGACACATTCGACGCTGATACACATATGG 1029
QY 677 cagctcggcgtacagcgctggaagagc'tggcgaactccacggggacatcgtcgccttc 736
Db 1030 CGGCGCGGAGATTGAGAAATTCGAGAGAACTGAGAAAGGATATCTGCATCGACTTC 1089
QY 737 aaggacgctgtcctctccgcgccagggggtgaccccaagaatcagagcatgatgctg 795
Db 1090 AGTGA-----ACTCATCTCCAGTACTCTGTGATGAGGAAAGATCCAGATGTGGTAGAG 1143
QY 797 cgtctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 856
Db 1144 GTGATCAAAATTCAGAGGCCAAAGTCATGCTGTTTCTCCAGTGGCCCAATCTTGAG 1203
QY 857 g'tcttctcaggctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 916
Db 1204 CCCCTCATCAAGAGATTTCTCCGCGCAATATCACGGGACAGATCTGGCTGGCCAGCGAG 1263
QY 917 gactgggcacatctccacgtaacatacacaatgtgccecgatccagggcatgtggaagctg 976
Db 1264 GCTTGCGCCAGGCTCTCTCCGTGATCCGCAAGCCTCAGTACTTCACGTTGTTGGCGCACCC 1323
QY 977 ctgggggtggccatccagagagagaagatccctggcc'tgaagagatt----- 1024
Db 1324 ATTGATTTGGCTCTAAGGCTGGGCAATCCAGGCTTCCGGGAATTCCTGAAGAGCTC 1383
QY 1024 -----tgaagatcctatgtcagaagctgatt----- 1052
Db 1384 CATCCAGGAGACTGTGTCACAATGGTTTGCCAGAGGATTGTGGGAAGAAACATTAAAC 1443
QY 1052 -----gtgtctccagaacttccagaagggctcgtgtgtgtgtgtgtgtgtgtgt 1096
Db 1444 TCCACCTTCAGAAAGGTGCAAAAGAGACCTTACCTGTGGAGAGGTAC 1503
QY 1097 -----cagctgcagaggg 1111
Db 1504 GAAGAAAGTGGCAGACAGTTTAGCAACAGCTGAGACGCTTCGACCCCTCTGTACAGGG 1563
QY 1112 tctcagccttccagacatgacacatgcccagccttgagaccttccatgagcgtcgc 1171
Db 1564 GATGAGAACATCAGCAGAGTGTCCAGACCCCTTCAATAGATTTACAGCCATTTAGCATATCC 1623
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OY	1172	taaatgta	tgaagcgtg	gtatagc	gtgagccca	ggcgtccca	gagctccca	gctctggatg	1231
Db	1654	TACAA	TGTGTCTTA	AGCAGT	ACTACT	CCATTGCC	AGCCCTTG	CAGATATATAT	ACTCTGC
OY	1232	aa	cttggagcc	ctg-----	ttgcagag	ccagct	ctacccc		
Db	1684	TTACT	TGGAGAGGG	CTCTTACCA	AAATGGCT	CTGTGAC	AGATCA	CAAGAAAT	TGAGGG
OY	1268	tggcagct	ctctcagcagat	ctacaag	gtgaatt	ctctctaca	taaga--	agac	gtba
Db	1744	TGGCAG	GGCTCGAAG	CAACCTA	AGGCACT	TAACCTTTA	CAAAACAT	ATGGGG	AGCAGGTG
OY	1325	gcattcga	tgaacaagg	ggagacc	ctcgtat	ataagac	taacgc	ctggagc	agat
Db	1804	ACCTTT	ATATGATGT	GTGTGT	GTACCTGT	GTGGAG	ACTATTC	ATCATCA	CTTGCAACTGTGC
OY	1385	ggacctga	atgaa	ctttgag	gtcattg	gtctgcct-----	ca	ctgtct	
Db	1864	CCAGAG	ATGTGCTCTCA	TCATCGT	TTTAAG	AGATGGGG	ATTTAC	AACTAT	TCCAAAG
OY	1430	ccaagtca	ctagaca	taataa	taagaca	aaatcc	agltg	ga	cgggaa
Db	1924	GGAGAA	AGACTCTTCA	TCAACAG	AGAAATCT	CTGTGG	ATGTGG	TTTCC	AGGAGGTG
OY	1490	ccgtgtga	aggtgt	taccag	ggagctgt	ctgaagg	gcacaca	aggtgt	cat---
Db	1984	CCCTTCT	CAACTCACTAC	CCAGAG	CTGCTGTG	CAGGAC	CAAGAAAG	GAATCA	TTAGAGG
OY	1547	tccaca	caatgt	ctctcag	gtgcat	ccctgtga	agcttgcag	ctatca	acagat
Db	2044	GAGCC	CACTCTCTT	TGATGTGT	GTGATGTG	CTCGAT	GTGGAG	ATATGT	CATAGACA
OY	1607	ga	acttca	acactctg	ccagcct	gtgtga	aacgaat	lygg	cccc
Db	2104	GATGCA	GTGCTCTTA	CAAGTGG	CCAGATG	ACTTGTG	CTCATATG	AACAC	CACTTCC
OY	1667	tgtcttca	acgcac	cggtggag	cttctgg	gtgcatga	aacat	ctctt	gtgt
Db	2164	TGCA	TTGGCAAG	AGATCG	ATGTCTGT	CTGTG	AGCGAG	CCCTTGG	ATGCCACTTCC
OY	1727	gcac	ctaa	caagctat	gtcgtcgtcgt	ctgat	ctgag	ctcgtcgt	ctcgtgag
Db	2224	CTCTTT	GCGGTCTT	CCACCTCC	CTGTTC	ATATGGGG	AGCCCA	AGCATG	CACTGTC
OY	1787	cttca	acgcct	gtgtgtg	aggtcag	ctggtg	agctgt	gtctct	ca
Db	2284	CGCAAC	CACTCTTGT	CAAGGG	CAACCA	CCAGAG	CTCTTCA	CTCTTCTT	CTTCTC
OY	1847	tgtga	ctgtg	aggtgtg	caagcc	ctcaag	cttctt	ggaa	gcca
Db	2344	CTGCTG	CTGCTCTT	CCACCTCC	CTGTTC	ATATGGGG	AGCCCA	AGCATG	CACTGTC
OY	1907	tgtgtg	ctga	ccccct	ctctctc	ctgaggt	ctgcac	ttctctc	ctcgt
Db	2404	CGCTTG	GGCCAG	CGGCGCTT	TGGCAT	CAGCTT	GTGTCT	GTCA	TCTCAT
OY	1967	cgct	ctct	caac	atg	gtcal	catctt	caag	tttct
Db	2464	AAAA	CAAC	CGTGTCT	CTCGGT	GTGAG---	GCCAA	GTCCCA	CGCTTCA
OY	2027	actt	ggg	ccca	aaac	cat	gtgtgc	cgga	atatt
Db	2521	AAGTGT	GGGGCT	CAACCTG	AGATTC	CTGTCT	GTCTTCT	GTGCA	CTTCA
OY	2087	tctc	ct	ctga	gtgtg	ctgca	atgtga	cccc	cgcc
Db	2581	GTCAT	CTGTGT	GATCTGT	GTACAC	CGGCGCC	CTCA	AGCTA	CCGCA
OY	2147	tctcc	ca	ctgtga	cttctgt	agtcaca	agatca	ctcgt	gtg
Db	2641	GAGG	ATGAT	CACTTCA	TCACTAC	AGGTG	CAAG	AGGTG	CCCTG
OY	2207	tctg	ca	caaca	catc	ctctc	ctacat	ga	ccctt

	Df	2701	ATGCGCTACACTGCCTGGCTGGCTGCCAATCTGTCTTTTTCCTTCAAGTCCCGGAAG	2760
	QY	2267	ctgcggaggaactataacgaaagcaaatgtgtaaccttcagcctgtccccaattcgta	2326
	Df	2761	CtGCGGGAATAATTCAATGAACCAAGTATCATCACCCTTAGCATGTATCTTTCTTCAIC	2820
	QY	2327	tccatgatcgtcttcctaccatgcatgtaaccaattaccaggagaagtactaacccgyc	2386
	Df	2821	GTCCTGATCTCTTCAATTCACCTTACGCTTAACACACCTTAAGCAAGTTGTCTTGCCGTA	2880
	QY	2387	aattgtcgtggcaggcgttgccacactctgtagtgcgcttaagcgcatttcctcta	2446
	Df	2881	GAGGAGTATGCGATCCTGGACGACGCTTTGGCTTGTGCGCTGATCTTTTCAACAAG	2940
	QY	2447	tgtcatgtatctcttcgcgtccagaactacaacaacaga	2487
	Df	2941	ACTTACATCATTTCTTCTTCAAGCCATCCGCAACACCATGSA	2981
	RESULT	3		
	VZ6964			
	ID	VZ6964 standard; cDNA to mRNA: 3809 BP.		
	AC	VZ6964:		
	DT	01-SEP-1998 (first entry)		
	DE	Human parathyroid calcium receptor 4.0 gene 4Kb fragment.		
	KM	ss: calcium ion concentration; parathyroid hormone; homeostasis;		
	OS	Kidney; calcium receptor; detection.		
	FH	Homo sapiens.		
	FT	Key	Location/Qualifiers	
	ET	CDS	373..3609	
	FT	/tag= a		
	ET	/product= "pHuPCAR 4.0 4kb fragment"		
	PD	US5763569-A.		
	PF	07-JUN-1998		
	PR	23-AUG-1995; 484565.		
	PR	23-AUG-1991; US-749451.		
	PR	11-FEB-1992; US-834044.		
	PR	21-AUG-1992; US-934161.		
	PR	12-FEB-1993; US-017127.		
	PR	23-FEB-1993; US-009389.		
	PR	22-OCT-1993; US-141248.		
	PR	19-AUG-1994; US-292827.		
	PR	21-OCT-1994; WO-012117.		
	PR	08-DEC-1994; US-353784.		
	PA	(BGMH) BRIGHAM & WOMENS HOSPITAL.		
	PI	(NESP-) NPS PHARM INC.		
	PI	Brown EM, Garrett JE, Hebert SC;		
	DR	WPI; 98-347412/30.		
	DR	P-PADB; W54846.		
	PT	Calcium receptor poly:peptide(s) - useful for drug screening or		
	PT	antibody production		
	PS	Example 27; Fig 49; 17app; English.		
	CC	The Human parathyroid calcium receptor gene encodes a 1078 amino acid		
	CC	protein. The tissue from which the receptor and receptors from bovine		
	CC	parathyroid and rat kidney are derived, respond to changes, and control		
	CC	changes, in calcium ion concentration, e.g., parathyroid hormone regulates		
	CC	Ca2+ homeostasis in blood and extracellular fluid, and kidney function		
	CC	altered through changes in Ca2+ levels in juxta glomerular and proximal		
	CC	tubule cells in the kidney. The purified receptors (produced		
	CC	recombinantly) can be used to screen for compounds that modulate calcium		
	CC	receptor activity, especially those that can be used to treat diseases		
	CC	associated with the receptors in these tissues. They can also be used		
	SQ	to raise antibodies for use in detection assays.		
		Sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T;		
	Query Match	6.4%; Score 166.2; DB 1; Length 3809;		
	Best Local Similarity	46.3%; Pred. No. 1.6e-33;		
	Matches 1130; Conservative 0; Mismatches 1143; Indels 168; Gaps 11.			
QY	206	tctgacagttcaaacgagcatggtcatalcacctcttccaagcatgcygttcaacggttqag	265	


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Db 550 TGTATCAGGTAAATTTCCGTGGGTTTCGTGGTTACAGCTATGATATTGGCATAAG 609
Qy 266 gagataaacactccacagctctgtcttcccaacatcacccctgggtatagaactctatgac 325
Db 610 GAGATAAACACAGCCAGCCCTTCTTCCCACTTGACGTGGGATACAGGATATTG 669
Qy 326 gtggctcagagctcttcaatgtct--atgcacacctgaaggttgcggccagca---- 379
Db 670 ACTTGCAACACCGTTTCTAAAGGCTTGGAAAGCCACCCCTGAGTTTGTGTCAAAACAA 729
Qy 379 --aggaaagagccactagaagatgcagagagatcttcgcaacctccctccaagtgtg 436
Db 730 ATTGATCTTTGAACTTGATGATGATTCGCAACTGCTCAGAGCAATTCCTCTACGATT 789
Qy 437 gcaactatgtgctgtgataaacacttgacagcagcgtctcaacctgtgcctctgaacct 496
Db 790 GCTGTGGTGGAGCACTGGCTCAGGCGTCTCCAGCGAGTGGCAATCTCTGGGCTC 849
Qy 497 ttcttgatggccctgtgtagctatgagcagcagcgtgactcactcagtgaggaaagcag 556
Db 850 TTTCATCATTCGCCAGGTGATGATGCTCTCCACAGCACTCTCAGCAACAAGATCAA 909
Qy 557 ttcccgctctcttgcagaccatcccccagcgataagtaaccaagtggaagtcatagtgcg 616
Db 910 TTCAAGTCTTTCCTCCGAAACCATCCCAATGATGAGCACAGGCCACATGCGCATGGCAGAC 969
Qy 617 ctctgtcagagctctcgcgtgtgtgtgatactcgcctcgtttgcaactatgtgtactaagg 676
Db 970 ATCATCGAGTATTTCCGCTGACACTGGGTGGGCAAAATTGGACGTGATGACGACTATGG 1029
Qy 677 cagctggcgcgtacagagcgcgtgagagagcttgccactccagcggagatctgctgccttc 736
Db 1030 CGCGCGGGGATTTGGAATTTCCGAGAGCAAGCTGAGGAAAGGATATTGCGATGACTTC 1089
Qy 737 aaggagctgtgtgctctctcccgcaagcgggtgacccaagatgacgcagatgatgtc 796
Db 1090 AGTGA-----ACTGATCTCCAGACTCTGATGATGAGNAAGATCCACATGTGGTAG 1143
Qy 797 cgtctgctcgaagccagagacacacgctgtgctgtgtctctcttaaccgacctgtgtga 856
Db 1144 GTGATTCMAAATTCACCGCCMAAGTCACTCGTGTGTTCTCCAGTGGCCAGACTTTGAG 1203
Qy 857 gtgtctctcaggtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 916
Db 1204 CCCCTCATCAAGAGATTTGTCGGCGCAATATCACGGGCAAGATGTGCTTGCCACGCGAG 1263
Qy 917 gactgtgacatctcgaatcacatcaccaatgtgcggagatccagggacatttggagcgtg 976
Db 1284 GCGTGGGCGACTCTCTCCCTGATCGCCATGCTGACTGACTTCAAGTGTGTTGGCGGCAC 1323
Qy 977 ctgggggtgtgtccatccagcagagacaagatccctgtgcctgaaggagt----- 1024
Db 1324 ATTGGATTCGCTTGAAAGCTGGGGAGATGCCAGGCTTCGCGAATTCCTGAGNAGGTC 1383
Qy 1024 -----tgaagagtcccttgcagggcagtgatg----- 1052
Db 1384 CATCCCAAGAGTGTGTCCAAATGGTTTTGGCAAGAGGTTTTGGGAAAGAAACATTTTAC 1443
Qy 1052 -----gtgtccccaagaatttgcacagaggggtcctgtgtgcgcactaac 1096
Db 1444 TGCCACCTCCMAAGAGTGGCAAAAGGACCTTACTGTGGAACCTTTCTGAGAGGTAC 1503
Qy 1097 -----cagcgtgtcagggag 1111
Db 1504 GAAAGAAAGTGCGCAGAGTTTACCAACAGCTCGACAGCCTTCGACCCCTCTGTACAGGG 1563
Qy 1112 tgtcagccttcacgacatgagacatgcccagcgttgagccttctccatlgagcgtcgc 1171
Db 1564 GATAGAAACATCAGCAGTGTGAGAGCCCTTACATAGATTACAGCATTTACGGATATACC 1623
Qy 1172 tacaatgtatagagctgtgtatgtgtgtgcccacggcctccacacagctcctggagagt 1231
|||||
Db 1624 TACAATGTACTTAGCAGTCTACTCCATTGCCACGCCCTTGCAAGATATATACCTGC 1683
Qy 1232 accctctggacctg-----tgcagagggccagcttacctcc 1267
Db 1684 TTACCTGGAGAGGGCTTTCACCAATGCGTCTGTGCAACATCAAGAAAGTTGAGCG 1743
Qy 1268 tggcagctcttcagcagatctacaagtgatcttccctctacataaga--aagactga 1324
Db 1744 TGGCAGGTCTCGAAGCACACTTAGCGCATCTAACTTTCAAAACATATAGGGGAGCAGTG 1803
Qy 1325 gcatctgatgacaagggggaacctctagttatatacatcatcgccttggagctggat 1384
Db 1804 ACCTTTGATGATGTGTGTGACCTGTGGGAACTATTCATCATCACTGACACTCTCC 1863
Qy 1385 ggaactgaatggacctttaggtgtatgtgtgacct-----cactgtct 1429
Db 1864 CCAAGAGATGGCTCCATCGTGTAAAGAGTGGGATTTACAACGTATGCCMAAG 1923
Qy 1430 ccagtcatctagaataaataagacaataatccagtgagcaggggaagaacaatcaggtg 1489
Db 1924 GGAAGAAAGACTCTTATCAACAGAGAGAAATCTGTGAGTGGGTCTCCAGGAGGTG 1983
Qy 1490 ccgtgtcagtggtgtacagggagctgtcgaaggccacacaggttgtcat--gggt 1546
Db 1984 CCTTTCCAACTGCAAGCCGAGACTGCTGCAAGGAGCAAGAAAGGATCATGAGGGG 2043
Qy 1547 tcccacacgtgtgtcctcagatgcataccctgtgaagcttggaaatttccaacagagt 1606
Db 2044 GAGCCACCTGCTGCTTGAAGTGTGAGAGTGTCTGATGGGAGTATGATGAGAACAA 2103
Qy 1607 gagcttcaacactgcagcccttgcagacagaaagatgggccccctgagggagctcagcc 1666
Db 2104 GATGCCAGTGGCTTTAACAAAGTCCCAAGATGACTTCTGCTCAATGAAACACACCTCC 2163
Qy 1667 tgccttcaacgcacggctgtgaggttcttggggtyggcataaccacatcttctgtgtata 1726
Db 2164 TGCAATGCCAAGAGATCGAGTTCTGTGAGAGAGGCCCTTTGGAGTGGCACTGACC 2223
Qy 1727 gcaagctaacagctattgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1786
Db 2224 CTCCTTCCGTCGCGGCGCATTTTCTACAGCCCTTGTGCTGGGTGATTTATCAAGTTC 2283
Qy 1787 ctccaacgcctgtgtgtgaggtcagctgagggatgagctgtgtgtgtgtgtgtgtgtgtgt 1846
Db 2284 CGCAACACACCATTTGTCAGAGCCACCAACGAGAGCTTCTTACTCTCTCTCTTTCTCC 2343
Qy 1847 ttggtatctggaggttgcaagcctctacagcttcttcgaggaagcccaaggtgtccgcgtg 1906
Db 2344 CTGCTGTGCTCTTCTCCAGTCCCTGTCTTCAATCGGGAGCCCCAGACTGAGCTGCG 2403
Qy 1907 ttgctgtcgaagccctcttctcctcgtgttgcaatttctcctctcctgtcgaacatc 1966
Db 2404 CGCCTGGCCAGCGCGGCTTTGGCATGAGTCTGTGCTGCACTCATGATCATCTGTG 2463
Qy 1967 cgtctctcaacatgtgtcatatctcaagtttctcacaagyaacccaatcttaccac 2026
Db 2464 AAAACCAACCTGTCTCTCTGCTGTTGAG--GCCAAGATCCCAACACAGCTTCCACCGC 2520
Qy 2027 acttgggcccacaaacatggtgtccggaatalctgtcatcttgacgtccacaggtctcatgtg 2086
Db 2521 AAGTGTGTGGGCTCAACCTGCAAGTCTCTGTGTGTTTCTGTGCTACACTTCATGAGATT 2580
Qy 2087 ttcctctgtctcaagtggtcttgcacatgtgaaccccaagcccaagggaggtacacagc 2146
Db 2581 GTCACTGTGTGATCTGCTTACACCGCGCCCTCAAGCTCAACCCCAACAGAGCTG 2640
Qy 2147 ttcgcccatctgtgtatcttggatgacagaggttcaacctgtgagcctccctgtgtgtgt 2206
Db 2641 GAGGATAGATCATCTTATCAGCTGCGACAGAGGGCTCCTCATGCGCTTGCTTCTG 2700
Qy 2207 ttgcacaacaacatcctcctctccatcagacacttgtctcagactaaccttgggtaaggaa 2266
Db 2701 ATCGGCTACACCTGCTGTGGGTGGCATGTGCTTCTTGTGCTTCAAGTCCGGAG 2760
|||||
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QY	2267	ctgcgcgggaacctataacgaagcaaatggtcaacctgaagccgtctccatccatcgta	2326
Db	2761	CTGGCGGAGACTTCATTGAAGACCAATTATCATCCTTGACATGCTATCTTCTTCAAC	2820
QY	2327	tccctgatccgtcttcttcacacatgctccagcattacacaggcagctaccacccgagtc	2386
Db	2821	GTCGGATTCCTCTTCATTTCCAGCCTATGCCAGCACCATGATGCAAGTTTCTCTGCGCTA	2880
QY	2387	aattgtcgcggagagggctcggccacctctgaigtggcggtctcagcgctattccctccaa	2446
Db	2881	GAGGTGATTGCCATTCCTGGCAGCCAGCTTTGGCTTGGCTGGCGTGCATCTTCTTCAACAAG	2940
QY	2447	tgctacgtgattctctctgcgcgtccgaagaactacaacacaga	2487
Db	2941	ATCTACATCATCTCTCTTCACAGCCATCCCGGACACACCATGGA	2981
RESULT	4		
ID	V82485		
AC	V82485	standard; cDNA to mRNA; 3809 BP.	
DT	19-MAR-1999	(first entry)	
DE	Human parathyroid calcium receptor pHPaCAR 4.0 encoding cDNA.		
KW	Parathyroid calcium receptor; Inorganic ion receptor; Osteoporosis;		
KW	calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;		
KW	spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;		
KW	neonatal distress; neurodegenerative disease; Alzheimer's disease;		
KW	Huntington's disease; Parkinson's disease; dementia; muscle tension;		
OS	depression; anxiety; ss.		
OS	Homo sapiens.		
FT	Key	Location/Qualifiers	
FT	CDS	373..3609	
FT		/*tag= a	
PN	US585868A-A.		
PD	12-JAN-1999.		
PF	07-JUN-1995; 480751.		
PR	07-JUN-1995; US-480751.		
PR	23-AUG-1991; US-749451.		
PR	11-FEB-1992; US-834044.		
PR	21-AUG-1992; US-934161.		
PR	12-FEB-1993; US-017127.		
PR	23-FEB-1993; US-009389.		
PR	22-OCT-1993; US-141248.		
PR	19-AUG-1994; US-292827.		
PR	21-OCT-1994; WO-012117.		
PR	08-DEC-1994; US-353784.		
PA	(BSPM) BRIGHAM & WOMEN'S HOSPITAL.		
PA	(NPSP-) NPS PHARM INC.		
P1	Balandrin MF, Brown EM, Del Mar EG, Garrett JE,		
P1	Hebert SC, Nemeth EF, Van Wageningen BC;		
DR	WPI: 99-119871/10.		
DR	P-PSDB: W89565.		
PT	Screening for calcium receptor-active compounds - by recombinant		
PT	expression of nucleic acid encoding calcium receptor and determining		
PT	the effect of compounds on calcium receptor activity		
PS	Claim 1; Fig 49; 176p; English.		
CC	A method has been developed of screening for a compound able to affect		
CC	one or more activities of a calcium receptor (CR) comprises: (A)		
CC	contacting a recombinant cell with a test compound, where the		
CC	recombinant cell comprises a recombinant nucleic acid expressing the		
CC	CR, provided that the cell does not have functional CR expression from		
CC	exogenous nucleic acid; (B) determining the ability of the test		
CC	compound to affect one or more activities of the calcium receptor; and		
CC	(C) comparing the ability with the ability of the test compound to		
CC	affect the one or more CR activities in a cell not comprising the		
CC	recombinant nucleic acid. The present sequence encodes human		
CC	parathyroid CR, designated a pHPaCAR 4.0. The nucleic acid sequence of		
CC	pHPaCAR 4.0 can be used as part of the recombinant nucleic acid in the		
CC	method described above. The compounds identified can be used to treat		
CC	diseases or disorders characterised by abnormal calcium homeostasis, e.g		
CC	hyperparathyroidism, osteoporosis and other bone and mineral-related		
CC	disorders. They can also be used for the treatment of diseases and		

CC disorders associated with disrupted Cat+ responses, e.g. seizures,
CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in
CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative
CC diseases such as Alzheimer's disease, Huntington's disease and
CC Parkinson's disease, dementia, muscle tension, depression, and anxiety.
50 Sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T;

Query Match	6.4%;	Score 166.2;	DB 1;	Length 3809;
Best Local Similarity	46.3%;	Pred. No. 1.6e-33;		
Matches 1130;	Conservative	0;	Mismatches 1143;	Indels 168;
				Gaps 11;

QY	206	tcctaaagcttcaagcgccatcgctctctcaacccttccaagccatcggttaccggtt	265
Db	550	TGTAATCAGGATTAATTTCCGTGGGTTTCCTCGTTACAGGCTATCATATTTTGGCATAG	609
QY	266	gagaataacaacatcccaagctctgtctcccaacatcaccccttgggttcaagactlatag	325
Db	610	GAGATAAAGACGACCGCCCTTCTTCCAACTTGAGCGTGGATACAGATATTGGAC	669
QY	326	gtgtgtcctcagagctcttccaatgtct---atgcacccttgaagggtgcccgcacga---	379
Db	670	ACTTGCACACCGTTTCTTAAGGCGCTTGGAAAGCCACTGAGTTTGTGTGCTCAAAACAA	729
QY	379	--aaggacagcgccactagatagacgaagaagattctgcacaccactctccaaagtggt	436
Db	730	ATTGATTTCTTTGAACCTTGATGATTTCTTCAACTGCTAGACACATTTCCCTTACGATT	789
QY	437	gcactcaattgagcctgataacaacttgcacacgctgtgcacacatgctgcgccttgcagcc	496
Db	790	GCCTGTGGTGGGACCACTGGCTTCAGGCGCTCCACGGCAGTGGCAATCTGCTGGGCTC	849
QY	497	ttctcgtaccccttgcacgtatagagcgagcagtgatctcagtgtggaaagcgcaag	556
Db	850	TTTACATTTCCCGAGTCAAGTTATGCGCTCTCCACAGCACTCTCAGCAACAAATCA	909
QY	557	ttcccgcctctcttgcagcaatccccagcagtaagtaccaggttgaaagtatatgtgcg	616
Db	910	TTCAAGTCITTTCTTCGGAACCATCCCAATGATGAGCAACCAAGCCACTGCATGGACAC	969
QY	617	ctgtgtcagaagctctgcgtcgtggtctcgtatctgcctgttgcagctatgtgactaag	676
Db	970	ATCATCAGATATTTCCGCTGGAACTGGGTGGGCACAATTTGCAGCTGATGAGACTATGG	1029
QY	677	caagctggcgtacaaagcgctgtgaagagcgtgcgcactccacaggggcatctgctgcctc	736
Db	1030	CGGCGGGGATGAGAAATTCGAGAGGAAGCTGAGGAAGGATATCTGCATGCACTTC	1089
QY	737	aaggaagctgtgcctctctccgccacagcggtgtgacccaagaatgcagcgcatgtctg	796
Db	1090	AGTGA-----ACTCATCTCCAGTCTCTGTGATGAGGAAGAAATCCACCATGTGTAG	1143
QY	797	cgctcgtcgcagcaagagcaacacgtgctgcgtctctctcaacgcgcacctgtgcgtga	856
Db	1144	GTGATTTAAATTCACAGGCCCAAGTCATCTGTGTTTCTCCAGTGGCCCAAGATCTTGAG	1203
QY	857	gtgtcttcacagctctgtgtgtcgtgcaccaaccgtacgttgcgaagtgtgatcgctccga	916
Db	1204	CCCCATATCAAGAGATTTGTCCGGCGCAATATCACGGGCAAGATCTGCTGGCAGGAG	1263
QY	917	gactgggcacatccacagtaacatcaccaaatgtgccggagatccagagcatgtggaa	976
Db	1264	GCGTGGCGCAGCTCTCCCTGTATCCGCAATGCTCAAGTACTTCCACAGTGTGGCGCAC	1323
QY	977	ctgggggtgtgcctcagcagagaagaagtcctctgtccgtgaaggggt-----	1024
Db	1324	ATTGGAATTCCTGTGAAGCTGGGCGAGATCCCAAGCCTTCGGGAATTTCTGAAGAGGTC	1383
QY	1024	-----tgaagagctcatgtctcagcagtgatg-----	1052
Db	1384	CATCCCAAGGAGTCTGTCCACATGTTTGGCCAAAGGATTTTGGGAAGAAACATTTAAC	1443
QY	1052	-----ggtgtctcccaagaattgcccaagaagggtctcgtgtgcgactaac	1096


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Db 1444 TGGCACCTCCAGAGGTGCAGAAAGACCTTTACTGTGGACACTTTCTGAGAGTGCAC 1503
1097 -----cagcgtgtgaaggag 1111
Db 1504 GAAGAAAGTGGCGACAGTTTAGCACAGCTGCAGACGCTTCGACCCCTCTGTGACGGG 1563
1112 tgcacgcttcacagacatggaacatgccgagcttgagccttcctcctcattgagcgcgcgc 1171
1564 GATGAGAACTACAGCACTGTGCAGACCCCTTAGCTACATAGATTACAGCAATTAGCGATTCC 1623
1172 tacaatgtatgtagcagctgtgtatgctgtgtgcacagcgccccaacagcctcttggagat 1231
1624 TACAATGTGACTAGTACGAGCTACTCTCATTTGCCACGCCCTTGGCAAGATATATATACCTGC 1683
1232 accttggagacctg-----tgcagagggccagcttacccc 1267
1684 TTACCTGGAGAGGGCTTTCCACCAATGGCTCTGTGCAGACATCAAGAAAGTTGAGCGG 1743
1268 tggcagcttccttcagcagatcacaaagtgaatttcctctacataaga--agactgta 1324
1744 TGGCAGGTCTCTGAAGCACTACGGCATCTAACTTTACAAACATATGGGGGAGCAGAGTG 1803
1325 gcaatgatacaaggagggagccctcaggtatatagacatcatcgacttggagctggaaat 1384
1804 ACCTTGATGATGTGTGTGACCTGTGTGGAGACTATTCATCATCAACTGCACCTCTCC 1863
1385 ggaacggaatggagaccttggagctatgtgttcgcct-----caactctc 1429
1864 CCAGAGATGTGCTCCATCGTGTTAAGGAAGTGGGTATTAACAAGTCTATGCCAAG 1923
1430 ccagttcatctagaataaataagacaaatccagtgcacaggaagaacaatcagctg 1489
1924 GGAGAAAGACTCTTCATCAACGAGAGAAATCTGTGAGATGGGTCTCTCAGGAGAGTG 1983
1490 cctgtgtcagtggttacagggagctgtctcgaaggagcaccagagttgtgcat---gggt 1546
1984 CCTTTCCTCCACTGCAGCCGACGACTGCTGTGGAGGACAGGAAAGGATCATGTAGAGGG 2043
1547 tccacacagctgtgtcgtgtcgtatgctcctgtggaagcttggagacttcccaacagagt 1606
2044 GAGCCCACTGCTGCTTTGAGTGTGTGAGTGTCTGATGGGAGTATAGTAGAGACA 2103
1607 gagcttcacacccgcgcgcctgtgtgacagagaagaatggcccccttggaggagctcagcc 1666
2104 GATGCCAGTGTCTGTAAACAGATGCCGATGACTTCTGTGCTCAATGGAACACACACTCC 2163
1667 tgccttcacagcaacgctgtgagcttcttggagggtggaatgaacccatctcttgtgtatta 1726
2164 TGCATTGCCAAGAGATCGAGTTCTGTCTGACGAGGAGCCCTTTGGATCGCACTACCC 2223
1727 ggaagctaacagctatagctgcgcgcgtgcgtatctggagactcgtgcgttgcctggcgt 1786
2224 CTCTTTGGCTGTGGGCAATTTCTGTACAGCCTTTGTGTGGGTGTGTTATCAAAATTTC 2283
1787 ctccacagcgtgtgtgaggtcagcgtgaggtgtagcgttgcctcccaagcgcgcgtcc 1846
2284 CGCAACACACCATGTGTCAAGGGCCACCAACGAGAGCTCTCTCACTCTCTCTCTTCTCC 2343
1847 ttgtgtagctggaggttgcagccttcacagcttcttcctggagagcccaagctgcgcgcgtgc 1906
2344 CTGCTCTGCTGCTTTCACACTCCCTCTTCTCTCATCGGAGAGCCCGACGACTGGAGCTGC 2403
1907 ttgtctgtcagagccctcttctctcgtgttgcacatttctctctcctcgttcgacaatc 1966
2404 CGCTCTCGCCAGCGCGGCTTTGGCATAGCTTGTGTCTGTGCAATCTCATCATCTCTGGTG 2463
1967 cgtctctcccaactggtcatcatcttcaaatcttcttcaacaggtacccacatcttaccac 2026
2464 AAACCAACACGTCCTCCCGTGGTGTGAG---GCCAAGATCCCCACACAGCTTCCACCGC 2520
2027 acttgggcccacaaacatggtgcgcgaataatgctcatgttcagcttccacagcttcattg 2086

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Db 2521 AAGTGTGGGGGCTCAAACTGACTTCCTGCTGTGCTTTCCTCTGCACCTTCAGCAGATT 2580
2087 ttctctgtctcaccgtgtgtgtgtgaatgtgacccccacagcccccagggagatccagcgc 2146
2581 GTCACTGTGTGATGTGGCTCTACACCGCGCCCCCTCAAGCTACCGCAACGAGGAGCTG 2640
2147 ttcccccacttggatgttcttgaagtgcacagagtaactcgtgtgggttccgtgtgct 2206
2641 GAGATGAGATCATCTTTCACTACAGCTGCGACAGAGGGCTCCCTCATGTGGCCCTTGCTC 2700
2207 ttgcacacacacatcctcctctccatcagaccttgcctgcacgtacctggttaaggaa 2266
2701 ATCGGCTACACCTCGCTGCGCTGCGCTGCATCTGCTTCTTCTTCTTCAAGTCCCGAAG 2760
2267 ctgcgggagacatataacgaagccaatgtgtactcttagcctgtgtcttccacttcgta 2326
2761 CTGCGGAGAACTTCATGAGCAAGTCAATCACTTCAAGCAATGCTCATCTTCTCATC 2820
2327 tccgtgacgcttcttcacacatgctccagatcttaccagggacagcttaccacccggtc 2386
2821 GTCTGGATCTCCTTCACTATCCAGCCTATGCCAGCAGCTTATGCAAGTTGTCTGTGCCGT 2880
2387 aatgtcctggcagaggtgtggcactctgaatggcgcgtctcagcgcatacttccctcaaa 2446
2881 GAGTGATTTGCCATCTCTGGAGCGCAGCTTGGCTGTGCTGTGGCGATCTTCTTCAACAAG 2940
2447 tgcctagtgatctctctgcgtccagactccaacaacagaga 2487
2941 ATCTACATCATCTCTTCAAGCCATCCCGACACCATCGA 2981

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RESULT 5

195857 standard; cDNA to mRNA; 5275 BP.

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AC 195857;
DT 08-MAY-1998 (first entry)
DE Bovine parathyroid cell calcium receptor 1 (BopCar 1) cDNA.
KW Bovine parathyroid cell calcium receptor 1; BopCar 1;
KM Calcium homeostasis; hyperparathyroidism; osteoporosis; ss.
OS Bos sp.
FH Key
FT Location/Qualifiers
FT CDS
FT 515..3772
FT /tag=a
FT /product= parathyroid_cell_calcium_receptor_1
PD US668938-A.
PD 18-NOV-1997.
PE 07-JUN-1995; 485588.
PR 07-JUN-1995; US-485588.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-017127.
PR 23-FEB-1993; US-009389.
PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (BGEV ) BRIGHAM & WOMENS HOSPITAL.
PA (NPSF-) NPS PHARM INC.
PI Brown EM, Fuller FH, Garrett JF, Hebert SC;
PI WPI; 98-008040/01.
DR P-PSDB; W38272.
PT DNA encoding calcium receptor polypeptide(s) - useful for
PT therapeutic purposes, e.g. hyperparathyroidism and osteoporosis
PS Claim 1; Columns 107-116; 174pp; English.
CC The present sequence encodes bovine parathyroid cell calcium
CC receptor 1 (BopCar 1).
CC The specification includes details of molecules that can modulate
CC one or more inorganic ion receptor activities, and antibodies and
CC antibody fragments targeted to inorganic ion receptor proteins. The
CC proteins, nucleic acids and antibodies may be used to treat
CC disorders by modulating one or more inorganic ion receptor
CC activities, preferably disorders of calcium homeostasis, e.g.

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CC hyperparathyroidism and osteoporosis.
SQ Sequence 5275 BP; 1277 A; 1476 C; 1315 G; 1207 T;
Query Match 6.1%; Score 157.2; DB 1; Length 5275;
Best Local Similarity 46.0%; Pred. No. 3.8e-31;
Matches 1156; Conservative 0; Mismatches 1168; Indels 168; Gaps 11;
QY 205 gtctgacagcttaacagcgccatgctatccaccccttccaaagcatcggtgtccacgttga 264
DB 694 gtctatccagctatatttccgagagatttgctgttaccgaacatattttccataga 753
QY 265 ggaataaacaactccaacagcttgcctccaacatccctggggtatgaactgtatga 324
DB 754 ggaataaacaactccaacagcttgcctccaacatccctggggtatgaactgtatga 813
QY 325 cgggtg---ctgagtgcttccaatgtctatgccaaccttgagggtgcccgcagcaagg 381
DB 814 cacttgtaaacacgctctttaaagccttggagggccaccctgagttgttgcccaagaa 873
QY 382 gacaggc-----cacctagaatgacagagatctctgcaacacatccctccaagtggt 435
DB 874 aattgaccttgaaccttgaatgattctgcaactgctcagagacatccctcttaccat 933
QY 436 ggaactcaattggcctgataaacaactgacaagcgtgtcaacacatgctgctgtgagccc 495
DB 934 cggagtggtggagctactgctgctgggcatctccacagagtgggccaaacctgagggt 993
QY 496 ttctcagtgccctgctgacagatagggagcagagtgatctcctgaagtgaggcgcaa 555
DB 994 ctcttaccatcccccaagctacgctatgctctctccagacagctcttcgcaaacgaatga 1053
QY 556 gtcccgctctcttgcgcacacatcccccagcgaataagtaacaggtggaagtaagtcg 615
DB 1054 attcagatctctctccgacacatattcccaatgaaacacagggccacggccatggctga 1113
QY 616 gctgcgcagagcttgcgctgggtctgcatctgcctcgttggaacgatagtgtactaagg 675
DB 1114 caatcatcgatctacttccgctggaaactgggagcaaatggcactgacatctactatgg 1173
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DB 1174 ccggccacagagatgagaaatttgcagagaaactgagagagagacatctgcattcgactt 1233
QY 736 caaggaacgtgtgtctctctccgcccagcggtgtgaacccaggaatcagcgacatgact 795
DB 1234 cagcga-----gctcatctcccaatctgatatgagaaagaaagatccagagtggtga 1287
QY 796 ggcgtcgtctgacagcaagcaacgctgtgtgtgtctctctcaacgcgcacatgctgtg 855
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QY 976 gctgggggtgtgacatccagcagagaagaatctcctgtgactgaaggagt----- 1024
DB 1468 caattgggtgtgttgaagctgggagatccagagcttccgggaattctctgcagaaagt 1527
QY 1024 -----tgaaaggtcctatgtctcagcagtgatgtgtgtgtgtgtgtgtgtgtgt 1066
DB 1528 ccacccacagaaattctgtccacaaatgttttgcgaagagatttggagaaacattttaa 1587
QY 1067 tgcacagaggtgtcctgtgtgcgca--ctaacagcgtgtcagggagtgtcagctttca 1124
DB 1588 ctgcacacctcaagagaggtcttaaaagcccatattacggtgagacacctctctgagagctca 1647
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DB 1648 cgaagaaagaggtgcccaggttaagcmaacagttccactgcttccgacctgtgacactgg 1707
QY 1170 -----c 1170
DB 1708 ggaaggaacatcagcagctgtcgagacatccttaccatgattttacacattttacgattatc 1767
QY 1171 ctacaatgtatgaagctgtgtatgtgtgtggcccagcctccacagctcctggtatg 1230
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QY 1231 taacctgtgga-----cctgtccagaagcccaagcttacc 1266
DB 1828 cataccctggagagagcgctcttccacaaacgcttctgcgcagatattcamaaggttgaaac 1887
QY 1267 ctggagcttctttagcagatctacaagtgaaattccctctacaata--gaagactgt 1323
DB 1888 ttggcaggtctgaaacacactcggcacttaatttttaccacaaatattggggagcgaact 1947
QY 1324 agcatcgaatgaacaaagggagccctcctcagttatataagacatcagcctgtggactgaa 1383
DB 1948 aactttcgatgaaatgagagacctggcagagaaactattccatcatcaactggcactcttc 2007
QY 1384 tggacctgaatggaccttgaggtcaattgtgtcgtc-----caatgtc 1428
DB 2008 cccagagagacggctccatagtgttttmaagaaattggatattcaaatgtctatgccaaaga 2067
QY 1429 tccagttcatctagaacataataaagcaaaatccaggtgacagcgggaagaacaatcaggt 1488
DB 2068 agcagagaaactcttcatatgaatgaataaataattcgtgagatggttttcanaagaggt 2127
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QY 1546 tcccccacactgtcgtcttgatgtgactgcccgtgtgaagctgggaacttctcaacagag 1605
DB 2188 ggaagccacactcgtgcttggatgtgtgaatgctgtgagggagttacagcagcagac 2247
QY 1606 tgaagctcacactgtccagcctgtgtgaaacagaagaatggcccctgaaaggagctcagc 1665
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QY 1666 ctgcttctcagcaccggttgagcttctgtgggtgagatgaacacatctcttgtgtat 1725
DB 2308 ctgcacatcgccaaagaaatgagattctgtgctgagacccagccttgcgagatgcactcac 2367
QY 1726 agcagctaaacagctatgctgtcgtctgattgtgagctcgtgctgtgtgtgtgtgtgt 1785
DB 2368 gctcttggctgtgctggcattttctctacacgcttgcgtgaggggcttcttcatcaagtt 2427
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QY 2026 cacttggcccaaaacacatgtgtcgggaatattgtcattgtcagctccacagctccatt 2085
DB 2665 gaagtgtgtgggggtcaacactgcagatctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2724
QY 2086 gtctcctgtctcagctgt 2145

Db	2752	TGTCATCTTGCCATTGGCTCATATACAGGCGCCCCCTCGAGCTACCGCAACCAACGAGCT	2784
Qy	2146	cttccccccatccgtgagatctcttgagtcacagagatcaactctgtggtcttccgtgagc	2205
Db	2785	GGAGGACAGGATCATCTTCATCACCTGCGCCAGAGGGCTCGCTCATGGCGCTTGCT	2844
Qy	2206	tttgcacacacatctctctctccatcagacacttgtcttgagcttaactgtgtaaga	2265
Db	2845	GATCGGCTACACTGCTTCCTGCGCCGACATCTCTTCTTGCCCTTCAAGTCCCGAA	2904
Qy	2266	atgcgcgagaaactataacagccaatgctgaccttaagcctgtctctccactcgt	2325
Db	2905	GCTGCCAGAACTTCAAGAACCCAGTTTCATCACCCTTAGCATGGTCTCATCTTTCAT	2964
Qy	2336	atccctgagatcgtcttcttccacatgctccagacattacacagagcagctaccacccggt	2385
Db	2965	CCTCTGAGATCTCTTCTATCCCGCCCTACGGCAGACACTTAGGCAAGTGTCTCTGCGT	3024
Qy	2386	caattgtctgcgcaaggctgagccactctgagtcgagcttaagcggctattctctccaa	2445
Db	3025	GGAGGTGATCGGCATCTCTGCGGCCAGCTTTGGCTTGCTGCTGTATCTTTCACAA	3084
Qy	2446	atgcacagtgatctctctgctgcctccagaactcaacacacacagaaacttaagcctccat	2505
Db	3085	GGTTCATCATCTCTCTTTCAGCCCTTCCGGAAACCATGAGAGAGGTGCTGACAGAC	3144
Qy	2506	ccaggaactaac 2517	
Db	3145	CGCGCACACGC 3156	

RESULT 6

ID V26962

V26962 standard; cDNA to mRNA; 5275 BP.

AC V26962:

DT 01-SEP-1998 (first entry)

DE Bovine parathyroid calcium receptor 1 gene 5kb fragment.

KW ss: calcium ion concentration; parathyroid hormone; homeostasis;

KW kidney; calcium receptor; detection.

OS Bos sp.

FH Key

FT CDS

FT Location/Qualifiers

FT 515..3772

FT /*tag= a

FT /product= "Bopcar 1 5kb fragment"

PN US5763569-A.

PD 09-JUN-1998.

PE 07-JUN-1995; 484565.

PR 23-AUG-1995; US-484565.

PR 23-AUG-1991; US-749451.

PR 11-FEB-1992; US-834044.

PR 21-AUG-1992; US-934161.

PR 12-FEB-1993; US-017127.

PR 23-FEB-1993; US-009389.

PR 22-OCT-1993; US-141248.

PR 19-AUG-1994; US-292827.

PR 21-OCT-1994; WO-012117.

PR 08-DEC-1994; US-353784.

PR (BGHM) BRIGHAM & WOMENS HOSPITAL.

PA (NPSF-) NPS PHARM INC.

PI Brown EM, Garret JE, Hebert SC;

PI WPI: 98-347412/30.

DR P-PSDB; WS4844.

PT Calcium receptor poly:peptide(s) - useful for drug screening or

PT antibody production

PS Example 25; Fig 47; 17app; English.

CC The bovine parathyroid calcium receptor gene encodes a 1085 amino acid

CC protein. The tissue from which this receptor and receptors from human

CC parathyroid and rat kidney are derived, respond to changes, and control

CC changes, in calcium ion concentration, e.g. parathyroid hormone regulates

CC Ca2+ homeostasis in blood and extracellular fluid, and kidney function

CC alters through changes in Ca2+ levels in juxtaglomerular and proximal

CC tubule cells in the kidney. The purified receptors (produced

CC recombinantly) can be used to screen for compounds that modulate calcium

CC receptor activity, especially those that can be used to treat diseases
CC associated with the receptors in these tissues. They can also be used
CC to raise antibodies for use in detection assays.
SQ Sequence 5275 BP; 1277 A; 1475 C; 1316 G; 1207 T;

Query Match 6.18; Score 157.2; DB 1; Length 5275;

Matches 1136; Conservative 0; Mismatches 1168; Indels 168; Gaps 11;

OY	205	gctctaagcgttcaacgcgcgatcgctatcacacctctccaaaccatggcgcttaaccgtttga	264
Db	694	GGGTATCAAGGTAATAATTTCGAGGAAATTTCCGTGGTACAAACTATGATATTTGCCATAGA	753
OY	265	ggagaataaacactccaacgcctctgtctccaacaatcacccctgggtagaagcatglatga	324
Db	754	GGAATTAACAAGCAGCATCCAGCCCTCTCTCTCCCAACATGCACCTGGGATACAGGATATTCGA	813
OY	325	cgttg-----ctcaaggctttccaatagtctatggccaacctgggggtggcccgcccaagag	381
Db	814	CACCTTGTAACACCCTGCTTTAAGCCTTTGGAGGCCAACCTTGAGTTTTGGGCCCAACAA	873
OY	382	gacaggc-----cacctagaagatbcagaagatcttcgaaccaactcctccaagstgct	435
Db	874	AATTACCTTTGAACCTTGATGANTTTTGCACTGCTCAGACGACATCCCCICTACAT	933
OY	436	ggcactcatlyggocctgtataaacactgacaagcytgtcaacaactgtgccccgttgaagccc	495
Db	934	CGCAGTGGTAGAGCTACTGGCTCGGGCATCTCCAACAGATGGCCAACTGCTGGGGCT	993
OY	496	tctctgttgccctggcgcacgtctbtgaagagagagcttgatctctcagtgaggaaagcaa	555
Db	994	CTTCTACATCCCCCAGGCTACACTATGGCTCTCCAGCGAGACTCTCTCACCAACAAAGMATCA	1053
OY	556	gtcccgctcctctctctggccaccatcccccagcataagtaaccaggtygaagatcatagtgcg	615
Db	1054	ATTCAAGTCCTTCCCTCCGACCATATCCCAATGATGMAACCCAGGCCACAGGGCATGGCTGA	1113
OY	616	gctgctgcagaagcttgagctggcttgatatctcgctgtggcaagctatggttgatacgg	675
Db	1114	CATCATCAGAGTACTTCCCTCGAAGCTGGGTGGGCCAATTCAGCTGACGATGACTATAGG	1173
OY	676	gcagctggcglaeaggsgctggagagacttgccaactccaaggsgacatctgcctgct	735
Db	1174	CCGGCCAGGAGATCCAGAAATTTCCAGAGGAAGCTGAGAGAGGGACATCTCATCTGACTT	1233
OY	735	caaggacgttggctgctctctccgcccaaggcggtgaccccaagagatgcagcgcatgct	795
Db	1234	CAGCGA-----GCTCATCTCCCAATACTGTGATGAGSAAAAGATCCAGAGGTGGTGA	1287
OY	796	ggcttgcctcgagagcaaggaaccaogtggctggctctctctcttaaocggcaactggcttgg	855
Db	1288	GGTGATCCAGAAATTCACCCGCCAAAGATATGTGGTCTTCCACAGCGGCCCAAGACTGGA	1347
OY	856	agtgctctcaagctctgtggtgtcggccaactctactgccaagtgtygatcgctccga	915
Db	1348	ACCCTGATCAAAGAAGATCTGTCCGGCGCAATATCAATCAATCAAGATCTGCTGCGCAGCGA	1407
OY	916	agactgyggccattctccacgtatcatcaaccaatgtgcccgggatlccaagggcatltggagcgt	975
Db	1408	GGCCCTGGGCCAGCTCTTCCCTGATTTGCTATCCCGAGATATTCATGCTGGTGGAGGAC	1467
OY	976	gctgggggtgcccataccagcagagacaagctccc-ggectgaaggaagt-----	1024
Db	1468	CATTGGGTTGGTTGAAGCTGGGCAATCCCAAGGCTCCGGGAATTCCTGCAGAAAGT	1527
OY	1024	-----tgaagatlocatgtlccaaggaagtgatgggtgtcccaagaact	1066
Db	1528	CCACCCCGAAGAACTGTGCCACATATGTTTTGCCAAGAGATTTTTGGGAAGAAATTTAA	1587
OY	1067	tggccagagggctcc-tggctgcgca--ctaacagctatgcaggagagtgtcaagcttca	1124
Db	1588	CTGCACCTCTGCAAGGGGTCTTAAGGGCCCAATTACCGGTGGACACCTCTCGAAGAGCTCA	1647

CC one or more activities of a calcium receptor (CR) comprises: (A)
CC contacting a recombinant cell with a test compound, where the
CC recombinant cell comprises a recombinant nucleic acid expressing from
CC provided that the cell does not have functional CR expression from
CC endogenous nucleic acid; (B) determining the ability of the test
CC compound to affect one or more activities of the calcium receptor; and
CC (C) comparing the ability with the ability of the test compound to
CC affect the one or more CR activities in a cell not comprising the
CC recombinant nucleic acid. The present sequence encodes bovine
CC parathyroid CR, designated a BopCAR 1. The nucleic acid sequence of
CC BopCAR 1 can be used as part of the recombinant nucleic acid in the
CC method described above. The compounds identified can be used to treat
CC diseases or disorders characterised by abnormal calcium homeostasis, e.g.
CC hyperparathyroidism, osteoporosis and other bone and mineral-related
CC disorders. They can also be used for the treatment of diseases and
CC disorders associated with disrupted Ca²⁺ responses, e.g. seizures,
CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in
CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative
CC diseases such as Alzheimer's disease, Huntington's disease and
CC Parkinson's disease, dementia, muscle tension, depression, and anxiety.
CC Sequence 5275 BP; 1277 A; 1475 C; 1316 G; 1207 T;

Query Match 6.1%; Score 157.2; DB 1; Length 5275;
Best Local Similarity 46.0%; Pred. No. 3.8e-31;
Matches 1136; Conservative 0; Mismatches 1168; Indels 166; Gaps 11;

QY 205 gctctacagcttcaaacgagccatgctatcaaccttccaagccatcggttaccggtga 264
Db 694 GGTGTACGATTAATTTCCGAGATTTTCGTGTACAGCTATGATTTGCAATAGA 753
QY 265 ggaataaacacacccacagctctctccacacacaccccgaggttgaactataga 324
Db 754 GCAATTAACACAGCACTCCAGCCCTTCTCCACATGACCTGGGATACAGATATTGCA 813
QY 325 cgtgtg----ctagaagcttccaatgctatgacacccctgaagtgcccgccacaag 381
Db 814 CACTGTAAACACCTGTCTAAAGCCTTGAGGCCACCTGATTTTGCGCCACAAACA 873
QY 382 gacaaagc-----caactagaaatgcagaagaatcttcgaacacactcccaagtg 435
Db 874 AATTACCTCTTTGAACCTTGATGATGTGCAACTGCTAGACGACATCCCTCTACCAT 933
QY 436 ggaactaatgagcctgtaaacacacacacacacacacacacacacacacacacac 495
Db 934 CGCACTGATGGAGCTACTGCTCGGCATCTCCACAGCAGTGGCAACCTGCTGGGCT 993
QY 496 ttctctgagccctgctgacgtatgagagcagcagcgtgaccccaagtgggaagcgcaa 555
Db 994 CTTTACATCCCCAGTCAGTATGCTCTCCACAGACACTCCCTACGACAAACAAATCA 1053
QY 556 gtcccgctctctctgacacacacacacacacacacacacacacacacacacac 615
Db 1054 ATTCAAGTCTTCTCCACACATACCAATGATGACACACGACGACGACGACGAC 1113
QY 616 gctgctgagagcctcgagctgagctgagctgagctgagctgagctgagctgagct 675
Db 1114 CATCATGAGTACTTCCCTGAGACTGGGTGGGCAATTGCACTGACGATGACTATGG 1173
QY 676 gcaagctgagcgttacaagcgtctgagagagcgtgacacacacacacacacacac 735
Db 1174 CCGGCGAGGATCGAGAGATTTCGAGAGAAAGCTGAGAGAGAGAGACATCTGATGACT 1233
QY 736 caaggaagctgctgctctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 795
Db 1234 CAGCA-----GCTCATCTCCCAATACTCTGATGAGAAAAGATCCAGCAAGTGTGGA 1287
QY 796 ggcctgagctcgagcagagacacacacacacacacacacacacacacacacacac 855
Db 1288 GGTGATCCAGATTTCCACCGCAAGTATGCTCTTCTTCTCCAGCGGCCACGACCTGGA 1347
QY 856 agtgctctcaggtctgctgctgctgctgctgctgctgctgctgctgctgctgctg 915
Db 915 agtgctctcaggtctgctgctgctgctgctgctgctgctgctgctgctgctgctg

Db 1348 ACCCTCATCAAGATGTCGCGGCAATATACAGCAGAGATGCTGCTGGCCAGCA 1407
QY 916 agactgggacatctcaagtaatacaccatgctgcccggatccagggcattggagagt 975
Db 1408 GGCCTGGGCGACCTTCTTCCTGATGCTATGCCGAGTATTTCCATGTGTGGGAGGC 1467
QY 976 gctgggggtggccatccagcagacacacacacacacacacacacacacacacac 1024
Db 1468 CATTTGGTTGGTTGAAAGCTGGGCACATCCAGGCTTCCGGGATTTCTGCAAGAA 1527
QY 1024 -----tgaagatctcattgccaagcagatgagtgctgctccagaact 1066
Db 1528 CCACCCAGAGAGTGTGTCACAAATGTTTGCCAGAGAGTTTGGAGAAACATTTAA 1587
QY 1067 tgcacagaggggtctgctgctgctgctgctgctgctgctgctgctgctgctg 1124
Db 1588 CTGCCACCTGCAAGAGGCTGTAAAGGCCCATTTACCGGTGACACCTCTCTAGAGGTCA 1647
QY 1125 gcaactgaaacatccgcagcagcttgagcctctccatgagcgtg----- 1170
Db 1648 CGAAGAGAGAGTGCACAGTTAAGCAACATCCACTCCCTTCCGACTCTGTGCATCG 1707
QY 1170 -----c 1170
Db 1708 GGAGAGAAACATCAGCAGTGTGAGACTCTTACATGATTAACATTTACGATATC 1767
QY 1171 ctacaatgtatgagcctggtatgctgctgctgctgctgctgctgctgctgctgctg 1230
Db 1768 CTACACGCTCTACTTAAAGCGCTCTACTCTCATTTGCTCATGCTTACAAAGATATAC 1827
QY 1231 taaccttgga-----cctgctgagagccagcctacc 1266
Db 1828 CATACCTGGAGAGGCGCTTTCACCAAGGTTCTCGCCCAATATCAAGAGTTGAAG 1887
QY 1267 ctggagctctctcagcagatctacaagtgaaatctcccttacaata---gaagactgt 1323
Db 1888 TTGGCAGGTCCTGAAAGACCGCGGACACTTAATTTACAGCAATATGGGGAGCAAGT 1947
QY 1324 agcatctgatacaaggggagacactctaggtatattatgacatcatcgctgagtgaa 1383
Db 1948 AACTTTCATGATGATGAGACACTGGAGGACATATTCATCATCACTGCACTGCACTCTC 2007
QY 1384 tggacctgaatgagccttgagcctgctgctgctgctgctgctgctgctgctgctg 1428
Db 2008 CCGAAGAGAGCGCTCATAGTGTTTAAGGAAGTTGGAATTACATGCTTATGCCAAGAA 2067
QY 1429 tccagttatctagacataaataagacacaaatccagtgagcagcaggaagaacatcag 1488
Db 2068 AGGACAGAGACTCTTCAATCATGATGAAATAATTTCTGAGATGATCTCAAGGAGGT 2127
QY 1489 ggcgtgtcagtggtgtacagcagcgtctcgaagggacacacaggttgatcat---ggg 1545
Db 2128 GCTTTCTTCAACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 2187
QY 1546 ttccac 1605
Db 2188 GGAGCCCACTGCTGCTTGAAGTGTGGAATGTCTGATGAGGAGTCAACGACGAGAC 2247
QY 1606 tgaagcttacaacctgccaagccttgtsaacaagaagaatggccctgagggagcctcagc 1665
Db 2248 AGATCAAGTGGCTGTGATTAAGTGCCCTGATGAGTCTGTGCTCAATGAAACACACTTC 2307
QY 1665 ctgctctcacaagcagcgtgaggtcttggtgtggtgagcagtaaacacacacacacac 1725
Db 2308 CTGCATCCCAAGAGAGATCGAGTTTCTGTGTGAGACCGAGCCCTTCCGGAATCGCACTAC 2367
QY 1726 agcagctacaac 1785
Db 2368 GCTCTTCTGCTGTGAGCAATTTTCTTCTACAGCCTTCTGCTGAGGCTCTTCACTAAATT 2427
QY 1786 tcttcacagcctctgtgaggtcagcgtgaggtgaggtgaggtgaggtgaggtgaggt 1845
Db 2428 CCGCAACAGCCCACTGCTCAAGGCGACCAACCGGAGCTCTCTATGCTCTTCTCTCTC 2487

QY	1846	ctgtgtatcgttgagggttgcaagccctctacagctctcttcgggaagcccaaggtgcccgtg	1905
Db	2488	cttgccttgcctgctcttccacgcttccctgcttcttcttcatcgggaagcccaagactgcagctg	2547
QY	1906	cttgcgtcgttcagccctctcttctctcgggttttgccatttctctctcctctgtctgacat	1965
Db	2548	ccgcctctgcgcacgcgcgccttcttgacatcaccttctgctcgtctgcattcgtgactcctgct	2607
QY	1966	ccgctctcttccaagtgtctatcttctcaagtttcttaccagaagttaccacacttcttaca	2025
Db	2608	GAAAAC---CAATGGGCTCTCTGCTGTTTGAAGCCAAAGATTCCACACAGCTTCACCG	2664
QY	2026	caattgggcccacaaacacatggtgcggaatattcgcattgttcagcttcacagctccatt	2085
Db	2665	GAAgGgGgGgGgGCTCAACTGCAGTTCGCGTGGCTTCCTCTGTGACTTCCTGACCTTCATGCAAT	2724
QY	2086	gttccctctgtctcaagtcgtgcttgcgaatgtgaccccaagcccaaggaagttaccagc	2145
Db	2725	TGTATCTGTGCCATTTTGGCTCAATACAGGCCCCCTTGAGCTACCGGACACAGACT	2784
QY	2146	cttcccccattcgtgtgattcttgagtgcacagaagttcaactcgtgtggttcctgtgyc	2205
Db	2785	GGAAGAGAGATCATCTTTCATCACCTGCCACAGGGCTGGCTCATAGGGCTTGGCTTCT	2844
QY	2206	tttcgcacacaaatccctctctctccatcagcaccttgtctgcagttactcgtgtaaga	2265
Db	2845	GATGGCTACACCTGCTTGGCTGCGGCACATCTCTTCTTGCGCTTCAGTCCCGGAA	2904
QY	2266	actcgcgagaaactataagaagaacaaatgtgcacttcagctcagctcctccacttgt	2325
Db	2905	GCTGCCAGAGAACTTCATATAAGCCAAAGTTTCATCACCTTCAGCATGCTCATCTTTTAT	2964
QY	2326	atctcgtatcgtcttcttccacaaatgtccagatttaccagaaggaactaacaccgcggt	2385
Db	2965	CGTGTGATCTCTTTCATCCCGCCCTACGCCACACACTTACGCAAGTTGTTGCGCGT	3024
QY	2386	caatgtctcgcagagggtgtgcacactcgtatggtgvcgttcacagcgtattctctccaa	2445
Db	3025	GGAAGTATGCCATCTGTGCGGCGCAGACTTTGGCTTGGCGCTGTATCTTTTACAA	3084
QY	2446	atgtcagtgattattctcgcgttcagaacttcaacacacagaaactttcagcctcat	2505
Db	3085	GGTTCATATATCTCTTTCAAAGCTTCCGGAAACACATTCAGAGAGTTCGCTGACGAC	3144
QY	2506	ccaggaactaac	2517
Db	3145	CGCGCACACGC	3156

RESULT	8
ID	T61381
AC	T61381 standard; cDNA to mRNA; 5006 BP.
DT	T61381;
DE	22-APR-1997 (first entry)
DE	Parathyroid calcium receptor coding sequence clone pPhuCar5.2.
KW	Calcium receptor; human parathyroid gland adenoma tumour; pPhuCar1;
KW	primary hyperparathyroidism; Xenopus oocyte; alternative splicing;
KW	variant; untranslated region; agonist; NPS R-467; NPS R-568;
KW	alternative transcription initiation; alternative polyadenylation; probe;
KW	human Car gene; isoform; ss.
OS	Homo sapiens.
FT	Key
FT	Location/Qualifiers
FT	436..3702
FT	/*tag -a
PN	/product- Calcium receptor
PD	W09612697-A2.
PD	02-MAY-1996.
PR	23-OCT-1995: U13704.
PR	21-OCT-1994: W0-U12117.
PR	08-DEC-1994: US-353784.
PA	(NPS-) NPS PHARM INC.

PI Balandra MF, Delmar EG, Moe ST, Nemeth EF, Van Wagenen BC:
DR WPL: 96-230520/23.
P-PSDS: W11888.
PT New di:arylalkyl amine cpds. useful for modulating inorganic ion
PT receptor activities - esp. for modulating effect of extracellular
PT calcium on cell surface calcium receptors, useful for treating e.g.
PT hyperparathyroidism, Paget's disease or osteoporosis
PS Example 1: Page 85-93; 221pp; English.
CC The sequences given in 161361-82 encode functional calcium receptors.
CC These sequences were isolated from human parathyroid gland adenoma
CC tumour using pHPaCaR.1 as a hybridisation probe. mRNA was isolated from
CC a 39 year old caucasian male diagnosed with primary hyperparathyroidism
CC and two clones of approx. 5 and 4 kb were identified. These cDNAs were
CC injected into Xenopus oocytes which were assayed for the presence of
CC functional calcium receptors. Both clone types gave rise to functional
CC calcium receptors as assessed by the stimulation of calcium-activated
CC chloride currents upon addition of appropriate calcium receptor agonists,
CC e.g. NPS R-167 and NPS R-558. Sequence analysis of the two cDNA clones
CC indicated the existence of at least two sequence variants differing in
CC the 3' untranslated region and which may result from alternative
CC polyadenylation. Sequence variation also exists in the 5' end of the
CC inserts. These sequence differences may have arisen due to alternative
CC transcription initiation and/or splicing. Three additional sites of
CC sequence variation occur within the coding regions of cDNA clones
CC pHPaCaR5.2 and pHPaCaR4.0 demonstrating that they encode distinct
CC proteins. Sequence analysis of the human CaR gene indicates that the
CC additional 30 bp in clone pHPaCaR5.2 as compared to pHPaCaR.0, results
CC from alternative mRNA splicing. This alternative splicing is predicted
CC to insert 10 additional amino acids into the CaR protein encoded by
CC pHPaCaR5.2 between residues 536 and 537 of the protein encoded by
CC pHPaCaR4.0. In addition pHPaCaR4.0 encodes Gln at position 925 and Gly
CC at position 990, whereas pHPaCaR5.2 encodes Arg at both equivalent
CC positions. The human CaR gene encodes for Gln and Arg respectively at
CC these positions. These two receptor isoforms may be functionally and/or
CC pharmacologically distinct.
SQ Sequence 5006 BP: 1228 A; 1376 C; 1220 G; 1182 T;

Query Match	5.9%	Score 152.6	DB: 1	Length 5006
Best Local Similarity	48.4%	Pred. No. 5.8e-30		
Matches 487	Conservative 0	Mismatches 514	Indels 6	Gaps 2
OY 1484	caggctgctctgtgtcaagtggtgtacacagggagactcttcggaagggaccacacaggtgtgtcat-	1543		
Db 2071	CAGGTGCCCCCTTCTCCAACTGCACGCCGAAGACTCCTTGCCAGGGACCAAGAAAGGATCAAT	2130		
OY 1543	--gggttccacacacactgctgtgtcttcgagtcagctatgcccctgtgaagctgaggacatttctcaac	1600		
Db 2131	GAGGGGGAGCCOACACTGCTGTGCTTTAGTGTGTGGAGTGTCTCGATGGGGAGATATGTAT	2190		
OY 1601	acgagtgagcttcacacactgtccagccctgtgtgaaacagaagaatggcccttgaaggagac	1660		
Db 2191	GAGACAGATGGCCAGTGCCTCTTAACAAAGTCCCAAGATGACTTCTGGTCCAAATGAGAACCC	2250		
OY 1661	tcagctgtctctcaacgacacggtggaagcttcttgggtgtgtcatgaaccatctcttgtgt	1720		
Db 2251	ACCTCTCTCATTTGCCAAGAGATCCAGTTCTGTGTGTGACGGACCCCTTGGGATGCCA	2310		
OY 1721	ctattgagcgttaacagcacttctgtctgtctgtcgtatggacattgcacgtctgagctgttgc	1780		
Db 2311	CTCACCCCTTTTGGCGTCTGGGCAATTTTCTGACAGCCTTTGTCTGTGGTGTGTTTATC	2370		
OY 1781	tgcgctctcacacagccctgtgtgtgagtcacagcttggggtaagctgtgtctctcactgtgt	1840		
Db 2371	AAGTTCGGCAACACACCCTATTGTCAAGGCCACCAACGAGAGCTTCTACTCTCTCTC	2430		
OY 1841	ggtctctgtgtagctgtggaattgacgctctaacagctctcttgcgggaagccacaggtgcc	1900		
Db 2431	TTTCTCCGCTGTGCTGTCTTCCAGTCCCTGTGTCTTCATGCGGGAGCCCAAGAGATGG	2490		
OY 1901	gagtgctgtgtggttcaagccctcttctctctcgtgtgttgcatttctctctctgtctgt	1960		
Db 2491	ACGTGCCCCCTGGCGCACCCGCTTTGGCATCAGCTTGTGCTGTGATCATCATCATCATC	2550		


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QY 1961 acatccgcctccctcccaactgggtacatcatctcaagttttctacacaaggtaccacattc 2020
Db 2551 CTGGTGAACCAACACCGTCTCTCTCGTGTGTTGAAG---CCAAGATCCCCACCACTTTC 2607
QY 2021 taccacacttggcccaaaaacacatgggtgcgggaatactgcatactgtccagctccacagtc 2080
Db 2608 CACCGCAAGTGTGGGGCTCAACCTGCAGTTCCTCTGTTTCTCTGCAACCTCATG 2667
QY 2081 cattgtctctctgtctcaagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 2140
Db 2668 CAGATTGTATCTGTGTATCTGTGCTCTACACCGCCCTCCCTCAAGCTACCGCAACCAAG 2727
QY 2141 cagcgcttcccccatctgtgtatctctgtgagtcacagagatcaactctgtggcttcagg 2200
Db 2728 GAGCTGGAGAGATGATATCTTTCATACAGTGCACAGAGAGGCTCTCATGGCCCTGGGC 2787
QY 2201 gtggtcttcgcacacaacatctctctccatcagacacttgcctgcagctcactcagtc 2260
Db 2788 TTCCTGATCGGCTACACCTGCTGCTGGCTGCATCTGCTTCTTCTTTCCTTTCAGTCC 2847
QY 2261 aagggaactgcgggaagaactataagaagcaaatgtgtcaacttcaagctctcctccac 2320
Db 2848 CGGAAGCTGCCGAGAACCTCAATGAAGCAAGTTTCATCAGCTTCAGCATGCTCATCTTC 2907
QY 2321 ttccgtatccctggtatcgcttctctccacatgctcagagattaccagggagagctaacctacc 2380
Db 2908 TTCATCGTGTGATATCTCTTCTTCCAGCTTCATGCCAGACCTATGGCAAGTTTGTCTT 2967
QY 2381 gcggtcaactgtgtgcagagctgcagcactctgaatgcgagcttccagcgctatctctc 2440
Db 2968 GCGGTAGAGCTGATTCCTCTCTGCGAGCCAGCTTGGCTGTGGCGTGCATCTTCTTC 3027
QY 2441 cctaagtgtacgtatctctcgcgcgtccagaactcacaacacaga 2487
Db 3028 AACAAGATCTACATCATTTCTTCAAGCCATCCCGACACCATCGA 3074

RESULT 9
T95858
ID T95858 standard; cDNA to mRNA; 5006 BP.
AC T95858.
DE 08-MAY-1998 (first entry)
DI Human parathyroid cell calcium receptor 5.2 (HupCar 5.2) cDNA.
KW Human parathyroid cell calcium receptor 5.2; HupCar 5.2;
KW Calcium homeostasis; hyperparathyroidism; osteoporosis; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 436..3702
FT /tag= a
FT /product= parathyroid_cell_calcium_receptor_5.2
FN US688938.A.
PD 18-JUN-1997.
PE 07-JUN-1995; 485588.
PR 07-JUN-1995; US-485588.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-017127.
PR 23-FEB-1993; US-009389.
PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (BGHM ) BRIGHAM & WOMEN'S HOSPITAL.
PA (NNSP-) NPS PHARM INC.
PI Brown EM, Fuller FH, Garrett JE, Hebert SC;
DR P-PSDB; M38273.
PT DNA encoding calcium receptor polypeptide(s) - useful for
PT therapeutic purposes, e.g. hyperparathyroidism and osteoporosis
PS Claim 15; Columns 117-126; 174bp; English.
CC The present sequence encodes human parathyroid cell calcium

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CC receptor 5.2 (HupCar 5.2).
CC The specification includes details of molecules that can modulate
CC one or more inorganic ion receptor activities, and antibodies and
CC antibody fragments targeted to inorganic ion receptor proteins. The
CC proteins, nucleic acids and antibodies may be used to treat
CC disorders by modulating one or more inorganic ion receptor
CC activities, preferably disorders of calcium homeostasis, e.g.
CC hyperparathyroidism and osteoporosis.
SQ Sequence 5006 BP; 1227 A; 1378 C; 1219 G; 1182 T;

Query Match 5.9%; Score 152.6; DB 1; Length 5006;
Best Local Similarity 48.4%; Pred. No. 5,8e-30;
Matches 487; Conservative 0; Mismatches 514; Indels 6; Gaps 2;

QY 1484 caggtgctgtgtcagtggtacagagagctgtcgaaggagccacacaggtgtgtcat- 1543
Db 2071 CAGGTGCTGTGTCCACAGTGCAGCGAGACTGCTGCGAGGACCAAGAAAGGATCATTT 2130
QY 1543 --gggtccacacactgtgtgtcagtggtacagagagctgtgagctgtggagcatcttccaac 1600
Db 2131 GAGGGGGAGCCCACTGCTGCTTGTGAGTGTGTGAGTGTCTGTGAGGGAGATAGTGTAT 2190
QY 1601 acgagtgaacttcaacactgtccagcctgtgtgaacagagaatggagccctgagggagagc 1660
Db 2191 GAGACAGATGCCAGTGTCTGTGAACAAGTCCCAAGTGACTTGTGTCCATAGAAACAC 2250
QY 1661 caagcctgtcttcaogaacggtgagttcttgggtggaatgaacccaactctcttgggtg 1720
Db 2251 ACCCTGCTGATGGCCAAAGAGATGAGATTTCTGTGTGAGACGAGCCCTTGTGATGCA 2310
QY 1721 ctattagcagcttaaacgttatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1780
Db 2311 CTACACCTTTTGGCGGTGTGGGCAATTTCTGACACCTTTGTGCTGGGTGTGTATTC 2370
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QY 1841 ggttcctgtgtagctgtggaagtgtcagccttcaagcctcttcgggaagccacagtgccc 1900
Db 2431 TTCTCCCTGCTGTGCTGTCTTCCAGCTCCCTGTCTTCATCTGAGGAGCCCAAGACTGG 2490
QY 1901 ggtgtcctgtctgtcagagccctcttctctcgggtgttgcatttctctcctcgtctg 1960
Db 2491 ACGTCCCGCTTGCAGCGAGCGGCTTTGGCAATCAGCTTCTGTGTGCACTCATAGCATC 2550
QY 1961 acatccgcctccctccaaactgtgtacatctcaagcttctacacaaggtaccacaatc 2020
Db 2551 CTGGTGAACCAACACCGTCTCTCTCGTGTGTTGAAG---CCAAGATCCCCACCACTTTC 2607
QY 2021 taccacacttggcccaaaaacacatgggtgcgggaatactgcatactgtccagctccacagtc 2080
Db 2608 CACCGCAAGTGTGGGGCTCAACCTGCAGTTCCTCTGTTTCTCTGCAACCTCATG 2667
QY 2081 cattgtctctctgtctcaagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 2140
Db 2668 CAGATTGTATCTGTGTATCTGTGCTCTACACCGCCCTCCCTCAAGCTACCGCAACCAAG 2727
QY 2141 cagcgcttcccccatctgtgtatctctgtgagtcacagagatcaactctgtggcttcagg 2200
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QY 2201 gtggtcttcgcacacaacatctctctccatcagacacttgcctgcagctcactcagtc 2260
Db 2788 TTCCTGATCGGCTACACCTGCTGCTGGCTGCATCTGCTTCTTCTTTCAGTCC 2847
QY 2261 aagggaactgcgggaagaactataagaagcaaatgtgtcaacttcaagctctcctccac 2320
Db 2848 CGGAAGCTGCCGAGAACCTCAATGAAGCAAGTTTCATCAGCTTCAGCATGCTCATCTTC 2907
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DB 2614 CACCGCTGCTTCGGCAGCAGCAGCTTGTGCTGTATCTCGGCACTCTTGGAAGACCAAT 2673
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QY 1976 caactgtaacatcatcattcaagattttaccagaagtaaccacattcaccacttggcc 2035
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 2674 CGGCTCTCTGATATTGA---AGCCAAATATACCCAGCTTCCACCGGAAGTGGTGG 2730
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QY 2036 caaacaatggtgcggaatattcgtcattgtcagctccacaggttccattgttctctgt 2095
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 2731 GGGCTCAACCTGCAAGTCTGCTGCTGCTTCTTCTTCCAGCTTCAATGAGATCTCATCTGC 2790
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 2096 ctcaactggttcgaatggtgaccccaagcccaaggaagtaaccaggttcccccatt 2155
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DB 2791 ATATCTGCTCTACACGGGGCCCTCTAGCTACCGCAACCATGAGCTGGAAGAGAA 2850
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QY 2156 ctggtatcttgatgagcagagagtaactctgtggtgcttctgtggttccgacac 2215
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QY 2216 aacatctctctctccacagcacccttctgtctgagctaccctgtgtaaggaactgcccag 2275
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DB 2911 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAT 2970
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QY 2276 aactataaggaagcaaatgtgtcaacctcagcctgctcctcacttctgtatccctggatc 2335
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DB 2971 AACCTTACAGCAAGCAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3030
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QY 2336 gcttcttccacatgctccagcattaccagagagtaactaccgagagcaatggtgtg 2395
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DB 3031 TCCCTTATTCACAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAT 3090
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
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DB 3091 GCCATTTTGGCAGCCAGCTTGGCTTACTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAT 3150
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 2456 attcttgcgcgtccagaactcaacaacacagaaacactttcaagcctccatc 2506
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 3151 ATCTCTTCAAGCCTTCCCGGAACACACATTGAGGAAGTCCGCTCCAGCACCC 3201
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

RESULT 15

V26965

V26965 standard; cDNA to mRNA; 4131 BP.

AC V26965;

DE 01-SEP-1998 (first entry)

DI Rat kidney calcium receptor 3A gene 4kb fragment.

KW ss: calcium ion concentration; parathyroid hormone; homeostasis;

OS kidney; calcium receptor; detection.

FH Rattus sp.

FT key

FT CDS Location/Qualifiers

FT /tag= a

FT /product= "RakCar 3A 4kb fragment"

PD US5763569-A.

PN 09-JUN-1998.

PE 07-JUN-1995; 484565.

PR 07-JUN-1995; US-484565.

PR 23-AUG-1991; US-749451.

PR 11-FEB-1992; US-834044.

PR 21-AUG-1992; US-934161.

PR 12-FEB-1993; US-017127.

PR 23-FEB-1993; US-009389.

PR 22-OCT-1993; US-141248.

PR 19-AUG-1994; US-292827.

PR 21-OCT-1994; WO-012117.

PR 08-DEC-1994; US-353784.

PA (BGM) BRIGHAM & WOMENS HOSPITAL.

PI (NPSF-) NPS PHARM INC.

PI Brown EM, Garrett JE, Hebert SC;

DR WPI: 98-347412/30.

DR P-PSDB: W54847.

PT Calcium receptor poly:peptide(s) - useful for drug screening or antibody production

PS Example 30; Fig 50; 174pp; English.
 CC The rat kidney calcium receptor gene encodes a 1079 amino acid protein.
 CC The tissue from which this receptor and receptors from bovine parathyroid
 CC and rat kidney are derived, respond to changes, and control changes. In
 CC calcium ion concentration, e.g. parathyroid hormone regulates Ca²⁺
 CC homeostasis in blood and extracellular fluid, and kidney function alters
 CC through changes in Ca²⁺ levels in juxtaglomerular and proximal tubule
 CC cells in the kidney. The purified receptors (produced
 CC recombinantly) can be used to screen for compounds that modulate calcium
 CC receptor activity, especially those that can be used to treat diseases
 CC associated with the receptors in these tissues. They can also be used
 CC to raise antibodies for use in detection assays.
 SQ Sequence 4131 BP; 988 A; 1170 C; 1052 G; 921 T;

Query Match 5.4%; Score 138.2; DB 1; Length 4131;
 Best Local Similarity 46.9%; Pred. No. 2.9e-26;
 Matches 502; Conservative 0; Mismatches 563; Indels 6; Gaps 2;

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QY 1439 ctgagataataagaacaaatccagtgcaggggaagaacaatcagtgctgtgtca 1498
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DB 2374 AAGGAGATGAGTCTTGTGCGTGAACGCCCTTGAATGCTCTCATCTCTTTGCG 2433
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DB 2434 GTCTGGGCAATTTCTGTGACCCCTTTGTGCTGGGTGTCTTATCAAGTTCGAAACACA 2493
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QY 1916 cagccctcttctctgtggtgttgccatttccctctcctgtcgtgacaaatccgcctctc 1975
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DB 2614 CAGCTGCTTTGGGCAATGCTTGTGCTGTATCTGTGATCTTGTGTAAGACCAAT 2673
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DB 2674 CGGCTCTCTGTAATTGA---AGCAAGATACCAACACAGCTTCCACCGGAAGTGGTGG 2730
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QY 2156 ctggtatcttgatgagcagagagtaactctgtggtgcttctgtggttccgacac 2215
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DB 2851 ATCATCTTATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAT 2910
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QY 2216 aacatctctctccacagcacttgtctgcaactacactgtgtaaggaactgcccag 2275
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Db	2911	ACGAGCTGGTGGGTGGCCATCTGGCTTCTTTTGCTTTAAATCCAGGAAGTACGAAG	2970
Qy	2276	aactataacgaagcgaaaatgltaccccttcacgcctctcccaattgtaacatgacatg	2335
Qy	2336	gcttcttcacacatgctcagaatcttaccagagagcttaccaccccggtcaatgctgtg	2395

AUTHORS	Hoon, M.A., Adler, E., Lindemeier, J., Battey, J.F., Ryba, N.J. and Zuker, C.S.
TITLE	Putative mammalian taste receptors: a class of taste-specific GPCRs with distinct topographic selectivity
JOURNAL	Cell 96 (4), 541-551 (1999)
MEDLINE	99159821
REFERENCE	2 (bases 1 to 2520)
AUTHORS	Hoon, M.A., Adler, E., Lindemeier, J., Battey, J.F., Ryba, N.J.P. and Zuker, C.S.
TITLE	Directed Submission
JOURNAL	Submitted (10-FEB-1999) Taste and Smell Unit, NIDCR, 10 Center Drive MSC 1188, Bethesda, MD 20892-1188, USA
FEATURES	location/Qualifiers
SOURCE	1. .2520

CDS

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/note="G protein-coupled receptor"
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/product="putative taste receptor TR1"
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QY	71 gcttccagctgcgaaggacagaaatcctctccagglltccagcctccctgaggaactcttc	130		
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QY	131 ctgagcagccgctgttctccctccatgtctgactctctgcaggtgtagacacagacctgtgt	190		
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QY	191 acaatttgcaggtctgcagagcttcaagcgccatgtgatccactcttccaagccaag	250		
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QY	251 cggttcacccgttgagagataaacaactccacagctctgcttccccaacaacacccctgggg	310		
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QY	311 tatgaactgtatgaagctgtgtcctcagaagcttccaaatgtctatgccaacctgaggtgccc	370		
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Qy	971	acggctgcctgggggtggtgcataccagcagagagaacaagttccctgcgtctaaagaggtttgaag	1030
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Qy	1091	actaacccagctgtgcgaaggggtgtcagcgtcttcacagacatgaaaatgcccgagtttga	1150
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Qy	1331	gatcaacaagggtgaccttaagttatattagcatcatcgctgcgtggaactgtgaatgtacct	1390
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Qy	1391	gaatggaactttgagtgcatgtgtctgcctcactgtctccagttcatctatagacataaat	1450
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Qy	1451	aagacaaaaatcgaatgtgcacggtggaagaagaacaatcgaatgtgctctgtatcagtgtgtacaag	1510
Db	1435	AAGACAAAAATCCAGTGTGCACGGGAAAGCAATACAGAGTCCCTGTGTCAAGTGTGTACACAG	1494

QY	1031	tcctatgtccagagcagatgagtgctccagaactctgcagaaaggggtccgtgtgagc	1093c
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QY	1091	actaacagactgtgtccagggagtgtcacgcttccagacatggaaacatgcccgagtgtga	1150b
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QY	1151	gccttcccatgagcgtctgcctacaaatgtgtatgagagcctgttatgctgtgtgccaaagc	1210b
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QY	1271	cagcttcctcagcagatctacaaggtgaatttcctctacataaagaagactgtagcattc	1330b
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QY	1331	gatgaacaaggggagccctctagtttatitgtacatcatatgcctggagactggatggact	1399a
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QY	1391	gaatgagaccttggagtcattgtgtctgcctcacgtctccagcttcattatagaataat	1450b
Db	1375	GAA TGAGAC TTTGAGATCATTTGGCTCTGCTCACTGTCTCCAGTTTCATCTGGACATTAAT	1433b
QY	1451	aagacaaaatccagctgtgcacgggaaagaacaatccagtgctctgtgtcagtgtgtaccag	1510b
Db	1435	AAGCAAAAAATCCAGTGTGCACGGGAAGAACAAATCAAGTCTCCTGTGTCAAGTGTGTACACAG	1494a


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QY 1511 gactgtctcagaagccacacaggttgatcattggtgtccaccactgtcttcgaatgc 1570
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Db 1495 GACTGTCTGCGACGGCACACAGGCTGTTGTGGTTCCACACCTCTCTGTGATGCT 1554
QY 1571 atgcacctgtaagcttggagacattctcaacacagatgagcttccacactgcagacctgt 1630
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QY 1631 ggaacagaaataatggcccttgagagagctcagccctgtcttcacgcacccgttgagttc 1690
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Db 2035 GGTTATTTGCTATGTTCAGCTCCAGGTCATTTGCTCATCTCTCTACATGGCTTGTA 2094
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QY 2231 atcagacacttgtctcagacttactggttaaggaactgcagagaaactaaagagcc 2290
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Db 2455 GAACTCAACAATACAGAAACATTTCAGGCTCCATCCAGAGACTACAGAGCGCTTGCGGC 2514
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Db 2515 ACTACC 2520
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RESULT 2
AF127390
LOCUS AF127390 2529 bp mRNA ROD 04-MAR-1999
DEFINITION Rattus norvegicus putative taste receptor TR2 mRNA, partial cds.
ACCESSION AF127390
VERSION AF127390.1 GI:4337087
KEYWORDS
SOURCE
ORGANISM Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 2529)
AUTHORS Hoon, X.A., Adler, E., Lindemeier, J., Battey, J.F., Ryba, N.J. and
Zuker, C.S.
TITLE Putative mammalian taste receptors: a class of taste-specific GPCRs
with distinct topographic selectivity
JOURNAL Cell 96 (4), 541-551 (1999)
MEDLINE 99159821
REFERENCE 2 (bases 1 to 2529)
AUTHORS Hoon, X.A., Adler, E., Lindemeier, J., Battey, J.F., Ryba, N.J.P. and
Zuker, C.S.
TITLE Direct Submersion
Submitted (10-FEB-1999) Taste and Smell Unit, NIDCR, 10 Center
Drive MSC 1188, Bethesda, MD 20892-1188, USA
FEATURES
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/db_xref="taxon:10116"
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/codon_start=1
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VYFVAETITAKVAIVGNMLATTINDIGRTDDDPNIMILSCHPNYRNLGTLNNTSMDL
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BASE COUNT 497 a 826 c 623 g 583 t
ORIGIN
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Query Match 15.9%; Score 409.2; DB 12; Length 2529;
Best Local Similarity 50.7%; Pred. No. 6,4e-81;
Matches 1242; Conservative 0; Mismatches 1168; Indels 42; Gaps 9;

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Db 83 CTGACTTCCACCTGGCGGGGACTTACTCTGGTGCGCTTTTACCCTTCATGCCACAG 142
QY 152 gctgcaggtgagaca--cagacctgtgtgacaagtttgcagagctgcagagctta 218
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Db 143 TGAAGACATCTCCACCTACCTACCTGACGAGTGCCCAAGTCAATGATTCACCATGA 202
QY 219 acggccatgtctatacctcttccaaagcatgaggttaccggttggaggaataaacaact 278
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D	380	TCTCTAAGAAGACTACAGCCAGTACTATGCCCCACAGTGGTGGCTGTACTATGGCCCCGACAACT	439
Q	459	ctgaacacgctgtltaaccaactgtgcctctgtagacccttctgtatgcccctgtgaact	518
D	440	CTGAGTCCGGCATTCAGCTGTCACCAACTTCTCTCTATTTCCATCTCCACAGATCCACAT	499
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D	500	ACAGCGCCATTCGCGACAACTGGGGGACAAAGGGCACTTCCCTAGCATGTACCCACAG	559
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D	560	TGCCAGGCGCACCCACCACTGAGGCGCATGGTGTGAGTGATGGTTTCACTTCCAAATGA	619
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D	740	CTGAGTCCAGCGCAGGTATGAGGTCCAGGAGACGAGACAACTGGGACCAATCTGGACAA	799
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Q	858	tgattcttcaggtctgtgtgtctgtgcacaacctgtgcacaagtgtgtatgcgtcccgaa	917
D	860	GCTTCTTTACAGAGTGTCTCCGCGTGAATTCACGGGTTTGTGTGATCGCCTGTAGT	919
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D	920	CTTGCGCTATCGACCCGATTTCTGCATTAACCTCAGGAGGTGGCCACACAGGGTACTTTTC	979
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D	1040	ACAAGCAGGGTATCCGTCCTTACACGACCAACTCGGGGAGACCTC-----AAC	1093
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Q	1158	ccatgaagcctgtgcataaagtgtltaagagctgtgtatgtctgtgcccacggtcccaac	1217
D	1154	GGGAGCGGTGTCTACAGGCTGTACGCGCAATTACGGGGTGGCCATGCTCTTCACA	1213
Q	1218	agctctcgtggaatgaactctcttggaaactgtgtccagaagcccagttacacccctgtgaacttc	1277
D	1214	GACTCTCCGCGCTGTAAACCGGGGTCCGCTGCACCAAGCAAAAGGCTTAACCGGTGGCGCTAC	1273
Q	1278	tccaagcagatctacaaggtgaatttcccttacaataagaagctgtgaatctcgatgtga	1337
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Qy	1458	aatccagttgacgaggaagacaaatcaagtcgagtcgtctgacgtgtgacagaggtctgc	1517
Db	1451	ATGTGCTCTGTATACACCCCAACAGGTTCCGTCTCATGTGTGCCAAGAGCTGCC	1510
Qy	1518	tcgaaggagccaaaggttggtcattggtttcccaaccaactgtctctgagtgagtcacct	1577
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Qy	1695	ggtgtgcatgaaaccaactcctttgtgtcattaaagcattaaagctattgtctgtctgc	1754
Db	1691	AGTGGCAGGAAGTGGCCCAACATCGTGGGCCATACTGGCGCCCTGGGCTTTAGTA	1750
Qy	1755	tgattggaatgctgagccgtttgacctgagcttcaacacgcgtgtgtgagtgcaagctg	1814
Db	1751	CACGTGGCAATCTTTTTCATCTCTGTGGAGACATTTCCAGACACCATATGTGCGTCGGCG	1810
Qy	1815	ggagtgagctgtgctctccatagctggtgtccctgttgtagctggaggttcagacctaca	1874
Db	1811	GTGGCCCAATGTCCTTCCATGATGTCGTGGCCCTGTGCTGTGGCTTGGGATGGTCCCG	1870
Qy	1875	gctcttcgggaagcccaacagtgagcccgagtcgtgctgagtgcaaccccttttctctcg	1934
Db	1871	TGTATGTGGGGCCCCCAAGGCTTCTCTATGCTTCTGTGCGACAGGCTTTTTCACCGCTC	1930
Qy	1935	ggtttgcacatttctctctctctcctgaaacatcgcctcttcacaaatgltatcatcttca	1994
Db	1931	GCTTCTCAATCTGCTATCTCTATCTCATACACGTCGCGCTTCCATATGCTGTGCTTCA	1990
Qy	1995	agttttctcaacaagagtaaccaattcttcaacacttggagcccaaaacatagtgccggaa	2054
Db	1991	AGATGGCAACAGCCCTGCGCAATGCTTCAAGTCTTTTGGATGCTGTACACAGGGCCCTATG	2050
Qy	2055	tatctgcattctgcaagctcacaaggtccattgttccctctgctc---caagtgactggcaa	2111
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Qy	2112	tttgagaccacagggcccacaaaggaagtaacagagcttcccccaltctggtattcttgagt	2171
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Qy	2172	gcaagaaggttcaactctgtgaggtcttcctgtgtgtgtcttggcaacaatatctctctca	2231
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Qy	2232	tcagcaactttgtctgcaagctaacctctgggtaaggaactgcggagaaactaataagaaacca	2291
Db	2231	TGCTGGGTTTACACTTTCGTTTACATGAGGCAAGAGAGTGCACCACTTACACAGAGGCCA	2290
Qy	2292	aatgtgtcaacttcaagctgtcctctcaactctcgatctctggatcttgctttcttcaacatg	2351
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Qy	2352	ccagcaatttccagagcaagctaacctaccacggcggttcaatgtctgtgcagggctggcaact	2411
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Qy	2412	tgagtgtagcttcagcggctatttctcccttaaaatgactagctagatctctcgcgtccag	2471
Db	2411	TCTGTGCATCTGCTTGGGATCTTGTGGCCCAAGTGTATCATATCTTTTCTTACCGG	2470

Oy	2472	aactaacacacagacacaccttcagcctccatccaggacacacagagccg	2523
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LOCUS	G09859	270 bp	DNA
DEFINITION	human STS CHLC.GCT15G02.P16729 clone GCT15G02.	STS	15-AUG-1995
ACCESSION	G09859		
VERSION	G09859.1	GI:941708	
KEYWORDS	STS sequence; primer; sequence tagged site.		
SOURCE	human vecor/pUC1 host-E.coli dut-ung+ (DH10B) Marker Selected genomic DNA prepared from XY individual of French nationality.		
ORGANISM	Homo sapiens		
	Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Carnarina; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 270)		
AUTHORS	Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buelow,K.H.		
TITLE	Cooperative Human Linkage Center		
JOURNAL	Unpublished (1995)		
COMMENT	Synonyms: GCT15G02, CHLC.GCT15G02.T16713		
	Contact: Dr. Jeffrey C. Murray		
	UofI		
	The University of Iowa		
	Department of Pediatrics, Iowa City, IA 52242, USA		
	Tel: (319) 356-3508		
	Fax: (319) 356-3347		
	Email: jeff-murray@uiowa.edu		
	Primer A: CTCACACAGGGTGCTCTAG		
	Primer B: TGGTGTTTTCGCTTTC		
	STS size: 124		
	PCR Profile:		
	denature: 30 seconds at 94 degrees C		
	annealing: 75 seconds at 55 degrees C		
	extension: 15 seconds at 72 degrees C		
	PCR cycles: 27		
	extension: 6 minutes at 72 degrees C		
Protocol:			
	Template: 30ng genomic DNA		
	Primer: each 1.5 pmole		
	dNTPs: each 200 uM		
	Taq Polymerase: 0.3 units		
	Total Vol: 10 ul		
Buffer:			
	MgCl2: 1.5mM		
	KCl: 50mM		
	Tris: 10mM		
	pH: 8.3.		
FEATURES			
source	Location/Qualifiers		
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STS	/organism="Homo sapiens"		
Primer_bind	95..218		
Primer_bind	95..114		
BASE COUNT	66 a complement(201..218)		
ORIGIN	90 c 75 g 39 t		
Query Match	7.1% Score 182.6; DB 13; Length 270;		
Best Local Similarity	79.9%; Pred. No. 1.5e-30;		
Matches 215; Conservative 0; Mismatches 54; Indels 0; Gaps 0;			
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Db	270	GGGAAGAAGAGATGGGCACTCTAGGGAAGCCAGACCTGCTTCCCGGCACTGTGGTGT	211
Oy	1691	ttggggttgcatgaaaccatctcttgggtgcatatagcagcctaaacagctatgctgctg	1750

[illegible]

QY 677 cagctggcgctacagcgctggagagctggcactccacgggagctatgctgccttc 736
DB 1030 CGGCGGGGCGATTGAGAAATTCGAGAGAGAGCTGAGAAAGGAGATATCTGCATCATTC 1089
QY 737 aagagcggtgggctcttcggccagggcggtgacccaaagtatgcgcgtatgtctg 796
DB 1090 AGTGA-----ACTCATCTCCAGTACTCTGATGAGAGAGATCATCATCTGGTAAAG 1143
QY 797 cgtcgtcgcagccagagaccagctggctgctgtctctcctcaacggcagctgtcga 856
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QY 917 gactgggcatctccagctaacatcactatgcccggagatccagggatttggagcgtg 976
DB 1284 GCGTGGGCGACCTCTCCCTGATCGCCATGCTCAGTACTTCCAGCTGGTGGCGGACCC 1323
QY 977 ctgggggtggcactccagagacaagctccctggcctgaagagat----- 1024
DB 1324 ATTGGATTGCGTCTGAAGGCTGGGAGATCCAGGCTTCCGGGATTTCTGAAGAGGTC 1388
QY 1024 -----tgaagagctctatgtccagcgagctgagt----- 1052
DB 1384 CATCCCAAGAGTCTGTCTCATATGTTTGGCAAGAGATTTGGAGAAACATTTAAC 1443
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QY 1097 -----caagtgtcagggag 1111
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QY 1385 ggaactgaatgagaccttgaagctatgtgtctgcct-----cactgctc 1429
DB 1864 CCAGAGATGGCTCATCGTGTTTAAGGAGTGGGTAATTACAGCTATGCCAAGAG 1923
QY 1430 ccaattcatcagacataaataagaacaaatcagtgagcagggagaaacaatacagtg 1489
DB 1924 GGAGAAAGACTTTCATACAGAGAGAGAAATCTGTGAGTGGTTCCTCCAGGAGGTG 1983
QY 1490 cctgtgtacgt 1546
DB 1984 CCTTCTCAACTGACCGGAGACTGCTGTGGAGGAGACCAAGAAAGGATCTTTAGGGG 2043
QY 1547 tccacacacgt 1606
DB 2044 GAGCCACTGT 2103
QY 1607 gagcttcaacctgcagccttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1666

DB 2104 GATGCCACTGCTCTTACCAATGCGCCAGATGACTTCTGTGTCATGAGAACCAACCTCC 2163
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DB 2164 TGCAATGCCAAGAGAGATGAGATTTCTGTGTGAGAGGAGCCCTTTGGAGATGACATACC 2223
QY 1727 gcaactaacacgtatgt 1786
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QY 1787 cttaacacgctgt 1846
DB 2284 CGCAACACACCATTTGTCAAGGCGCCACCAAGAGAGCTCTCTACCTCTCTCTCTCTCC 2343
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DB 2344 CTGCTGTGCT 2403
QY 1907 ttgt 1966
DB 2404 GCGCTGGCGCCAGCGGCGCTTGGCATCAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 2463
QY 1967 cgtctcttccacatgt 2026
DB 2464 AAAACCAACCGTGTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2520
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DB 2521 AAGT 2580
QY 2087 ttccctgtctcagctgt 2146
DB 2581 GTCATCTGT 2640
QY 2147 ttcccccatcgt 2206
DB 2641 GAGGATGATCATCTTATACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2700
QY 2207 ttgcac 2266
DB 2701 ATCGGCTACCTGCTGT 2760
QY 2267 ctgcggagaaactaaacgaagccaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2326
DB 2761 CTGCGGAGAACTTCAATGAGCCAAAGTATCATCTTACAGATCATCTTCTTATC 2820
QY 2327 tccgt 2386
DB 2821 GTCTGGATCTCTTATTCAGCGCTATGCGACGACTATGCAAGTGTGTGTGTGTGTGT 2880
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DB 2881 GAGGTGATGTGATCTGT 2900
QY 2447 tgcatagtatctctgcgcgtccagaaactcaacaacacaga 2487
DB 2941 ATCTACATCATCTTCTCAAGCCATCCCGCAACACATCGA 2981

RESULT 5
LOCUS AR028467 3809 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5858684.
ACCESSION AR028467
VERSION AR028467.1 GI:5940440
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3809)
Nemeth,E.F., Brown,E.M., Hebert,S.C., Garrett,J.E. Jr., Van
Wageningen,B.C., Balandrin,M.F. and Del Mar,E.G.

Db 2521 AAGGTGGGGGCTCAACCTGCACTTCTGCTGTTTCTCTGACCTTCATGACAGAT 2580
Oy 2087 ttctctgtctcaagctgagctgcaatgagacccacagccacacagagagtagacagc 2146
Db 2581 GTCACTGTGTGATGCTGCTTACACCGCCGCCCTTCAAGCTACCGCAACAGAGCTG 2640
Oy 2147 ttcccccatctgagatctctgagtgacacagaggttcaactctgtgagctctctgagct 2206
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Oy 2207 ttgcacacacacatctctctctcctacacagaccttctgtcagactacagtgagaa 2266
Db 2701 ATCCGCTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
Oy 2267 ctgcagagac 2326
Db 2761 CTGCGGAGAACTTCATGAGAGCCAGTTGATCACTACCTTCATGCTCATCTTCTGCTG 2820
Oy 2327 tctctgagct 2386
Db 2821 GTCGTGATCTCTCTCATTCACGCGCTATGCGACGCTATGCGAAGTTGCTGCTGCGTA 2880
Oy 2387 aatgtctgagagagctgagcactctgagtgagctgagctgagctgagctgagctgag 2446
Db 2881 GAGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
Oy 2447 tgcctgagct 2487
Db 2941 ATCTACATCATCTCTCTCAAGCCATCCCGCAACACATCGA 2981

RESULT 6
LOCUS 175053 3809 bp DNA PAT 03-APR-1998
DEFINITION Sequence 3 from patent US 5688938.
ACCESSION 175053
VERSION 175053.1 GI:3011194
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3809)
AUTHORS Brown,E.M., Fuller,F.H., Hebert,S.C. and Garrett,J.E. Jr.
TITLE Calcium receptor-active molecules
JOURNAL Patent: US 5688938-A 3 18-NOV-1997;
FEATURES
source 1..3809
BASE COUNT 910 a 1071 c 979 g 849 t
ORIGIN

Query Match 6.4%; Score 166.2; DB: 5; Length 3809;
Best Local Similarity 46.38; Pred. No. 4.9e-27;
Matches 1130; Conservative 0; Mismatches 1143; Indels 168; Gaps 11;

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Oy 266 gagaataaacaactcaacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 325
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Oy 326 gtgtgtcagagcttcccaatgtct--atgcacacctgagagtgccgcagcagcagcagc 379
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Db 730 ATTGATTTCTTGAACCTTGATGAGTTCTGCAACTGCTCAGACACATTCCTCTACGATT 789

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AUTHORS	1 (bases 1 to 3783) Garrett,J.E., Capuano,I.V., Hammerland,L.G., Hung,B.C., Brown,E.M., Hebert,S.C., Nemeth,E.F. and Fuller,F.		
TITLE	Molecular cloning and functional expression of human parathyroid calcium receptor cDNAs		
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AUTHORS	Direct Submission		
TITLE	Submitted (07-FEB-1995) James E. Garrett, Molecular Biology, NPS Pharmaceuticals, Inc., 420 Chippewa Way, Salt Lake City, UT 84108, USA		
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 3234)
 Freichel,M., Zink-Dorenz,A., Holloschl,A., Hafner,M., Flockeziel,V. and Raue,F.
 TITLE Expression of a calcium-sensing receptor in a human medullary thyroid carcinoma cell line and its contribution to calcitonin secretion
 JOURNAL Endocrinology 137 (9), 3842-3848 (1996)
 MEDLINE 96343808
 REMARK GenBank staff at the National Library of Medicine created this entry [NCBI g1dbsg 179653] from the original journal article. This sequence comes from Fig. 6.
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K	E	YWORDS	Calcium-sensing receptor; PCar1 gene.	
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R	E	ERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;	
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J	O	URNAL	Pearce,S.H.S.	
R	E	MARK	Direct Submission	
R	E	REFERENCE	Submitted (16-AUG-1994) S.H.S. Pearce, MRC Molecular Medicine	
R	E	REFERENCE	Group, Collier Bldg, Royal Postgrad Med School, London W12 ONN, UK	
R	E	REFERENCE	revised by [3] MAT	
R	E	REFERENCE	2 (bases 1 to 3234)	

FEATURES	source	location/Qualifiers
AUTHORS	Pearce, S.H.S. and Thakker, R.V.	
JOURNAL	Unpublished	
REFERENCE	3 (bases 1 to 3234)	
AUTHORS	Pearce, S.H.S.	
TITLE	Direct Submission	
JOURNAL	Submitted (05-DEC-1994) S.H.S. Pearce, MRC Molecular Medicine Group, Collier Bldg, Royal Postgrad Med School, London W12 0NN, UK	
COMMENT	On Dec 7, 1994 this sequence version replaced g1.556648.	
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DEFINITION Mus musculus calcium-sensing receptor (CaSR) mRNA, alternatively spliced, complete cds.

ACCESSION AF110179

VERSION AF110179.1 GI:4731164

KEYWORDS

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.

AUTHORS Oda,Y., Tu,C.-L., Mauro,T. and Blikle,D.

TITLE The calcium-sensing receptor and its alternatively-spliced form in murine epidermal differentiation

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 4319)

AUTHORS Oda,Y., Tu,C.-L., Mauro,T. and Blikle,D.

TITLE Direct Submission

JOURNAL Submitted (10-NOV-1998) 190 Dermatology, VA Medical Center - San Francisco, 4150 Clement Street, San Francisco, CA 94121, USA

FEATURES

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ORIGIN

Query Match 6.3%; Score 162; DB 12; Length 4319;

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DEFINITION	Ca(2+)-sensing receptor [cattle, parathyroid gland, mRNA, 5249 nt]				
ACCESSION	S67307				
VERSION	S67307.1	GI:453108			
KEYWORDS					
SOURCE	Bos taurus parathyroid gland.				
ORGANISM	Bos taurus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bos.				
AUTHORS	1 (bases 1 to 5249) Brown, E.M., Gamba, G., Riccardi, D., Lombardi, M., Butters, R., Kitor, O., Sun, A., Hediger, M.A., Lytton, J. and Hebert, S.C.				
TITLE	Cloning and characterization of an extracellular Ca(2+)-sensing receptor from bovine parathyroid				
JOURNAL	Nature 366 (1993), 575-580 (1993)				
MEDLINE	94077182				
REMARK	Genbank staff at the National Library of Medicine created this entry [NCBI g1569 140593] from the original journal article.				
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ORIGIN					
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SOURCE	Unknown.		
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AUTHORS	Nemeth,E.F., Brown,E.M., Hebert,S.C., Garrett,J.E. Jr., Van		
TITLE	Method of screening calcium receptor-active molecules		
	Waghen,B.C., Balandrin,M.F. and Del Mar,E.G.		

Journal	Patent: US 5858684-A 1 12-JAN-1999;	Location/Qualifiers
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VERSION 175051.1
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AUTHORS Brown,E.M., Fuller,F.H., Hebert,S.C. and Garrett,J.E. Jr.
TITLE Calcium receptor-active molecules
JOURNAL Patent: US 5588938-A 1 18-NOV-1997;
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Query Match 6.1%; Score 157.2; DB 5; Length 5275;
Best Local Similarity 46.0%; Pred. No. 4,7e-25;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	143.2	6.1	5275	4	US-08-943-986-1	Sequence 1, Appl1
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6	138.4	5.9	3809	1	US-08-485-588-3	Sequence 3, Appl1
7	138.4	5.9	3809	2	US-08-484-565-3	Sequence 3, Appl1
8	138.4	5.9	3809	3	US-08-480-751-3	Sequence 3, Appl1
9	138.4	5.9	3809	4	US-08-943-986-3	Sequence 3, Appl1
10	138.4	5.9	3809	5	US-08-353-784-3	Sequence 3, Appl1
11	132.6	5.7	5006	1	US-08-485-588-2	Sequence 2, Appl1
12	132.6	5.7	5006	2	US-08-484-565-2	Sequence 2, Appl1
13	132.6	5.7	5006	3	US-08-480-751-2	Sequence 2, Appl1
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26	72	3.1	3919	5	US-08-367-264-5	Sequence 5, Appl1
27	70.8	3.0	2961	4	US-08-407-875-1	Sequence 1, Appl1
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32	55	2.4	3321	2	US-08-485-270-1	Sequence 1, Appl1

33	55	2.4	3219	4	US-08-687-289A-3	Sequence 3, Appl1
34	55	2.4	3219	4	US-08-687-289A-4	Sequence 4, Appl1
35	55	2.4	3321	5	US-08-367-264-1	Sequence 1, Appl1
36	51.6	2.2	4300	1	US-08-041-535-1	Sequence 1, Appl1
37	51.6	2.2	4300	2	US-08-463-642-1	Sequence 1, Appl1
38	51.6	2.2	4300	2	US-08-455-602-1	Sequence 1, Appl1
39	51.6	2.2	4300	2	US-08-465-157-1	Sequence 1, Appl1
40	51.6	2.2	4300	6	PCT-US91-09422-1	Sequence 1, Appl1
41	51.6	2.2	5236	6	PCT-US91-09422-16	Sequence 16, Appl1
42	50.2	2.2	3330	1	US-08-072-574-1	Sequence 1, Appl1
43	46.2	2.0	4085	1	US-08-072-574-7	Sequence 7, Appl1
44	46.2	2.0	4181	1	US-08-072-574-9	Sequence 9, Appl1
45	46.2	2.0	2997	6	PCT-US94-14989-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-485-588-1
Sequence 1, Application US/09485588
Patent No. 5688938
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
NUMBER OF INVENTION: MOLECULES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/005


```
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TEXT: 67-5510
INFORMATION FOR SEQ ID NO.: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5275 base pairs
TYPE: nucleic acid
STANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 515..3769
OTHER INFORMATION:
US-08-485-588-1
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Query Match	6.1%;	Score 143.2;	DB 1;	Length 5275;
Best Local Similarity	47.3%;	Pred. No. 5.5e-28;		
Matches 501: Conservative	0;	Mismatches 553;	Indels 6;	Gaps 2

QY	1233	ctaaacataatgagaccacaacacagatggcaggaagaacacacaggtgtctaagct	1292
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QY	1293	gtgtgtccagcgactgtctctgaaggcaca--cagcgagtgttacyggtttccatcac	1349
Db	2138	AACGCAAGTGCAGACTGCTGGCAGGGAGACAGAAAGAAATGAAATGAGGGAGGCCAAC	2197
QY	1350	tgtctgttttagtgtgtgtgtccctgttggggtctgggaccttctacaagaagcgactctac	1409
Db	2198	TGCGCTTTTGAAGTGTGGAAATCTCTGAAGGGGAGTAAAGGACGAGACATCAATCAAGT	2257
QY	1410	agaatgcagccttgttgaacagagaagtgtagccatggaggaagccagacgcgtgtcccg	1469
Db	2258	GCCGTGATATAGATGACCTGATGACTTCTGTGTCATATGAACACACTTCTGCAATGCC	2317
QY	1470	cgcacttggtgtgttttgtgtcttcgttgaacacacctcttgggtgtgtgtgcaactaac	1529
Db	2318	AAGGAGATCGAGTTTGTGTGTGGACCGAACCTTGTGGGATCGCACTCAAGCTTTTGT	2377
QY	1530	acgctgtctgtctgtctgtctgtgttggaaactgtgcgcttctgtgctgcaactagaacc	1588
Db	2378	GTCGTGGGCAATTTTCCACACAGCCTTGTGCTGGGGGCTTATATCAAGTTCCGCAACAG	2437
QY	1590	ccgtgtgtgaggttcaagaaggggcgcgctgtgtcttctatgtctgggtccctgtgcaga	1649
Db	2438	CCCATGCTCAAGGCCACCAACCGGAGACTCTCTAATCTCTTCTCTTCCCTGCTGTGC	2497
QY	1650	gtagtgtgcagcctctaagtctctcttcttgggaacccacaagaagcgtgtgctgttagc	1709
Db	2498	TGCTTTCAGACGTCCTGTTCTTCAATGGGGAGCCCAAGAGCTGAGACGAGCGCCCTGGGC	2557
QY	1710	caggcctcttgcaccttggtttcaacaactcttcgtctgcctgacagttcgtctcaatc	1768
Db	2558	CAGCGGACCTTTGGACATCACTTCGTGCTCTGATCTCGCATCTCGTATCCTGTGAAAAACAT	2617
QY	1770	caactaatcatcatcacaagtttccacaagaagtaacctaatctacacagccctggctc	1828
Db	2618	CGGGTCTCTCTGTTGTGAG--GCCAAGATTTCCACACAGCTTCCACCGGAGATGGTGG	2674
QY	1830	caaaacacagtgctgagccgtgttgtgatgatcagctcagcgccacgctgttactgt	1889
Db	2675	GGGCTCAACTGCAAGTTCCTGCGTGCTTCTGTGACCTTCAATGAGATTTGATCAATCTGT	2734
QY	1890	ctaacttggcttgggtgtgtgtggaaccacagtctgtctaggaatcacagcgcttccocat	1949
Db	2735	GCAATTTGGCTCAATACAGCGCCCTCGAGCTACCCGACACACAGAGCTGGAGAGACAG	2794
QY	1950	ctgtgtgtgtctgtgagtgcaagagacaacatccctgtgtgtctatactgtcctctctac	2009
Db	2795	ATCATCTTCATCACTTCGACAGAGGGCTGCTCATATGGCCCTGGGCTTCTGTATGGCTAC	2854

QY	2010	aatggcctccctccatcaagtcgctttgctgcgcagctaaccttgcgaaggaagacttccaaag	2069
Db	2855	ACCGCTGTGTGGCCGCCCATCTGCTTCTTCTTGCGCTTCAAGTCCCGGAAGCTGCGAAG	2914
QY	2070	aactacaacgaaggccaatgctacccctcaagccgcgtctcttaacttgcgtgctcbyagtc	2129
Db	2915	AACCTTCATTAACCCAAAGTTCATACACTTCACACATGCTCATCTTCTTCATGCTGGATC	2974
QY	2130	gcctctctccacacagccagcgtctccagccagccagctacccgtccgcgcgcacacatgag	2189
Db	2975	TCTTTATCCCGCCCTACGCCAGCAATTACGCCAAGTTGTCGTGCGCTGAGAGTATC	3034
QY	2190	gctggcgctgaagcagccttgaagcagcgcgctcgatcttctgcctaaagtgcgaagtg	2249
Db	3035	GCCATCTGTGGCGGCCAGCTTTGGCTGTGCTGGGCTGATCTTCTTTCACAAAGCTTACATC	3094
QY	2250	atactctgcgcgcagagcttcaacacagacagagcacttc	2289
Db	3095	ATCCTCTTCAAGCCTTCCCGGAACACATCGAGAGAGTCC	3134

RESULT 2
 US-08-484-565-1
 : Sequence 1, Application US/08484565
 : Patent No. 5763569
 :
 : GENERAL INFORMATION:
 : APPLICANT: Edward M. Brown
 : APPLICANT: Steven C. Hebert
 : APPLICANT: James E. Garrett, Jr.
 : TITLE OF INVENTION: CALCULUS RECEPTOR-ACTIVE
 : TITLE OF INVENTION: MOLECULES
 : NUMBER OF SEQUENCES: 20
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Lyon & Lyon
 : STREET: First Interstate World Center
 : STREET: Suite 4700
 : STREET: 633 West Fifth Street
 : CITY: Los Angeles
 : STATE: California
 : COUNTRY: USA
 : Zip: 90071
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PASTSRO
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/484,565
 : FILING DATE: 7 June, 1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA: Including application
 : PRIOR APPLICATION DATA: described below: 9
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/353,784
 : FILING DATE: 9 December, 1994
 : APPLICATION NUMBER: PCT/US/94/12117
 : FILING DATE: 21 October, 1994
 : APPLICATION NUMBER: U.S. 08/292,827
 : FILING DATE: 23 August, 1994
 : APPLICATION NUMBER: U.S. 08/141,248
 : FILING DATE: 22 October, 1993
 : APPLICATION NUMBER: U.S. 08/009,389
 : FILING DATE: 23 February, 1993
 : APPLICATION NUMBER: U.S. 08/017,127
 : FILING DATE: 12 February, 1993
 : APPLICATION NUMBER: U.S. 07/934,161
 : FILING DATE: 21 August, 1992
 : APPLICATION NUMBER: U.S. 07/834,044
 : FILING DATE: 11 February, 1992
 : APPLICATION NUMBER: U.S. 07/749,451
 : FILING DATE: 23 August, 1991
 : ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 515..3769
OTHER INFORMATION:
US-08-480-751-1

Query Match 6.1%; Score 143.2; DB 3; Length 5275;
Best Local Similarity 47.3%; Pred. No. 5.5e-28;
Matches 501; Conservative 0; Mismatches 553; Indels 6; Gaps 2;

QY 1233 ctaacataatgagacaaatccagtgacaggaagaaaccaccaggtgcttaagtct 1292
DB 2078 CTCTTCATCATGATGATAAAATCTGTGGAGTGTCTCAAGGAGGTGCTTCTCC 2137
QY 1293 gtgtgtccagcagctgtcttgaaggagac--cagcagtggttacgggttccatcac 1349
DB 2138 AACGCAAGTCAGAGCTGCTGCTGAGGAGCAGGAAAGAAATCATTTAGGGGAGCCACC 2197
QY 1350 tgcgtcttgagtggtgtccctgtgaggtctggaacctctctcaacaagagagctctac 1409
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QY 1470 cgcactgtgtgttttggcttgcgtgagacacaccttctgtgtcgtgcagctaac 1529
DB 2318 AAGGAGATCGAGTTCTGTCTGTGACGAGCCCTTCGGGATCGCACTCAGCTTTTGT 2377
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DB 2378 GTGCTGGGCAATTTCTCTACAGCCTTGCTGTGGCGCTCTTCATCAAGTTCCGACACG 2437
QY 1590 ccgtgtgtgagtgacagagggggcgccgtgtgtcttctttagtgcgggctccctgcagca 1649
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DB 2618 CGGCTCTCTCGGTTGTGAG--GCCAAGATTTCCCAACAGCTTCCACCGGAAGTGGTG 2674
QY 1830 caaacaacaggtgtgcgccttctgtgtagatcagctcagggccagcagctcatatgt 1889
DB 2675 GGGCTCAACCTGCAAGTTCTGCTGTCTCTCTCTGACCTTCATGACGATTTGATCTGT 2734

QY 1890 ctaactgtgtgtgtgtgtgagacccactgctcgttaggaaataccagcgcttccccc 1949
DB 2735 GCATTTGGCTCAATATAGGCGCCCTCGAGCTACCGCAACAGAGCTGAGAGAGAG 2794
QY 1950 ctggtgactgtcctgagtgacagagaccactccctgggtctcatctgctctctac 2009
DB 2795 ATCATCTTCATCACCTCCGAGGAGGCTCCCTCATGCGGTGGGCTTCCATGAGTGGCTAC 2854
QY 2010 aatggcctctctccatcaatgctgtcctgtgcctgagctgtgtaaggctggcaag 2069
DB 2855 ACCTGCTTGGCGGCGCATCTGCTTCTTCTGCTTCAAGTCCGGAAGCTGCCAGAG 2914
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QY 2190 gctgggtgagcagcagcctgagcagcagcctgctggtgtattctgtcctaagtctag 2249
DB 3035 GCCATCTTGGCGGCGCATCTTGGCTTGTGCTGCTGCTGATCTTCTTCAACAAAGTCTACATC 3094
QY 2250 atcctctgcccgcagacctcaacacagcacagcagcttcc 2289
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RESULT 4

US-08-943-986-1
Sequence 1, Application US/08943986
Patent No. 5962314
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCULUM RECEPTOR-ACTIVE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
City: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,986
FILING DATE: 03-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127

APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 209/069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 515..3769
OTHER INFORMATION:
US-08-353-784-1

Query Match 6.1%; Score 143.2; DB 5; Length 5275;
Best Local Similarity 47.3%; Pred. No. 5,5e-28;
Matches 501; Conservative 0; Mismatches 553; Indels 6; Gaps 2;

QY 1233 ctaaacataatgagaccacaaatccagtcgagcgaagaacacccagtgctcaagtc 1292
DB 2078 CTCTTCATCATGATGATAAATAATCTGTGAGTGTCAAGGAGAGGCTTCTCC 2137
QY 1293 gtgtgtccagcagctgtcttgaaaggcac---cagcagtggttaagtggttcatac 1349
DB 2138 AACTGAGTCGAGCTCTGCGGAGGAGCAGGAAGAAATCATTTAGGGGAGCCACC 2197
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QY 1950 ctgtgtatgt 2009
DB 2795 ATCATCTTCATCACCTGCGCACAGGCGCTGCTCATGCGCTGGCTTCCGATGCGCTAC 2854
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DB 2855 ACCTGCTGTGCGCGCCATCTCTCTTCTGCTTCAAGTCCGGAAGCTGCCAGAG 2914
QY 2070 aactacaagcagcacaatgt 2129
DB 2915 AACTTCATTAACCAAGTTCATCAGCTTCAAGTCTCATCTTCTTCATCGTGTGATC 2974
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QY 2190 gctgt 2249
DB 3035 GCATCTCTGCGGCGCAGCTTGT 3094
QY 2250 atcctctgcccagcagcctcaacagcagcagcagcagcagcagcagcagcagcagcagcagc 2289
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RESULT 6
US-08-485-588-3
Sequence 3, Application US/08485588
Patent No. 5688938
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 373..3606
OTHER INFORMATION:
US-08-485-568-3

Query Match 5.9%; Score 138.4; DB 1; Length 3809;
Best Local Similarity 47.0%; Pred. No. 8.4e-27;
Matches 498; Conservative 0; Mismatches 556; Indels 6; Gaps 2;

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DB 1933 CTCTTATCAACAGAGAGAAATCCTGTGAGTGGTTCTCCAGGAGAGTGCCTTCTCC 1992
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QY 1410 agaagccagccttctggaacagaagatgagcactgagggaggaaccagcctgtcccg 1469
DB 2113 GCCTGTAAACAAGTGCACAGATGCTTGTGTCATGAGAACACACACCTCTGCAATGCC 2172
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DB 2173 AAGGAGATCGAGTCTTGTGTGAGACGACCTTTGGAGTGCACCTCCTTTTGGC 2232
QY 1530 acgcagcagcgtgctgctgtgtgtgagactgctgtgtgtgtgtgtgtgtgtgtgtgtgt 1589
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DB 2293 CCCATTGTCAAGGCGACCAACGAGAGCTCTCTACTCTCTCTCTCTCTCTCTCTCTCT 2352
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DB 2413 CAGCGCGCCTTTGGCATGAGCTGTGCTGTGCATCTCAATGCATCTCTGTGAACCAAC 2472
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DB 2473 CGTGCTCTCTGTGTGTGTGAGG--CCAAAGATCCCGACACCTTCCACCGGAGGTGG 2529
QY 1830 caaacacacgt 1889
DB 2530 GGGCTCAACCTGCAATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2589
QY 1890 ctaactgt 1949
DB 2590 GTGATCTGTGCTGTACACCGCGCGCCCTCAAGCTAACCCAGACCTGGAGATGAG 2649
QY 1950 ctgt 2009
DB 2650 ATCATCTTCAATCACGCTGCACAGAGGGCTCCCTCAAGGCGCTGTGGCTTCTGTATG 2709
QY 2010 aatgscctccctccatcagtgsccttgcctgtgagcgtacccgtgtgtgtgtgtgtgtgt 2069
DB 2710 ACCTGCTGT 2769
QY 2070 aactaacagagggccaaatgtgtacacctcagcctgtgtgtgtgtgtgtgtgtgtgtgtgt 2129
DB 2770 AACTCATATGAAGCCAAATGTATCATACCTTCAAGCATGCTCATCTTCTGTGTGTGTGT 2829
QY 2130 gctctcttcaacacagcgccagcgtctctgagcggcaagatctgtgtgtgtgtgtgtgt 2189
DB 2830 TCTTTCATTTCCAGCTTATGACGACCTATGACACCTATGCAAGTTTGTCTGTGCGGTG 2889
QY 2190 gctgt 2249
DB 2890 GCCATCTTGGACCGCAGCTTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2299
QY 2250 atcccttgc 2289
DB 2950 ATTCTTCAAGGCATTCGCCGACACATCGAGGAGTGTC 2989

RESULT 7
US-08-484-565-3
Sequence 3, Application US/08484565
Patent No. 5763569
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,565
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: Including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784


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CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 373..3605
OTHER INFORMATION:
US-08-480-751-3

Query Match 5.9%; Score 138.4; DB 3; Length 3809;
Best Local Similarity 47.0%; Pred. No. 8.4e-27;
Matches 498; Conservative 0; Mismatches 556; Indels 6; Gaps 2

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[illegible]


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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943.986
FILING DATE: 03-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 373..3606
OTHER INFORMATION:
US-08-943-986-3

Query Match          5.98; Score 138.4; DB 4; Length 3809;
Best Local Similarity 47.08; Pred. No. 8.4e-27;
Matches 498; Conservative 0; Mismatches 556; Indels 6; Gaps 2;

QY 1233 ctaacataatgagacaaatccagtcgacggaagaacacccagctgctgaagctc 1292
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DB 1933 CTCTTATCAACGAGGAAATCTTGAGTGGTTCTCCAGGAGGCTCTTCTCC 1992
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1293 gtagtccagcagctgcttgaaggcaccagcgag---tggttaagggtttccatcac 1349
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1993 AACTGCAGCCGAGACTCTGCGACGGGACCAAGAAAGGATCATGAGGGGAGCCACC 2052
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1350 tggctgttgaagtggtgcccctggtgggctgggaaccttccaaagaagcagagcttac 1409
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2053 TGCTGCTTGAAGTGTGGAGTGCTCGATGGGAGATAGTGTGAGAGAGATGCCAGT 2112
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QY 1410 agatgcagccttgtagaagaagtgaggcaccctgagggaagcagagactgctccg 1469
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DB 2113 GCCTGTAAACAAGTCCAGATGACTTGTGTCATATAGAACACACACTCTCTGCAATGCC 2172
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QY 1470 cgcactgtgtgttttggtcttcgtagacacacaccttgggtgctgctggcagctaac 1529
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DB 2173 AAGGAGATCGAGTTTGTGTGGACGAGGCCCTTGGGATCGCACTCACCCCTTTGCC 2232
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QY 1530 acgctgctgctgctgctgctgctgagcagcagcagcagcagcagcagcagcagcagc 1589
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DB 2233 GTGCTGGGCAATTTCTGACAGCCTTTGTGCTGGGTGTATTATCAAGTCCGCAACACA 2292
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QY 1590 ccgtgtgtgaggtcaggaaggcgccgctgtgttcttatgtgtggtccctggcagca 1649
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DB 2293 CCCTATTCAAGGCGACCAACCGAGAGCTCTCTACTCTCTCTCTCTCTCTCTCTCTCTGC 2352
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QY 1650 gtagtggcagcctctatggctcttcttgggaaacccaagagcctgctgttctgaagc 1709
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DB 2353 TGCTTCCAGCTCCCTGCTTCTCATCGGGAGCCCGACGACGAGAGCTGCCCTGCGCG 2412
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QY 1710 caggccctcttgcccttggtttcaacatcttcctgctgctgagagtgctcatc 1769
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DB 2413 CAGCGGCTTTGGACATCACCTTCGTGCTGATCTCATCTCTGTGGAAACCAAC 2472
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QY 1770 caactaatcatctctcaagtttccaccaggtaccctcatcttaccagcgtgtgtc 1829
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DB 2473 CGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2529
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QY 1830 caaaccagcgtgtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1889
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DB 2530 GGGCTCAACCTGAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2589
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QY 1890 ctactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1949
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DB 2590 GTGATCTGGCTTACACCGCGCCCTCAAGCTACCGCAACCGAGAGCTGAGATGAG 2649
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QY 1950 ctgtgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2009
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DB 2650 ATATCTTATCACTGACGTGACGAGGAGGCTCCCTATGAGCCTGTGGGCTTCTGATGGCTAC 2709
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QY 2010 aatggcctcctctcatcagtcagtccttgcctgagctagctgtgtgtgtgtgtgtgtgt 2069
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DB 2710 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2769
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QY 2070 aactaaagagggccaatgtgtcaccctcagcctcctcctcctcctcctcctcctcctc 2129
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DB 2770 AACTTCATTAAGCAAGTTCATCCTTCACTGATCTCTCTCTCTCTCTCTCTCTCTCTCT 2829
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QY 2130 gctctcttaccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2189
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DB 2830 TCCTTATTTACAGCTATATGCAACACTATATGCAATTTGTCTCTGCTAGAGGTGATT 2889
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QY 2190 gctgagcctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2249
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DB 2890 GCCATCTGACAGCAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2949
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QY 2250 atcctctgcccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2289
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2950 ATTCTCTTCAAGCAATCCGCAACACCATCGAGAGGTGC 2989
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RESULT 10
US-08-953-784-3
; Sequence 3, Application US/08353784
; Patent No. 6011068
; GENERAL INFORMATION:
; APPLICANT: Edward F. Nemeth, Edward M.
; APPLICANT: Brown, Steven C. Hebert,
; APPLICANT: Bradford C. Van Wagenen, Mannel
; APPLICANT: F. Baladrin, Forrest H. Fuller,
; APPLICANT: Eric G. DelMar, and Scott T. Moe
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
```


COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Hebert, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5006 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 436..3699
OTHER INFORMATION:
US-08-485-588-2

Query Match 5.7%; Score 132.6; DB 1; Length 5006;
Best Local Similarity 50.4%; Pred. No. 3.1e-25;
Matches 414; Conservative 0; Mismatches 389; Indels 18; Gaps 3;

QY 10 agctcaatgagcgtctaccacctctccagcgtatgagcgtgagtgaggagata 69
DB 619 AGGTATATATTTCCGTGGTTCGTTGCTGATGAGGCTATGATATTGATCCATGAGAGAGATA 678
QY 70 aacaactccagcgccgtcgtcccaaatcacacctggggtaccagcgtatgagtgt 129
DB 679 AACGACGACCCAGCCCTTCTTCCCACTTGACGCTGGGATACAGGATATTGACACTTGC 738
QY 130 tctgactctgcacatg---tgatgcacgctgagagtgctctccc-----tgcca 177
DB 739 AACACCTTTCTAAGGCTTGGAAGCCACCTGAGTTTGTGCTCAAAACAAATGAT 788
QY 178 ggggaacacacacataagctcccaaggagacctctcacatctcccttaaggtgctgca 237
DB 799 TCTTGAACCTTGATGAGTTCTGCAACTGCTCAGAGACATTCCTCTACGATTGCTGTG 858

QY 238 gtgatggccttacagcaaccacgctgtccaccacagccgctgctgagcccttc 297
DB 859 GTGGAGCAACTGGCTCAGGCCCTCTCCACGGCAGTGGAATGCTGTGGGCTCTTCTAC 918
QY 298 ctgtgcatatagctatgagcagcagcagcagcagcagcagcagcagcagcagc 357
DB 919 ATTCCAGAGTCAAGTATGCTCTCCAGAGACTCTCAGCAACGAATCAATCAAG 978
QY 358 tcttctctgacacatcccaatgacatgacagtgagagacatgctgctgctg 417
DB 979 TCTTCTCCGAAACATCCCAATGATGAGCAGCAGCCACTGCGATGCGACATCATC 1038
QY 418 caaagtcggtgagcctgacatctctggttgagcagcagtcagcagcagcagcagc 477
DB 1039 GATATTTCCGCTGGAACTGAGTGGGACACATTCAGCTGATACACATATGGCGCGG 1098
QY 478 ggggtgcagcactgtagaagcagcctggtcagggagcagcagcagcagcagc 537
DB 1099 GGGATTGAGAAATTCGAGAGGAACTGAGAAAGGATATCTGATCGACTCACTGAA 1158
QY 538 atatgcccctctctgcccagctggtgagatgagagatgagcctatgagccac 597
DB 1159 CTGATCTCCAGTACTGTGATGAGAAAG---GATCAGCATGTGTAGAGTGATT 1212
QY 598 gcccaagccgagccacgctggtgtgttttccagccgagctgagcagcagctgt 657
DB 1213 CAATAATTCACGGCCCAAGATCATGCTGTTTCTCCAGTGGCCCAATCTTGAGCCCTC 1272
QY 658 ttgagtcgctggtgtgacacacactgactggaaggtgtggtgctcagaagcctg 717
DB 1273 ATCAGAGAGATTGTCCGGGCAATATCACGGGCAAGATCTGGCTGCCAGCGAGCTGG 1332
QY 718 gccctctcagcagacatcactggtggtggtggtggtggtggtggtggtggtg 777
DB 1333 GCCAGCTCTCCTGATTCGCATGCTCTCACTGATCTTCAAGTGTGGTGGCGACCAATTGA 1392
QY 778 gtggccatccagaagagagctgtccctgagcctgaagcgt 818
DB 1393 TTGCTGTGAGGCTGGCAGATCCAGGCTTCCGGGATTT 1433

RESULT 12
US-08-484-565-2
Sequence 2, Application US/08484565
Patent No. 5763569
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,565
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below: 9

APPLICATION NUMBER: 08/353,784

FILING DATE: 9 December, 1994

APPLICATION NUMBER: PCT/US/94/12117

FILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 23 August, 1994

APPLICATION NUMBER: U.S. 08/141,248

FILING DATE: 22 October, 1993

APPLICATION NUMBER: U.S. 08/009,389

FILING DATE: 23 February, 1993

APPLICATION NUMBER: U.S. 08/017,127

FILING DATE: 12 February, 1993

APPLICATION NUMBER: U.S. 07/934,161

FILING DATE: 21 August, 1992

APPLICATION NUMBER: U.S. 07/934,044

FILING DATE: 11 February, 1992

APPLICATION NUMBER: U.S. 07/749,451

FILING DATE: 23 August, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Heber, Sheldon O.

REGISTRATION NUMBER: 38,179

REFERENCE/DOCKET NUMBER: 213/006

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ. ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 5006 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

FEATURE:

NAME/KEY: CDS

LOCATION: 436..3699

OTHER INFORMATION:

US-08-484-565-2

Query Match 5.7% Score 132.6; DB 2; Length 5006;

Best Local Similarity 50.4%; Pred. No. 3,1e-25;

Matches 414; Conservative 0; Mismatches 389; Indels 18; Gaps 3;

QY 10 agctcaatgagctggtacacaccccttccagcgtatgagcgttgaggaagata 69

DB 619 AGGTATATTCCTGGGTTCCGTGTACAGGCTATGATATTGCCATAGAGAGATA 678

QY 70 aacaaccacagccgctgctgacacacacccctgsggtacacagctgatgagtgat 129

DB 679 AACAGCAGCCGCTCTTCTTCCCACTTGACGCTGGGATACAGATATTGACACTTGC 738

QY 130 tctgactctgccaatg---tgatgccaagcttgagagtgctctccc-----tgcca 177

DB 739 AACACCGTTTGAAGCCTTGGAAGCCACCTGAGTTTGTGTGCAAAACAAATTGAT 798

QY 178 gggcaacaacacatagagctccaagagagccttctccactatcccttaagtgctgcca 237

DB 799 TCTTTGAACCTTGATGAGTTCTGCACTGCTCAGAGCACTTCCCTTACATGCTGTG 858

QY 238 gtgattgagctgacagcacaaccgctgctgcaacacagcgcgcctctgagcccttc 297

DB 859 GTGGAGCACTGGCTCAGGGGCTCTCCACGCGCAGTGGCAATTCGTGGGCTCTTCTAC 918

QY 298 ctggtgataatactgctgagcagcagcagcagcagcagcagcagcagcagcagcagc 357

DB 919 ATTCCCGAGTGATGCTCTCCCTCCAGACAGCTCAGCAACAACAATCAATTCAG 978

QY 358 tcttctctgagcaccatcccaagcaagcagcagcagcagcagcagcagcagcagcagc 417

DB 979 TCTTCTCCGACCACTCCCAATGATGAGCAGCAGGCGCACTGCCATGCGAGACATCATC 1038

QY 418 cagaagctgagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 477

DB 1039 GAGTATTTCGCTGGAAGTGGGTGGCACAATTCAGCTATGACGACTATGGGCGCG 1098

QY 478 ggggtcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 537

DB 1099 GGGATTGAGAAATTCGAGAGGAGAGTGAAGGAGATCTCATTCAGACTTCAAGTAA 1158

QY 538 atcagcctctctctgcccagcagcagcagcagcagcagcagcagcagcagcagcagc 597

DB 1159 CTCATCTCCAGTACTGTGATGAGAGAGA-----GATCCAGCATGTGTGAGAGTAT 1212

QY 598 gccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 657

DB 1213 CAATATTCAGCGCCCAAGTATGATGTTTCTCCAGTGCGCCAGATCTGAGCCCTC 1272

QY 658 ttcgagctcgtgctgac 717

DB 1273 ATCAAGAGATTTGCCGCGCATATCACGGGCAAGATCTGGCTGGCCAGCGAGCCTGG 1332

QY 718 gccctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 777

DB 1333 GCCAGCTCTCTCCATGATCGCATGCTCTCAGTACTTCCACGTGTGTTGGCGGCACTTGA 1392

QY 778 gtggcaccagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 818

DB 1393 TTCGCTGTGAAGGCTGGGCAATCCAGGCTTCGGGGAATT 1433

RESULT 13

US-08-480-751-2

Sequence 2, Application US/08480751

Patent No. 5858684

GENERAL INFORMATION:

APPLICANT: Edward F. Nemeth

APPLICANT: Edward M. Brown

APPLICANT: Steven C. Hebert

APPLICANT: Forrest H. Fuller

APPLICANT: James E. Garrett, Jr.

TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE

NUMBER OF INVENTION: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: First Interstate World Center

STREET: Suite 4700

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PASTSEO

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,751

FILING DATE: 7 June, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: described below: 9

APPLICATION NUMBER: 08/353,784

FILING DATE: 9 December, 1994

APPLICATION NUMBER: PCT/US/94/12117

FILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 23 August, 1994

APPLICATION NUMBER: U.S. 08/141,248

FILING DATE: 22 October, 1993

APPLICATION NUMBER: U.S. 08/009,389

[illegible]

ET US-763568-A. /product- "BOPAR 1 5kb fragment"
 FN 09-JUN-1998.
 PD 07-JUN-1995; 484565.
 PF 07-JUN-1995; US-484565.
 PR 23-AUG-1991; US-749451.
 PR 11-FEB-1992; US-834044.
 PR 21-AUG-1992; US-934161.
 PR 12-FEB-1993; US-017127.
 PR 23-FEB-1993; US-009389.
 PR 22-OCT-1993; US-141248.
 PR 19-AUG-1994; US-292827.
 PR 21-OCT-1994; WO-012117.
 PR 08-DEC-1994; US-353784.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PA (NPSP-) NPS PHARM INC.
 PI Brown EM, Garrett JE, Hebert SC;
 DR WPI: 98-347412/30.
 P-PSDB: W54844.
 PT Calcium receptor poly:peptide(s) - useful for drug screening or
 PT antibody production
 PS Example 25; Fig 47; 174pp; English.
 CC The bovine parathyroid calcium receptor gene encodes a 1085 amino acid
 CC protein. The tissue from which this receptor and receptors from human
 CC parathyroid and rat kidney are derived, respond to changes, and control
 CC changes, in calcium ion concentration, e.g. parathyroid hormone regulates
 CC Ca2+ homeostasis in blood and extracellular fluid, and kidney function
 CC alters through changes in Ca2+ levels in juxtaglomerular and proximal
 CC tubule cells in the kidney. The purified receptors (produced
 CC recombinantly) can be used to screen for compounds that modulate calcium
 CC receptor activity, especially those that can be used to treat diseases
 CC associated with the receptors in these tissues. They can also be used
 CC to raise antibodies for use in detection assays.
 SQ Sequence 5275 BP; 1277 A; 1475 C; 1316 G; 1207 T;

Query Match	6.1%	Score 143.2	DB 1	Length 5275
Best Local Similarity	47.3%	Prod. No. 2.6e-26		
Matches 501	Conservative 0	Mismatches 555	Indels 6	Gaps 2
QY 1233	ctaacaataatgaagaccnaaatccagatgagcagcggnaaagaaccaccaggtgcttaagtct	1292		
DB 2078	ctcttcattcatatgatgaaagaaaaattttgttgatgatgatatttctcaaggagagtgctttttctcc	2137		
QY 1233	gtgtgttccagcgacgactgtcttgaagggagac---cagcgagtgtttacaggtttccatcac	1349		
DB 2138	aaactcagacgacgactgctgctgcagaggaacagaaagagaaatcatgttagggggagagccacac	2197		
QY 1350	tgctgcttttagtgtgtgtccctctgtgggctcttgagaccttcctcaacaagaagagctctcac	1409		
DB 2198	tgtctcttttgatgtgttggaatgtcttcttagggagagtacagagacagacacaaatgcamaot	2257		
QY 1410	agatccagcccttgygnaacagaagaagtgygnaacttgygnaagcagaagccgtctcccg	1469		
DB 2258	gcccttgatgaatgacctgcatgacaccttctgtgttcaattgaagaaacacacatttctgcacatggcc	2317		
QY 1470	cgcactgtgtgtgtttttgtgcttgcgttgagcacacacctctgtgtgtcgtgagactaac	1529		
DB 2318	aaggaagatcgaatttctctctcgtcagacacagcccttccggatgtgacactacgctcttttgt	2377		
QY 1530	acgctgtgctgtcgtcgtcgtcttggagactgtgcgtctgttttgccttgcagactagacacc	1589		
DB 2378	gngctggggcatttttctctacacaccttgcngctggcgcttctcatcagaatttccgacaacacg	2437		
QY 1590	cctgtgtgtgaggttcagcagagggggcccgcctgtgtctttcttatgtcgtggctcctctgcagaca	1649		
DB 2438	cccatcgtcacaagggccacacacacggagagcttccatcttcttcttcccttccctgccttccg	2497		
QY 1650	ggtatggcagcgtctatagctcttcttgggnaaccacaagagcccggtgtctgtctacgc	1709		
DB 2498	tgtcttctccagcttccctgttttcatcagggggagcccccagagactggaagtgccgctggccg	2557		
QY 1710	cagggcccttctgaccttgcattcacacatctctcctgtcctgtcctacaaattcgtcatc	1769		

OY	1830	caaaaccccgctgctggcgccttcttgtagtaagctcaaggcgccagcgtatattgt	1869
Db	2675	GGGCTCAACCGTCAGACTTCTCTGTGTCTCTCTCTGCACATTTCAAGATTGATGT	2734
OY	1890	ctaacttgcgtgtygtgtgtgaccaccaactgccttcaggaatacacagcgtcccccac	1949
Db	2735	GCCATTGTGGCTCAATACAGCGCCCCCTTGAGCTAACGCCAACCAGAGCTGAGGACGAG	2794
OY	1950	ctgtgtgatgcttgtagtgcacagagaacaacctcccttggtcctaacatgcgtcccttac	2009
Db	2795	ATCATCTTCAATCACCTGGCCACGAGAGGCTCGCTCATGGCGGGCTTCGTATCGGCTAC	2854
OY	2010	aatggccccctcccatcagtcagtcctttgcctgaagctaacctcgggtaaagactgccag	2069
Db	2855	ACGTCCTTGCTGCGCGGCATCTGCTCTCTTCTTGCGCTTCAAGTCCCGGAAGCTCCAGAG	2914
OY	2070	aactacaacagagccaatatgtgtcaaccttcagcctgcctcttcaacttcgtgtccctgatac	2129
Db	2915	AACCTTCATTAAGAAGCAATGTTATCATCCTTTCAGATGCTCATCTTTCATCAGTCTGATC	2974
OY	2130	gcctcttcaccaaagcgccagcgtcttaagacggcaagraactcgtcctcggccacaatgatg	2189
Db	2975	TCTTTCAATCCCCTGCTACGCGAGCACTTACGGAATGCTGCTTGGCGTGGAGGTGATC	3034
OY	2190	gctgggcgtgaagacgcttgagcagcgcctcgtgtgttatcttcgtcagatagtaagtgtg	2249
Db	3035	GCCATCCCTGGGGGCGGACGTTTGCGTCTGCTGGCCGTATCTTTCATCAACAAGTCTACATC	3094
OY	2250	atcccttcgcgcgccacagacctcaacagacagagactctcc	2269
Db	3095	ATCCCTTTCAGACCTTCCCGGAAACACCATCCAGAGAGGTGC	3134
RESULT	4		
ID	T61382	standard; cDNA to mRNA; 3809 BP.	
AC	T61382;		
DT	22-APR-1997	(first entry)	
DE	Parathyroid calcium receptor coding sequence clone pNucPAR.0.		
KW	Calcium receptor; human parathyroid gland adenoma tumour; pNOCARL;		
KW	primary hyperparathyroidism; Xenopus oocyte; alternative splicing;		
KW	calcium-activated chloride current; agonist; NPS R-467; NPS R-568;		
KW	variant; untranslated region; alternative polyadenylation; probe;		
KW	alternative transcription initiation; pNucPAR.2; pNucPAR.0;		
OS	human Car gene; isoform; ss.		
PN	Homo sapiens.		
FT	Key	Location/Qualifiers	
FT	cds	373..3609	
FT	/product=	Calcium receptor	
FT	/note=	"Pages 94-95 are missing from the specification,	
FT		sequence information was obtained from the Epo"	
DR	WO9612697-A2.		
PD	02-MAY-1996.		
PE	23-OCT-1995; U13704.		
PR	21-OCT-1994; WO-U12117.		
PR	08-DEC-1994; PR-353784.		
PA	(NPSP-) NPS PHARM INC.		
P1	Balandrin MF, Delmar EG, Moe ST, Nemeth EF, Van Wagenen BC;		
DR	WPI; 96-230520/23.		
P1	p-PDSB; W11889.		
PT	New di:arylalkyl amine cpds. useful for modulating inorganic ion		
PT	receptor activities - esp. for modulating effect of extracellular		
PT	calcium on cell surface calcium receptors, useful for treating e.g.		
PT	hyperparathyroidism, Paget's disease or osteoporosis		
PS	Example 1; Page 93-100; 231pt. English.		
CC	The sequences given in T61381-82 encode functional calcium receptors.		
CC	These sequences were isolated from human parathyroid gland adenoma		
CC	tumour using pNOCARL as a hybridisation probe. mRNA was isolated from		
CC	a 39 year old caucasian male diagnosed with primary hyperparathyroidism		
CC	and two clones of approx. 5 and 4 kb were identified. These cDNA's were		
CC	infected into Xenopus oocytes which were assayed for the presence of		

Query Match	5.9%	Score 138.4	DB 1:	Length 3809
Best Local Similarity	47.0%	Pred. No. 3,6e-25		
Matches 498	Conservative 0	Mismatches 556	Indels 6	Gaps 2
OY 1233	ctaacataaagagaccaaatccagctgacggaagaacaccaggtgctcaagtct	1292		
DB 1933	ctcttcatcacaagagagaaaaatcctgttgagattgggttccaggagagtgcccttctcc	1992		
OY 1293	gtgtgtccagcgacgtcttctgaaggacacgagag---tggtacgggtttccatcac	1349		
DB 1993	aaactcacccgacgagatgctctggcagagacaaagaaaagcatttgaaggagccacac	2052		
OY 1350	tgctgctttgagtggtgtccctggtggcgcttgagaccttctcaacaaggcgagctctac	1409		
DB 2053	tgcctctttgagatgtgtgagagtgctctgattgggagatagatgacagatggcagct	2112		
OY 1410	agatgcagacctgtgagacaagaagatgagacctgaaggagaaagcagacgtcttcccg	1469		
DB 2113	gcctttacacagatgccacagatgacttctgtgctcattgaaacacacacctcttcgattggc	2172		
OY 1470	cgcactgtgtgttttttggtcttgcgtgagacacacctcttggtgctgtctggcagctaac	1529		
DB 2173	aaggaatgcagatttctgtgcgtgagacgagcccttggagatgcactacacctctttggcc	2232		
OY 1530	acgtgcgcgtcgtcgtcgtcgtcttgagacctgctgtgcgtgttgcctggcagacctagaacac	1589		
DB 2233	gttgctgggacatttttcttgacacgctttgtgtgctgggtgttttatcaagtccgacaaaca	2292		
OY 1590	ccgtgtgtgaggtcagcagagggcgccgtcgtgtcttcttatctgtagcccttgagcagca	1649		
DB 2293	cccatgtgtcagagccacacacacagagacgtctcttaccttctctcttcttccctgtcgtgc	2352		
OY 1650	ggtagtgagcagcctatagcttcttggggaacccacaaaggcgtcgtgtgtgtctagcag	1709		
DB 2353	tgcttcttcacagctccctgttcttcatcggggagccccaagactggacgctggcgccgtgcgc	2412		
OY 1710	cagcgcctcttgcacctggtttcaacacatctcctgcgtcctgcctgaagttgcgtatc	1769		
DB 2413	cagccggccttttgagcatcagcttctgtcttctcatctcatctgcattcgtgtgaaacacac	2472		
OY 1770	caacatcatcatcttaagttttccacacaaagtaacctaaactctacacagccttggc	1829		
DB 2473	cgtgtcttctcgtgtgttttgagc---ccaagatcccccacacagctttccacgcgaagtgtgc	2529		
OY 1830	caaaacacagtggtcgtgcgtgtgtgtatgatcagactcagcgccagcgtgtctatctgt	1889		
DB 2530	ggcgtcacaacgtgcatttctcgtgtgtgttttcttctgcaccttcatgacagattgtcactgt	2589		
OY 1890	ctaactgtcgtgtgtgtgtgtgagcccaactgcctgcttagggaaatacagcgcttcccac	1949		

[illegible]

Query Match	5.9%	Score 138.4	DB 1	Length 3809
Best Local Similarity	47.0%	Prod. No. 3.6e-25		
Matches 498	Conservative 0	Mismatches 556	Indels 6	Gaps 2
QY 1233	caaacataaataagaaacccaataatccagctcagtcacggaagaaccaccagctcgaagctc	1292		
Db 1933	ctcttcatcaccagagagaaaatctctgtgagatgggctctccaggagagtgcccttcttc	1992		
QY 1293	gtgtgtccagagcagctgtctttgaaggacacacagagag---tggtacgggtttccatcac	1349		
Db 1993	aaactgcaccccgagatgccttgacagagacacagaaagagatcatgagggagagccacac	2052		
QY 1350	tgtctctcttgagtggtgtccctgttgagcttgagacctccctcaacaagaagagctctac	1409		
Db 2053	tgtctctttagatgtgtgagagtgcttcttagtgggagtgatgtagtagacacatgccagt	2112		
QY 1410	agatgcagaccccttgagacagaagaagtggtgacacctgaggaagcagacagctgtcccg	1469		
Db 2113	gccctgtaacagatgccacagatgacttctgtgctcatgaaacacacacccctctgcatggc	2172		
QY 1470	cgcagcttgagtgcttttttggtcttgccgttagcacacctcttggtgtcgtcagagctaac	1529		
Db 2173	aaggaatgcgaattctctctgagacagagacccctttggagatgcacatccctctttggcc	2232		
QY 1530	aagctgctgctgtcgtctgtctgttgagacagtcgtgccccttgcttgagacatagacac	1589		
Db 2233	gtgctggggcatttttctctacagacctttgtgctgggtgtgtttatgaagtccggacaaca	2292		
QY 1590	ccgtgtgtgaggtcagcagaggggcccgcctgtgtcttcttatgtcttgagctcccttgaca	1649		
Db 2293	cccatgttgcacagggcacacacagacagatctctctacccctcttccctgctctgc	2352		
QY 1650	ggtatgagagcctctataggtctctttggggagaccacaagaagcccggtgctgtgaagc	1709		
Db 2353	tgtcttctccagctccctgtcttcttcttcaacggggagcccccagagactgcagtgccgtgcc	2412		
QY 1710	cagggccctctcttccctgtgtttcacacatcttccctgctcgtcctacagttcgtcatatc	1769		
Db 2413	cagccggccttggcagatcagctctgtctctgcatatcagatctctgtgaaaacacac	2472		
QY 1770	caac	1829		
Db 2473	cgtgtccctctgt	2529		
QY 1830	caaac	1889		
Db 2530	gggctcaccctgacatctctgt	2589		
QY 1890	ctaacttgctgt	1949		
Db 2590	gtgactgtgctgt	2649		
QY 1950	ctgt	2009		
Db 2650	atcatcttcatcactgt	2709		
QY 2010	aatgtgcctctctctcatctagtgctcttgctgtcagctacacttggttaagactgtcagag	2069		
Db 2710	acctgtcgt	2769		
QY 2070	aactcagaagagcccaaatgt	2129		
Db 2770	aaattcaatgaagcccaaatgt	2829		
QY 2130	gacctctcacaacagcagcgtctcaagaagcaagtaacgtcctgcgggccaacatgtatg	2189		
Db 2830	tcttctcatctcagccttattgacacagacacatagcagagttgtgtctgtgcgttaaggtgat	2889		
QY 2190	gctgt	2249		
Db 2890	gccatctctgt	2949		

(NPSP-) NPS PHARM INC.
PI Balandrin MF, Delmar EG, Moe ST, Nemeth EF, Van Wageningen BC;
DR WPJ. 96-230520/23.
P-PSDS: W11688.
PI New di:arylalkyl amine cpds. useful for modulating inorganic ion
P-PSDS: W11688.
PT receptor activities - esp. for modulating effect of extracellular
PT calcium on cell surface calcium receptors, useful for treating e.g.
PT hyperparathyroidism, Paget's disease or osteoporosis
PS Example 1; Page 85-93; 231pp; English.
CC The sequences given in 161381-82 encode functional calcium receptors.
CC These sequences were isolated from human parathyroid gland adenoma
CC tumour using pBOPCRL as a hybridisation probe. mRNA was isolated from
CC a 39 year old caucasian male diagnosed with primary hyperparathyroidism
CC and two clones of approx. 5 and 4 kb were identified. These cDNA's were
CC injected into Xenopus oocytes which were assayed for the presence of
CC functional calcium receptors. Both clone types gave rise to functional
CC calcium receptors as assessed by the stimulation of calcium-activated
CC chloride currents upon addition of appropriate calcium receptor agonists
CC e.g. NPS R-667 and NPS R-568. Sequence analysis of the two cDNA clones
CC indicated the existence of at least two sequence variants differing in
CC the 3' untranslated region and which may result from alternative
CC polyadenylation. Sequence variation also exists in the 5' end of the
CC inserts. These sequence differences may have arisen due to alternative
CC transcription initiation and/or splicing. Three additional sites of
CC sequence variation occur within the coding regions of cDNA clones
CC pHPuCAR5.2 and pHPuCAR4.0 demonstrating that they encode distinct
CC proteins. Sequence analysis of the human Car gene indicates that the
CC additional 30 bp in clone pHPuCAR5.2 as compared to pHPuCAR4.0, results
CC from alternative mRNA splicing. This alternative splicing is predicted
CC to insert 10 additional amino acids into the Car protein encoded by
CC pHPuCAR5.2 between residues 536 and 537 of the protein encoded by
CC pHPuCAR4.0. In addition pHPuCAR4.0 encodes Gln at position 925 and Gly
CC at position 990, whereas pHPuCAR5.2 encodes Arg at both equivalent
CC positions. The human Car gene encodes for Gln and Arg respectively at
CC these positions. These two receptor isoforms may be functionally and/or
CC pharmacologically distinct.
SQ Sequence 5006 BP: 1228 A; 1376 C; 1220 G; 1182 T;

Query Match	5.7%	Score 132.6	DB 1.1	Length 5006
Best Local Similarity	50.4%	Pred. No. 11e-23		
Matches 414	Conservative	0	Mismatches 389	Indels 18
			Gaps	
QY	10	agctcaatgaacatgagctgacaccacctctctccaggcgtatgcyggttgaagata	69	
Db	619	AGGTAATATTTCGGGGGTTTGGCTTGATACAGGCATATATTTCCTACAGAGATA	678	
QY	70	aacaacatccacgycgcctgctgcccacaatcacccctggggatcacagctgatgtygt	129	
Db	679	AACACACAGCCCGCCCTTCTTCCCAACTTGACGCTGGGATACAGGATATTGGACATTGC	738	
QY	130	tctgactctgcgaagc---tgatgccaagctggagagtgctctccc-----tgcca	177	
Db	739	AACACCGTTTCTAAAGCCCTTGGAAGCCACCCCTGAGTTTGTGGCTCAAAAACAAATTGAT	798	
QY	178	gggcacacacacatagagctcccaagagagacctctccactatccctccatgctgcga	237	
Db	799	TCTTGAACCTTGATGAGATTCTGCAACTGCTCAGAGCAATTCCTCTACGATGCTG	858	
QY	238	gtgattggccttgacagcaccaacccgtgctgccaaccaagccgcctctgagcccttc	297	
Db	859	GTGGAGACAACCTGAGGCTCAGGCGCTCTCCACAGGAGATGGCAAAATCGCTGGGGCTCTTCTAC	918	
QY	298	ctgtagcatattagctatgcygcgcagcagcggaaogcttagagtgtaagcggagatccc	357	
Db	919	ATTCCCCAGGTAGTTATGCTCTCTCCACACAACCTCTTAGCAACAAGATACAAATTCAAG	978	
QY	358	tcttcctgcgcacacatccccaatgacaagtacagtgtagacacatgctgctgc	417	
Db	979	TCTTCTCTCCGCAACATCCCAATATATATGACACACAGGCCACATGCCATGACATATC	1038	
QY	418	cagaagcttcgggtgacactgcatctctctggttgccagcagtgacactatgagccta	477	

Db	1039	GAGATTTTCGGCTGGAACTGGGTGGGACAAATTGCAGCTGATGAGACTACTATGGGGGCGC	1098
Qy	478	gggggtgcaggacactgtggaacacgagccctgtgcacggggcatctgtcatcttcaagrac	537
Db	1099	GGGATTTGAGAAATTCGAGAGCGAGCAAGCTGAGGAAGGAGATATCTGCATGCATTCAGTGAA	1158
Qy	538	atcatgccccttctctgcccaagtgtgscgattgagagatgtcaatgtcctcatgscacactg	597
Db	1159	CTCATCTCCAGTACTCTGTATGGGAAGA-----GATCCACCATGTGTATGAGGTGATT	1212
Qy	598	gccccaggccgggacgcacgcgtgtgtgttttttcacgcggcagcttgscagagtgctt	657
Db	1213	CAAAATTCACAGGGCCAAAGTCATCGTGGTTTCTCCAGTGGGCCAGATCTTGAGGCCCTC	1272
Qy	658	ttcagatccgttggltgctgacccaactctgacttggcaaggtgtgtgtgcctcagaagcctgtg	717
Db	1273	ATCAAGAGAGATTGTCCGGGCCAATATCACGGGCAAGATCTGTGCTGGCCAGCGAGGCTCGG	1332
Qy	718	ggccttcctccaggacacatcatcttgggtgtgcccgagatccagcgcatctgggaatgtgtctggc	777
Db	1333	GCCAGCTCTCCCTGTAGTCGCATGCTCTCACTTCCACAGTGGTGGGGCCACCAATTGGA	1392
Qy	778	gtggccatccagaagaggggtcttcccttgsccttgaaggcgctt	818
Db	1393	TTCCGCTCTGAAGGCTGGCGAGATCCCAAGGCTTTCGGGAATT	1433

RESULT	9	
ID	T86166	
AC	T86166	standard; DNA; 4000 BP.
DT	02-DEC-1997	(first entry)
DE	Nucleotide sequence of pCAR/RI.	
KW	Chimeric receptor; extracellular domain; seven transmembrane domain;	
KW	intracellular cytoplasmic tail domain; metabotropic glutamate receptor;	
KW	MGR; calcium receptor; CR; mGluR; G protein-coupled receptor;	
KW	neurological disease; ss.	
OS	Chimeric - Homo sapiens.	
EH	Key	Location/Qualifiers
FT	cds	41..3700
FT		/*tag= a
FT		/product= pCAR/RI
PN	MO9705252-A2.	
PD	13-FEB-1997.	
PF	25-JUL-1996.	U12336.
PR	26-JUL-1995.	US-001526.
PA	(NPSF-) NPS PHARM INC.	
P1	Fuller FH, Hamnerland LG, Krapcho KJ;	
DR	WPI: 97-145690/13.	
P	P-PSDB: W25763.	
PT	Chimeric receptors comprising metabotropic glutamate receptor and	
PT	calcium receptor - used for screening for neurologically active	
PT	compounds	
PS	Example 3; Fig 3; 177bp; English.	
CC	This sequence encodes a chimeric receptor. The chimeric receptor	
CC	comprises an extracellular domain, a seven transmembrane domain, and	
CC	an intracellular cytoplasmic tail domain, and a sequence of at least	
CC	6 contiguous amino acids is homologous to a sequence of a metabotropic	
CC	glutamate receptor (MGR), and a sequence of at least 6 contiguous amino	
CC	acids is homologous to a sequence of a calcium receptor (CR). The	
CC	chimeric receptor may be used for screening for compounds that bind to	
CC	or modulate the activity of MGR or CR and for determining the site of	
CC	action of a CR active compound. The compounds can be used in the	
CC	treatment of neurological diseases and disorders. They can also be	
CC	used as diagnostic agents. Chimeric receptors such as this, allow the	
CC	coupling of certain functional aspects of an MGR with certain functional	
CC	aspects of a CR. They allow for more efficient high-throughput screening	
CC	of compounds.	
CC	Sequence 4000 BP; 955 A; 1128 C; 1010 G; 907 T;	

Query Match 5.7%; Score 132.6; DB 1; Length 4000;
Best Local Similarity 50.4%; Pred. NO. 1e-23;

Matches	414	Conservative	0	Mismatches	389	Indels	18	Gaps	3
QY	10	agcttcaatgacatgctgactaccactcttcacgactatgcccgttgaagaaata	69						
Db	224	AGGTTAATTTCCTCGGTGGTTTCGTGTACAGGCTATGATTTTGGCTTAGAGGAGATA	283						
QY	70	aacaactccagggccctctgctcccaataacaccctggggtaccagctgtatgtgtct	129						
Db	284	AACACACAGCCCAAGCCCTTCTTCCCAACTGAGCGTGGGATACAGGATATTGACACTTGC	343						
QY	130	tctgactctgccaatg----tgatgcacagctcgaagtgcctcc-----tgcca	177						
Db	344	AACACCGTTTCTTAAGGCGCTTGSAGACCAACCTCTGATTTTGTGTCTTAACAACAAATTGAT	403						
QY	178	gggcaaccaacacatagatcctccaagagaagactcttcacatctccctacggtgtctgga	237						
Db	404	TCTTGAACCTGTGATGAGTGTGCAACTGCTCAGAGACATTCCTCCCTGATGGTGTG	463						
QY	238	gtgatgtggccttgaagaaccacacccgtgtctgcacacacagccgcctctgtgaccttc	297						
Db	464	GTGGAGGACACTGGCTCAGGCGCTCTCCACAGGGAGTGGCAAAATCTGTGGGCTTCTTCTAC	523						
QY	298	ctggtgcataatagactatgcccagcagcagagagacgctacagcttgaagggcagatccc	353						
Db	524	ATTCCCCAGGTCAGTATTATGCTCTCTCCAGACAACTCTCTTAGCAACAGAAATTAATTCAAG	583						
QY	358	tcttctctgcgcacacatccccaatagacatgacagtgagtgaaacatagtgtctgtctg	417						
Db	584	TCTTCTCTCCGACCATCCCAATGATGAGCACAGGCCATGCGCATGGCAGCATCATC	643						
QY	418	cagaagcttcgggttgacctgtgatctctctgtgttgccagcagctgaagcactatggaagcta	477						
Db	644	GAGTATTTCGCTGGACGTGGGTGGGACAAATTCACGTGATGAGACATATGGCGGCGG	703						
QY	478	gggggtgcagcagcttggagaacacagggccctgtgcagggagatctgacttcttcaagagac	537						
Db	704	GGGATTGAGAAATTCGAGAGAGGAACTGAGGAAAGGAGATATCTGCACTTCACATTCACTGA	763						
QY	538	atcatgacctctctcgcagcaggtggcgaatgagagatcagctgcctcatgcccacactg	597						
Db	764	CTCATCTCCCACTACTCTGATGAGGAAGA-----GATCAGACATCTGTTAGAGTGATT	817						
QY	598	gcccaaggccggagccacacgctgctgtgttcttccacgcggcagcttggccaggggtgtt	657						
Db	818	CAAAATTCACAGCGCCAAAGTCAATCGTGTGTTCTCCAGTGGCCCAAGATCTTAGCCCCCTC	877						
QY	658	ttcagctccgtgtgtctgacacacactgactgtgccaaggtgtgtgtgcctcccaagcctgtg	717						
Db	878	ATCAAGGAGATTTGTCGGGGCAATATCACAGGGCAAGATTTGGCTGGCCAGCGCATCTGG	937						
QY	718	gccctctccagcagacatcacatcgtgggtgcccggagatcccaagcagatggatgtgtgtc	777						
Db	938	GCCACTCTCTCCCTGATCCCAATGCCATGCCCTAGTACTTCCACTGTGGTGGCGGACACATGGA	997						
QY	778	gtggccatccagaagaagggctgtcccttgagccttgaaggcgtt	818						
Db	998	TTCGCTCTGAAGGCTGGGCAGATCCACAGGCTTCGGGGAATT	1038						
RESULT 10									
TS	195858	standard: cdna to mRNA: 5006 BP.							
AC	T95858:								
DT	08-MAY-1998	(first entry)							
DE	Human parathyroid cell calcium receptor 5.2 (hnpCar 5.2)	cdna.							
KW	Human parathyroid cell calcium receptor 5.2; hnpCar 5.2;								
KW	calcium homeostasis; hyperparathyroidism; osteoporosis; ss.								
OS	Homo sapiens.								
FT	Key	Location/Qualifiers							
FT	CDS	436..3702							
FT		/*tag= a							
PN	US568938-A.	/product= parathyroid_cell-calcium_receptor_5.2							

PD 18-NOV-1997.
PF 07-JUN-1995; 485588.
PF 07-JUN-1995; US-485588.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-017127.
PR 23-FEB-1993; US-009389.
PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (BGHM) BRIGHAM & MOXENS HOSPITAL.
PA (NOSP-) NPS PHARM INC.
PI 3iCON EM, Fuller FH, Garrett JE, Hebert SC;
D3 WPI, 98-008040/01.
D3 P-5SD8; w38273.
PT DNA encoding calcium receptor polypeptide(s) - useful for
PT therapeutic purposes, e.g. hyperparathyroidism and osteoporosis
PS Claim 15; Columns 117-126; 174pp; English.
CC The present sequence encodes human parathyroid cell calcium
CC receptor 5.2 (HupCar 5.2).
CC The specification includes details of molecules that can modulate
CC one or more inorganic ion receptor activities, and antibodies and
CC antibody fragments targetted to inorganic ion receptor proteins. The
CC proteins, nucleic acids and antibodies may be used to treat
CC disorders by modulating one or more inorganic ion receptor
CC activities, preferably disorders of calcium homeostasis, e.g.
CC hyperparathyroidism and osteoporosis.
SQ Sequence 5006 BP; 1227 A; 1378 C; 1219 G; 1182 T;

[illegible]


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Db      1159  CTCATCTCCCACTACTCTGATGATGAGGAGA-----GATCAGAGATGTGGTATAGAGTGATT 1212
Oy      598  gccacgacggcgggcgccacgcgtcgctggtgttcttcttcacgcggcagttgcccaggtgtt 657
Db      1213  CAAATTTCCACGCCCAAAATCATCTGCTGTTTCTCCAGTGGGCCCAATCTTGAGCCCTTC 1272
Oy      658  ttccgactccgctgggtctgtgacacacctgactgtgcgaagtgttggtccctccagaagcttg 717
Db      1273  ATCAAGGAGATTGTCTCCCGCCCAATATACGGGCGCAAAATCTGGCTGGCCAGCGAGGCTCG 1332
Oy      718  gccctctccagcgacatcacctctgggtggtccggagatccagcgcattgagatggtcctgggc 777
Db      1333  GCCAGCTCTCTCCTGATGCCCATGCTTCAGTACTTCCAGCTGGTTTGCGGCAACATTGGA 1392
Oy      778  gtggccatccagaagaaggctgtctcctgtgacctgaagcgtt 818
Db      1393  TTCGCTCTGAAAGCTGGGCGAGATCCGAGGCTTCCGGGAATT 1433

RESULT  11
ID      V26963
AC      V26963 standard; cDNA to mRNA; 5006 BP.
DT      01-SEP-1998 (first entry)
DE      Human parathyroid calcium receptor 5.2 gene 5Kb fragment.
KW      ss; calcium ion concentration; parathyroid hormone; homeostasis;
OS      Homo sapiens.
FH      Key
FT      CDS
          Location/Qualifiers
          436..3702
          /*tag= a
          /product= "pHUPCAR 5.2 5kb fragment"

FN      US5763369-A.
PD      09-JUN-1998.
PF      07-JUN-1995; 484565.
PR      07-JUN-1995; US-7484565.
PR      23-AUG-1991; US-749451.
PR      11-FEB-1992; US-834044.
PR      21-AUG-1992; US-834161.
PR      12-FEB-1993; US-017127.
PR      23-FEB-1993; US-009389.
PR      22-OCT-1993; US-141248.
PR      19-AUG-1994; US-292827.
PR      21-OCT-1994; WO-012117.
PR      08-DEC-1994; US-353784.
PA      (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA      (NPSF ) NPS PHARM INC.
PI      Brown EM, Garrett JE, Hebert SC;
WI      98-347412/30.
DR      P-PSDB; WS4845.
DR      P-PSDB; WS4845.
FT      Cdc10m receptor poly:peptide(s) - useful for drug screening or
FT      antibody production
PS      Example 27; Fig 48; 174pp; English.
CC      The Human parathyroid calcium receptor gene encodes a 1088 amino acid
CC      protein. The tissue from which this receptor and receptors from bovine
CC      parathyroid and rat kidney are derived, respond to changes, and control
CC      changes, in calcium ion concentration, e.g. parathyroid hormone regulates
CC      Ca2+ homeostasis in blood and extracellular fluid, and kidney function
CC      alters through changes in Ca2+ levels in juxtaglomerular and proximal
CC      tubule cells in the kidney. The purified receptors (produced
CC      recombinantly) can be used to screen for compounds that modulate calcium
CC      receptor activity, especially those that can be used to treat diseases
CC      associated with the receptors in these tissues. They can also be used
CC      to raise antibodies for use in detection assays.
CC      Sequence 5006 BP; 1228 A; 1376 C; 1220 G; 1182 T;

Query Match 5.7%; Score 132.6; DB 1; Length 5006;
Best Local Similarity 50.4%; Pred. No. 1,1e-23;
Matches 414; Conservative 0; Mismatches 389; Indels 18; Gaps 3

10 agctcaatgagcatggtaccacacctcttcacaggtcgtacgtcggttggtgagagata 69

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Db	619	AGGATATATTTCCTGGGTTTCCTGGTTACAGGCGATATATTTCCTAGACAGATA	678		
Qy	70	aacaactcaacgagccctgctgcccacaatcacccctgggtacaaagctglatgattggt	129		
Db	679	AACAGCAGCCAGCCGCTCTTCCCACTTGACGCTGGATACAGGATATTGGACACTGC	738		
Qy	130	ctgagccctgcaaatg---tgatgagcagagctggagatgctctcc-----tgcga	177		
Db	739	AACACCGTTTCTAAGGCGCTTGGAAGCGACCCCTGAGTTTGTGTGCTAAACAAATTCAT	798		
Qy	178	gggacaacacacatagagctccacaagaagaccccttcacactctccctcctacggtgtgca	237		
Db	799	TCTTTGAACCTTGATGAGTCTTCGCACTGCTCAGACAGCAATTCCTCTACAGATTCTGTG	858		
Qy	238	gtgatgtggccttgacagacacaaacgltgtgcacacaagccgcgcctctgaagcccttc	297		
Db	859	GTGGAGAGCACTGGCTCAGGCGTCTCCACAGCGCAGTGGCAATCTCTGGGCGCTTCTAC	918		
Qy	298	ctgtgatatattgactatgctggtggccacagcagagagcagctgaggtgtagaagcgagatccc	357		
Db	919	ATTCGCCAGGCTGAGTTATGCTCTCTCCACAGACTCTCTGACACAAATCAATCAATTCAG	978		
Qy	358	tccttcctgcgcacatccccaatgacaagtacacaggtgtagaacatgctgtctgtgtg	417		
Db	979	TCTTTCTCTCGAAGCACTCCCAATATGATGAGCAGCGCACAGCATGGCAGACATCATC	1038		
Qy	418	cagaagctcggtgtgagacctggtatctctctgtgtgtgcagcagtgacgactatgtagcagcta	477		
Db	1039	GAGTATTTCCGCTGGAACCTGGTGGGCGCAATTCGACGTGATGACGACTATGGGGCGCG	1098		
Qy	478	gggtgtcagagcactcgtgagaaacccagcccgctgcagggcgatctgattgcttcaagagac	537		
Db	1099	GGGATTAGAAGATTCGACAGGAGAGCTGAGGAAGGAGATATCTGATCTGACTTCAGTAA	1158		
Qy	538	atcatgcccctctctgcgcccaggtggtgcagatgtagagagtgcagtgctcatgcyccacctg	597		
Db	1159	CTCATCTCCAGTACTCTGATGAGGAAGA-----GATCCACATCTGTGTAGAGTGAATT	1212		
Qy	598	gcccagagccggggccacacgctcgtgtgtgttttcttcacgcccggcagltgycagaagtgctt	657		
Db	1213	CAAAATTCACAGCGCCAAAGCATGCTGATGTTTCTCCAGTGGCCCGACGATCTTGAGCCCTTC	1272		
Qy	658	ttcgaagctcgtgtgtctgacacaacccgactgtagaagatgtgtgtctcctcagaagccctgg	717		
Db	1273	ATCAGAAGGAGATTGTCCGCGCCCAATATCACGGCCAAAGATCTGGCTGGCCAGCGAGCCCTGG	1332		
Qy	718	gcccctccacagcacaatcactatggtgggtgcccggagatccacagcagatgtggtgtgtggtc	777		
Db	1333	GCCAGCTCTCTCCGATCGATCGCATGCTCTAGTACTTCCAGTGTGTTGGCGGCACCATTTGGA	1392		
Qy	778	gtggccatcacaagaagaggtctgcccctgagccctgaaagcgctt	818		
Db	1393	TTCGCTCTGAAGGCTGGCGAGATCCCGAGGCTTCGCGGAATT	1433		
RESULT 12					
ID	V82484	standard; cDNA to mRNA; 5006 BP.			
AC	V82484				
DT	19-MAR-1999	(first entry)			
DE	Human parathyroid calcium receptor pHPuPar 5.2 encoding cDNA.				
KW	Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;				
KW	calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;				
KW	spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;				
KW	neonatal distress; neurodegenerative disease; Alzheimer's disease;				
KW	Huntington's disease; Parkinson's disease; dementia; muscle tension;				
OS	Homo sapiens.				
FM	Key	Location/Qualifiers			
FT	CDS	436..3702			
FT	/*tag= a				
FN	US5858684-A				

PD 12-JAN-1999.
 PF 07-JUN-1995: 480751.
 PR 07-JUN-1995: US-480751.
 PR 23-AUG-1991: US-749451.
 PR 11-FEB-1992: US-834044.
 PR 21-AUG-1992: US-934161.
 PR 12-FEB-1993: US-017127.
 PR 23-FEB-1993: US-009389.
 PR 22-OCT-1993: US-141248.
 PR 19-AUG-1994: US-292827.
 PR 21-OCT-1994: WO-012117.
 PR 08-DEC-1994: US-353784.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PA (NPSF-) NPS PHARM INC.
 PI Balandrin MF, Brown EM, Del Mar EG, Garrett JE,
 PI Hebert SC, Nemeth EF, Van Wagenen BC;
 DI WPI: 99-119871/10.
 DR P-PSDB; W89564.
 PT Screening for calcium receptor-active compounds - by recombinant
 PT expression of nucleic acid encoding calcium receptor and determining
 PT the effect of compounds on calcium receptor activity
 PS Claim 1: Fig 48: 176p; English.
 CC A method has been developed of screening for a compound able to affect
 CC one or more activities of a calcium receptor (CR) comprises: (A)
 CC contacting a recombinant cell with a test compound, where the
 CC recombinant cell comprises a recombinant nucleic acid expressing the CR,
 CC provided that the cell does not have functional CR expression from
 CC endogenous nucleic acid; (B) determining the ability of the test
 CC compound to affect one or more activities of the calcium receptor; and
 CC (C) comparing the ability with the ability of the test compound to
 CC affect the one or more CR activities in a cell not comprising the
 CC recombinant nucleic acid. The present sequence encodes human
 CC parathyroid CR, designated a phurCAR 5.2. The nucleic acid sequence of
 CC phurCAR 5.2 can be used as part of the recombinant nucleic acid in the
 CC method described above. The compounds identified can be used to treat
 CC diseases or disorders characterised by abnormal calcium homeostasis, e.g.
 CC hyperparathyroidism, osteoporosis and other bone and mineral-related
 CC disorders. They can also be used for the treatment of diseases and
 CC disorders associated with disrupted Ca²⁺ responses, e.g. seizures,
 CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in
 CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative
 CC diseases such as Alzheimer's disease, Huntington's disease and
 CC Parkinson's disease, dementia, muscle tension, depression, and anxiety.
 SQ Sequence 5006 BP: 1228 A: 1376 C: 1220 G: 1182 T:

Query Match 5.7%; Score 132.6; DB 1; Length 5006;
 Best Local Similarity 50.4%; Pred. No. 1, ie-23;
 Matches 414; Conservative 0; Mismatches 389; Indels 18; Gaps 3;

QY 10 agcttcaatgaagcatggtcaccacttccaggtatgaggttgaggaata 69
 Db 619 AGGATATATTTCGTGGGTTTCGTGTACAGGCTATGATATTTCGCAAGAGGAATA 678
 QY 70 aacaactccagggccgtgcgtcccaacatcaacctgtggtggtgagtgatgtgt 129
 Db 679 AACGACAGCCCAAGCCTTCTTCCCACTTGACGCTGGGATACAGATATTGACACTTGC 738
 QY 130 tctgactcgtccaatg--tgatgcaagcgtgagagtgctctccc-----tgcca 177
 Db 739 AACACGCTTCTTCTGAAGCCTTGGAAGCCACCTGAGTTTGTGTCTCAAAACAAATGAT 798
 QY 178 gggcaaacacacataagagctcccaagagagacttccacattcccttaagtgctgca 237
 Db 799 TCTTGAACCTTGATGAGTTCTGCAACTGCTCAGAGACACATTCCTCTACGATTGCTGTG 858
 QY 238 gtgaattggcgtgacacacacacacgcgtgcgtcccaagcgcgtgcgtgagcccttc 297
 Db 859 GTGGAGCACTGGCTAGAGGCTGTCCACGGCACTGGCAATATGCTGGGGCTTTCTTAC 918
 QY 298 ctggtgcatattagcatatgagcagcagcagcagcagcagcgtgaaagcagcagtatccc 357
 Db 919 ATTCCCAAGTCAAGTATGCTCTCTCCAGACACTCTCTCAGCAACAAGAAATCAATTCAG 978

QY 358 tcttctctgcacacccatccccaatgacaagttagagacatgtgctgctgctg 417
 Db 979 TCTTCTCTCCGAACCATCCCAATGATGACACAGCCACTCCGACAGACATATATC 1038
 QY 418 cagaagttcgggtgagacttgatccctctgtgttgccagcagtgacgactatggcagcta 477
 Db 1039 GAGTATTCTCGCTGGAACTGGGTGGGACAAATTGCAGCTATATGACGACTTGGGGCGCG 1098
 QY 478 ggggtgcagcgacatggaagaccagccctggtcaggggcactctgcatctgttccaaggc 537
 Db 1099 GGGATTGAGAAATTCGACAGAGAACTGAGAGAAAGGGAATATCTGCACTTCAGTGAA 1158
 QY 538 atatgacctctctgcccagggggcgatgagaagatgtagtgccctcaagccacctg 597
 Db 1159 CTATCTCCAGTACTTGTATGAGGAAGA-----GATCCAGCATGTGGTAGAGTGATTT 1212
 QY 598 gcccaaggccggcccaacccgtgcgtgtgtttttccagcccgagttgscagggtgtt 657
 Db 1213 CAAATTCACAGGCGCAAGATCATGCTGTCTTCTCCAGTGGCCACATCTTAGCCCTC 1272
 QY 658 ttcgagtcgtggtgctgacaaacctgactgcgaaggtgtggtgcgtcagaagcctg 717
 Db 1273 ATCAAGGAGATGTTCGGGCGCAATATCACCGCAAGATCTGCTGGCGACGAGGCGCTGG 1332
 QY 718 gcccttccagcgacatcactggtgggtgcccggatctccagcttggatgtg-gctgggc 777
 Db 1333 GCCAGCTCTCCCTGATGCGCATGCTCCTACTTCCACGTGGTGTGGCGCACCATTTGA 1392
 QY 778 gtggcattccagaagagggctgtccctggcctgaagcgct 818
 Db 1393 TTGCGCTTGAAAGCTGGGCAAGTCCAGGCTTCCGGGAATT 1433

RESULT 13
 ID T89290 standard: cDNA; 4131 BP.
 AC T89290:
 DT 27-MAR-1998 (first entry)
 DE Dogfish shark kidney calcium receptor related protein cDNA.
 KW Calcium receptor related protein; Car-RP; dogfish shark; SKCar-RP;
 KM Polyclonal-sensing receptor; aquaculture; fish farming;
 OS Salinity tolerance; ss.
 OS Squalus acanthias.
 FH Key Location/Qualifiers
 FT CDS 439..3519
 FT /tag- a
 FT /tag- b
 FT polyA_site 4076..4113
 FT W09735977-A1.
 PN 02-OCT-1997.
 PF 27-MAR-1997: U05031.
 PR 27-MAR-1996: US-622738.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PI Brown E, Harris HW, Hebert S;
 DI WPI: 97-489640/45.
 DR P-PSDB; W32059.
 PT New isolated Aquatic polyvalent cation-sensing receptor - used to
 PT develop products for increasing or decreasing the salinity tolerance
 PT of fish for use in aquaculture
 PS Claim 2: Fig 4A-F: 57p; English.
 CC This cDNA clone codes for dogfish shark kidney calcium receptor
 CC related protein (SKCar-RP, see W32059), an aquatic polyvalent
 CC cation-sensing receptor (PVCr). It was isolated from a shark
 CC kidney cDNA library using a rat kidney calcium receptor cDNA as
 CC probe. Also claimed are: a probe comprising the 4131 bp SKCar-RP
 CC sequence; an isolated PVCr present in the plasma membrane of
 CC aquatic species, especially on the apical membrane of epithelial
 CC cells of elasmobranch fish, particularly from cells found in the
 CC collecting duct or late distal tubule in the kidney; intestine,
 CC gill, rectal gland, gonad or brain; an antibody that specifically
 CC binds to a PVCr; and a method of screening for aquatic PVCr
 CC agonists and antagonists. Modulation of the expression of the

